

METHOD FOR THE DETECTION OF GENE TRANSCRIPTS IN BLOOD AND USES THEREOF

RELATED APPLICATION(S)

This application is a continuation-in-part of Application No. 10/268,730 filed on
5 October 9, 2002, which is a continuation of U.S. Application No. 09/477,148 filed January 4,
2000, now abandoned, which claims the benefit of U.S. Provisional Application No.
60/115,125 filed on January 6, 1999.

TABLES

This application includes a compact disc in duplicate (2 compact discs: Tables copy 1
10 and Tables copy 2), which are hereby incorporated by reference in their entirety. Each
compact disc contains the following files (corresponding to Tables 2 – 4) :

| FILES NAMES | SIZE | DATE OF CREATION |
|--|-----------|---------------------|
| TABLE 2 | 1,991,680 | 6/11/2003 |
| 15 TABLE 3A (GeneListFigure8.hyperten) | 223,744 | 6/18/2003 |
| TABLE 3B (GeneListFigure9.obesity) | 240,640 | 6/18/2003 |
| TABLE 3C (GeneListFigure10.allergies) | 165,376 | 6/18/2003 |
| TABLE 3D (GeneListFigure11.syst.ster) | 161,792 | 6/18/2003 |
| TABLE 3E (GeneListFigure12.hyper) | 483,328 | 6/18/2003 |
| 20 TABLE 3F (GeneListFigure13.obesity) | 291,328 | 6/18/2003 |
| TABLE 3G (GeneListFigure14.diabetes) | 238,080 | 6/18/2003 |
| TABLE 3H (GeneListFigure15.hyperlipidemia) | 267,264 | 6/18/2003 |
| TABLE 3I (GeneListFigure16.lung) | 160,768 | 6/18/2003 |
| TABLE 3J (GeneListFigure17.bladder) | 1,511,424 | 6/18/2003 |
| 25 TABLE 3K (GeneListFigure18.bladder) | 1,262,592 | 6/18/2003 |

| | | | |
|---|--|---------|-----------|
| | TABLE 3L (GeneListFigure19.cad) | 348,160 | 6/18/2003 |
| | TABLE 3M (GeneListFigure20).ra | 513,024 | 6/18/2003 |
| | TABLE 3N (GeneListFigure21.depression) | 248,320 | 6/18/2003 |
| | Table 3O (GeneListFigure22).ra | 95,232 | 6/18/2003 |
| 5 | Table 4 | 276,480 | 6/19/2003 |

SEQUENCE LISTING

The application includes a sequence listing submitted on compact disc in triplicate (3 compact discs: SEQ LIST COPY 1, SEQ LIST COPY 2 and SEQ LIST COPY 3 (Computer readable form), the contents of which are hereby incorporated by reference in its entirety.

10 Each compact disc contains the following file:

| FILE NAME | SIZE | DATE OF CREATION |
|-----------------------------|---------|------------------|
| Sequence listing (CDS 1516) | 117,888 | 6/16/2003 |

BACKGROUND

The blood is a vital part of the human circulatory system for the human body.

15 Numerous cell types make up the blood tissue including monocytes, leukocytes, lymphocytes and erythrocytes. Although many blood cell types have been described, there are likely many as yet undiscovered cell types in the human blood. Some of these undiscovered cells may exist transiently, such as those derived from tissues and organs that are constantly interacting with the circulating blood in health and disease. Thus, the blood

20 can provide an immediate picture of what is happening in the human body at any given time.

The turnover of cells in the hematopoietic system is enormous. It was reported that over one trillion cells, including 200 billion erythrocytes and 70 billion neutrophilic leukocytes, turn over each day in the human body (Ogawa 1993). As a consequence of

25 continuous interactions between the blood and the body, genetic changes that occur within the cells or tissues of the body will trigger specific changes in gene expression within blood. It is the goal of the present invention that these genetic alterations be harnessed for

diagnostic and prognostic purposes, which may lead to the development of therapeutics for ameliorating disease.

For example, isoformic myosin heavy chain genes are known to be generally expressed in cardiac muscle tissue. In the rodent, the (MyHC gene is only highly expressed in the fetus and in diseased states such as overt cardiac hypertrophy, heart failure and diabetes; the (MyHC gene is highly expressed shortly after birth and continues to be expressed in the adult heart. In the human, however, (MyHC is highly expressed in the ventricles from the fetal stage through adulthood. This highly expressed (MyHC, which harbours several mutations, has been demonstrated to be involved in familial hypertrophic cardiomyopathy (Geisterfer-Lowrance *et al.* 1990). It was reported that mutations of (MyHC can be detected by PCR using blood lymphocyte DNA (Ferrie *et al.*, 1992). Most recently, it was also demonstrated that mutations of the myosin-binding protein C in familial hypertrophic cardiomyopathy can be detected in the DNA extracted from lymphocytes (Niimura *et al.*, 1998).

Similarly, APP and APC, which are known to be tissue specific and predominantly expressed in the brain and intestinal tract, are also detectable in the transcripts of blood. These cell- or tissue-specific transcripts are not detectable by Northern blot analysis. However, the low number of transcript copies can be detected by RT-PCR analysis. These findings strongly demonstrate that genes preferentially expressed in specific tissues can be detected by a highly sensitive RT-PCR assay. In recent years, evidence has been obtained to indicate that expression of cell or tissue-restricted genes can be detected in the certain peripheral nucleated blood cells of patients with metastatic transitional cell carcinoma (Yuasa *et al.* 1998) and patients with prostate cancer (Gala *et al.* 1998).

In the prior art, there is a need for large samples and/or costly and time-consuming separation of cell types within the blood (Kimoto (1998) and Chelly *et al.* (1989; 1988)). The prior art, however, is deficient in non-invasive methods of screening for tissue-specific diseases. The present invention fulfills this long-standing need and desire in the art.

SUMMARY OF THE INVENTION

The present invention relates generally to the molecular biology of human diseases. More specifically, the present invention relates to a process using the genetic information contained in human peripheral whole blood for the diagnosis, prognosis and monitoring of
5 genetic and infectious disease in the human body.

This present invention discloses a process of using the genetic information contained in human peripheral whole blood in the diagnosis, prognosis and monitoring of genetic and infectious disease in the human body. The process described herein requires a simple blood sample and is, therefore, non-invasive compared to conventional practices used to detect
10 tissue specific disease, such as biopsies.

The invention is based on the discovery that gene expression in the blood is reflective of body state and, as such, the resultant disruption of homeostasis under conditions of disease can be detected through analysis of transcripts differentially expressed in the blood alone. Thus, the identification of several key transcripts or genetic markers in
15 blood will provide information about the genetic state of the cells, tissues, organ systems of the human body in health and disease

The present invention demonstrates that a simple drop of blood may be used to determine the quantitative expression of various mRNAs that reflect the health/disease state of the subject through the use of RT-PCR analysis. This entire process takes about three
20 hours or less. The single drop of blood may also be used for multiple RT-PCR analyses. It is believed that the present finding can potentially revolutionize the way that diseases are detected, diagnosed and monitored because it provides a non-invasive, simple, highly sensitive and quick screening for tissue-specific transcripts. The transcripts detected in whole blood have potential as prognostic or diagnostic markers of disease, as they reflect
25 disturbances in homeostasis in the human body. Delineation of the sequences and/or quantitation of the expression levels of these marker genes by RT-PCR will allow for an immediate and accurate diagnostic/prognostic test for disease or to assess the efficacy and monitor a particular therapeutic.

One object of the present invention is to provide a non-invasive method for the diagnosis, prognosis and monitoring of genetic and infectious disease in humans and animals.

In one embodiment of the present invention, there is provided a method for detecting
5 expression of a gene in blood from a subject, comprising the steps of: a) quantifying RNA from a subject blood sample; and b) detecting expression of the gene in the quantified RNA, wherein the expression of the gene in quantified RNA indicates the expression of the gene in the subject blood. An example of the quantifying method is by mass spectrometry.

In another embodiment of the present invention, there is provided a method for
10 detecting expression of one or more genes in blood from a subject, comprising the steps of: a) obtaining a subject blood sample; b) extracting RNA from the blood sample; c) amplifying the RNA; d) generating expressed sequence tags (ESTs) from the amplified RNA product; and e) detecting expression of the genes in the ESTs, wherein the expression of the genes in the ESTs indicates the expression of the genes in the subject blood.
15 Preferably, the subject is a fetus, an embryo, a child, an adult or a non-human animal. The genes are non-cancer-associated and tissue-specific genes. Still preferably, the amplification is performed by RT-PCR using random sequence primers or gene-specific primers.

In still another embodiment of the present invention, there is provided a method for
20 detecting expression of one or more genes in blood from a subject, comprising the steps of: a) obtaining a subject blood sample; b) extracting DNA fragments from the blood sample; c) amplifying the DNA fragments; and d) detecting expression of the genes in the amplified DNA product, wherein the expression of the genes in the amplified DNA product indicates the expression of the genes in the subject blood.

25 In yet another embodiment of the present invention, there is provided a method for monitoring a course of a therapeutic treatment in an individual, comprising the steps of: a) obtaining a blood sample from the individual; b) extracting RNA from the blood sample; c) amplifying the RNA; d) generating expressed sequence tags (ESTs) from the amplified RNA product; e) detecting expression of genes in the ESTs, wherein the expression of the

genes is associated with the effect of the therapeutic treatment; and f) repeating steps a)-e), wherein the course of the therapeutic treatment is monitored by detecting the change of expression of the genes in the ESTs. Such a method may also be used for monitoring the onset of overt symptoms of a disease, wherein the expression of the genes is associated with the onset of the symptoms. Preferably, the amplification is performed by RT-PCR, and the change of the expression of the genes in the ESTs is monitored by sequencing the ESTs and comparing the resulting sequences at various time points; or by performing single nucleotide polymorphism analysis and detecting the variation of a single nucleotide in the ESTs at various time points.

10 In still yet another embodiment of the present invention, there is provided a method for diagnosing a disease in a test subject, comprising the steps of: a) generating a cDNA library for the disease from a whole blood sample from a normal subject; b) generating expressed sequence tag (EST) profile from the normal subject cDNA library; c) generating a cDNA library for the disease from a whole blood sample from a test subject; d) generating
15 EST profile from the test subject cDNA library; and e) comparing the test subject EST profile to the normal subject EST profile, wherein if the test subject EST profile differs from the normal subject EST profile, the test subject might be diagnosed with the disease.

In still yet another embodiment of the present invention, there is provided a kit for diagnosing, prognosing or predicting a disease, comprising: a) gene-specific primers;
20 wherein the primers are designed in such a way that their sequences contain the opposing ends of two adjacent exons for the specific gene with the intron sequence excluded; and b) a carrier, wherein the carrier immobilizes the primer(s). Preferably, the gene-specific primers are selected from the group consisting of insulin-specific primers, atrial natriuretic factor-specific primers, zinc finger protein gene-specific primers, beta-myosin heavy chain gene-specific primers, amyloid precursor protein gene-specific primers, and adenomatous
25 polyposis-coli protein gene-specific primers. Further preferably, the gene-specific primers are selected from the group consisting of SEQ ID Nos. 1 and 2; and SEQ ID Nos. 5 and 6. Such a kit may be applied to a test subject whole blood sample to diagnose, prognose or predict a disease by detecting the quantitative expression levels of specific genes associated
30 with the disease in the test subject and then comparing to the levels of same genes expressed

in a normal subject. Such a kit may also be used for monitoring a course of therapeutic treatment or monitoring the onset of overt symptoms of a disease.

In yet another embodiment of the present invention, there is provided a kit for diagnosing, prognosing or predicting a disease, comprising: a) probes derived from a whole blood sample for a specific disease; and b) a carrier, wherein the carrier immobilizes the probes. Such a kit may be applied to a test subject whole blood sample to diagnose, prognose or predict a disease by detecting the quantitative expression levels of specific genes associated with the disease in the test subject and then comparing to the levels of same genes expressed in a normal subject. Such a kit may also be used for monitoring a course of therapeutic treatment or monitoring the onset of overt symptoms of a disease.

Furthermore, the present invention provides a cDNA library specific for a disease, wherein the cDNA library is generated from whole blood samples.

Other and further aspects, features, and advantages of the present invention will be apparent from the following description of the presently preferred embodiments of the invention. These embodiments are given for the purpose of disclosure.

BRIEF DESCRIPTION OF THE DRAWINGS

The above-recited features, advantages and objects of the invention, as well as others which will become clear, are attained and can be understood in detail, more particular descriptions of the invention briefly summarized above may be had by reference to certain embodiments thereof which are illustrated in the appended drawings. These drawings form a part of the specification. It is to be noted, however, that the appended drawings illustrate preferred embodiments of the invention and therefore are not to be considered limiting in their scope not be considered to limit the scope of the invention.

Figure 1 shows the following RNA samples prepared from human blood; Figure 1A: Lane 1, Molecular weight marker; Lane 2, RT-PCR on APP gene; Lane 3, PCR on APP gene; Lane 4, RT-PCR on APC gene; Lane 5, PCR on APC gene; Figure 1B: Lanes 1 and 2, RT-PCR and PCR of (MyHC, respectively; Lanes 3 and 4, RT-PCR of (MyHC from RNA prepared from human fetal and human adult heart, respectively; Lane 5, Molecular weight marker.

Figure 2 shows quantitative RT-PCR analysis performed on RNA samples extracted from a drop of blood. Forward primer (5'-GCCCTCTGGGGACCTGAC-3', SEQ ID No. 1) of exon 1 and reverse primer (5'-CCCACCTGCAGGTCCTCT-3'', SEQ ID No. 2) of exons 1 and 2 of insulin gene. Blood samples of 4 normal subjects were assayed. Lanes 1, 3, 5 and 7 represent overnight "fasting" blood sample and lanes 2, 4, 6 and 8 represent "non-fasting" samples.

Figure 3 shows quantitative RT-PCR analysis performed on RNA samples extracted from a drop of blood. Lanes 1 and 2 represent normal healthy person and lane 3 represents late-onset diabetes (Type II) and lane 4 represents asymptomatic diabetes.

Figure 4 shows multiple RT-PCR assay in a drop of blood. Primers were derived from insulin gene (INS), zinc-finger protein gene (ZFP) and house-keeping gene (GADH). Lane 1 represents normal person. Lane 2 represents late-onset diabetes and lane 3 represents asymptomatic diabetes.

Figure 5 shows standardized levels of insulin gene (Figure 5A) and ZFP gene (Figure 5B) expressed in a drop of blood. The first three subjects were normal, second two subjects showed normal glucose tolerance, and the last subject had late onset diabetes type II. Figure 5C shows standardized levels of insulin gene expressed in each fractionated cell from whole blood.

Figure 6 shows the differential screening of human blood cell cDNA library with different cDNA probes of heart and brain tissue. Figure 6A shows blood cell cDNA probes vs. adult heart cDNA probes. Figure 6B shows blood cell cDNA probes vs. human brain cDNA probes.

Figure 7 graphically shows the 1,800 unique genes in human blood and in the human fetal heart grouped into seven cellular functions.

Figure 8 shows a diagrammatic representation of gene expression profiles of blood samples from individuals having both osteoarthritis and hypertension as compared with gene expression profiles from normal individuals.

Figure 9 shows a diagrammatic representation of gene expression profiles of blood samples from individuals who were identified as having both osteoarthritis and who were obese as described herein as compared with gene expression profiles from normal individuals

5 Figure 10 shows a diagrammatic representation of gene expression profiles of blood samples from individuals who were identified as having both osteoarthritis and allergies as described herein as compared with gene expression profiles from normal individuals.

Figure 11 shows a diagrammatic representation of gene expression profiles of blood samples from individuals having osteoarthritis and who were subject to systemic steroids as described herein as compared with gene expression profiles from normal individuals.

10 Figure 12 shows a diagrammatic representation of gene expression profiles of blood samples from individuals having hypertension as compared with gene expression profiles from samples of both non-hypertensive and normal individuals.

Figure 13 shows a diagrammatic representation of gene expression profiles of blood samples from individuals who were identified as obese as described herein as compared
15 with gene expression profiles from normal and non-obese individuals

Figure 14 shows a diagrammatic representation of gene expression profiles of blood samples from individuals who were identified as having type 2 diabetes as described herein as compared with gene expression profiles from normal and non-type 2 diabetes individuals.

Figure 15 shows a diagrammatic representation of gene expression profiles of blood
20 samples from individuals who were identified as having hyperlipidemia as described herein as compared with gene expression profiles from normal and non-hyperlipidemia patients.

Figure 16 shows a diagrammatic representation of gene expression profiles of blood samples from individuals who were identified as having lung disease as described herein as compared with gene expression profiles from normal and non lung disease individuals.

25 Figure 17 shows a diagrammatic representation of gene expression profiles of blood samples from individuals who were identified as having bladder cancer as described herein as compared with gene expression profiles from non bladder cancer individuals.

Figure 18 shows a diagrammatic representation of gene expression profiles of blood samples from individuals who were identified as having advanced stage bladder cancer or early stage bladder cancer as described herein as compared with gene expression profiles from non bladder cancer individuals

- 5 Figure 19 shows a diagrammatic representation of gene expression profiles of blood samples from individuals who were identified as having coronary artery disease (CAD) as described herein as compared with gene expression profiles from non-coronary artery disease individuals

- 10 Figure 20 shows a diagrammatic representation of gene expression profiles of blood samples from individuals who were identified as having rheumatoid arthritis as described herein as compared with gene expression profiles from non-rheumatoid arthritis individuals.

Figure 21 shows a diagrammatic representation of gene expression profiles of blood samples from individuals who were identified as having depression as described herein as compared with gene expression profiles from non-depression individuals.

- 15 Figure 22 shows a diagrammatic representation of gene expression profiles of blood samples from individuals who were identified as having various stages of osteoarthritis as described herein as compared with gene expression profiles from normal individuals.

Figure 23 shows RT-PCR of overexpressed genes in CAD peripheral blood cells identified using microarray experiments, including PBP, PF4 and F13A.

- 20 Figure 24 shows the the "Blood Chip", a cDNA microarray slide with 10,368 PCR products derived from peripheral blood cell cDNA libraries. Colors represent hybridization to probes labeled mth Cy3 (green) or Cy5 (red) . Yellow spots indicate common hybri dization between both probes. In slide A, normal bl ood cell RNA samples were labeled with Cy3 and CAD blood cell RNA samples were labeled with Cy5. In slide B, Cy3 and Cy5 were switched to
25 label the RNA samples. (Cluster analysis revealed distinct gene expression profiles for normal and CAD samples.)

DETAILED DESCRIPTION

In accordance with the present invention, there may be employed conventional molecular biology, microbiology, and recombinant DNA techniques within the skill of the art. Such techniques are explained fully in the literature. See, e.g., Sambrook, Fritsch & Maniatis, "Molecular Cloning: A Laboratory Manual (1982); "DNA Cloning: A Practical Approach," Volumes I and II (D.N. Glover ed. 1985); "Oligonucleotide Synthesis" (M.J. Gait ed. 1984); "Nucleic Acid Hybridization" [B.D. Hames & S.J. Higgins eds. (1985)]; "Transcription and Translation" [B.D. Hames & S.J. Higgins eds. (1984)]; "Animal Cell Culture" [R.I. Freshney, ed. (1986)]; "Immobilized Cells And Enzymes" [IRL Press, (1986)]; B. Perbal, "A Practical Guide To Molecular Cloning" (1984). Therefore, if appearing herein, the following terms shall have the definitions set out below.

A "cDNA" is defined as copy-DNA or complementary-DNA, and is a product of a reverse transcription reaction from an mRNA transcript. "RT-PCR" refers to reverse transcription polymerase chain reaction and results in production of cDNAs that are complementary to the mRNA template(s).

In addition to RT-PCR, other methods of amplifying may also be used for the purpose of measuring/quantitating tissue-specific transcripts in human blood. For example, mass spectrometry may be used to quantify the transcripts (Koster et al., 1996; Fu et al., 1998). The application of presently disclosed method for detecting tissue-specific transcripts in blood does not restrict to subjects undergoing course of therapy or treatment, it may also be used for monitoring a patient for the onset of overt symptoms of a disease. Furthermore, the present method may be used for detecting any gene transcripts in blood. A kit for diagnosing, prognosing or even predicting a disease may be designed using gene-specific primers or probes derived from a whole blood sample for a specific disease and applied directly to a drop of blood. A cDNA library specific for a disease may be generated from whole blood samples and used for diagnosis, prognosis or even predicting a disease.

The term "oligonucleotide" is defined as a molecule comprised of two or more deoxyribonucleotides and/ or ribonucleotides, preferably more than three. Its exact size will depend upon many factors which, in turn, depend upon the ultimate function and use of the

oligonucleotide. The upper limit may be 15, 20, 25, 30, 40 or 50 nucleotides in length. The term "primer" as used herein refers to an oligonucleotide, whether occurring naturally as in a purified restriction digest or produced synthetically, which is capable of acting as a point of initiation of synthesis when placed under conditions in which synthesis of a primer extension product, which is complementary to a nucleic acid strand, is induced, i.e., in the presence of nucleotides and an inducing agent such as a DNA polymerase and at a suitable temperature and pH. The primer may be either single-stranded or double-stranded and must be sufficiently long to prime the synthesis of the desired extension product in the presence of the inducing agent. The exact length of the primer will depend upon many factors, including temperature, source of primer and the method used. For example, for diagnostic applications, depending on the complexity of the target sequence, the oligonucleotide primer typically contains 15-25 or more nucleotides, although it may contain fewer nucleotides. The factors involved in determining the appropriate length of primer are readily known to one of ordinary skill in the art.

As used herein, random sequence primers refer to a composition of primers of random sequence, i.e. not directed towards a specific sequence. These sequences possess sufficient complementarity to hybridize with a polynucleotide and the primer sequence need not reflect the exact sequence of the template.

"Restriction fragment length polymorphism" refers to variations in DNA sequence detected by variations in the length of DNA fragments generated by restriction endonuclease digestion.

A standard Northern blot assay can be used to ascertain the relative amounts of mRNA in a cell or tissue obtained from plant or other tissue, in accordance with conventional Northern hybridization techniques known to those persons of ordinary skill in the art. The Northern blot uses a hybridization probe, e.g. radiolabelled cDNA, either containing the full-length, single stranded DNA or a fragment of that DNA sequence at least 20 (preferably at least 30, more preferably at least 50, and most preferably at least 100 consecutive nucleotides in length). The DNA hybridization probe can be labelled by any of the many different methods known to those skilled in this art. The labels most commonly employed for these studies are radioactive elements, enzymes, chemicals which fluoresce

when exposed to ultraviolet light, and others. A number of fluorescent materials are known and can be utilized as labels. These include, for example, fluorescein, rhodamine, auramine, Texas Red, AMCA blue and Lucifer Yellow. A particular detecting material is anti-rabbit antibody prepared in goats and conjugated with fluorescein through an isothiocyanate.

5 Proteins can also be labeled with a radioactive element or with an enzyme. The radioactive label can be detected by any of the currently available counting procedures. The preferred isotope may be selected from ^3H , ^{14}C , ^{32}P , ^{35}S , ^{36}Cl , ^{51}Cr , ^{57}Co , ^{58}Co , ^{59}Fe , ^{90}Y , ^{125}I , ^{131}I , and ^{186}Re . Enzyme labels are likewise useful, and can be detected by any of the presently utilized colorimetric, spectrophotometric, fluorospectrophotometric, amperometric or

10 gasometric techniques. The enzyme is conjugated to the selected particle by reaction with bridging molecules such as carbodiimides, diisocyanates, glutaraldehyde and the like. Many enzymes which can be used in these procedures are known and can be utilized. The preferred are peroxidase, (-glucuronidase, (-D-glucosidase, (-D-galactosidase, urease, glucose oxidase plus peroxidase and alkaline phosphatase. U.S. Patent Nos. 3,654,090,

15 3,850,752, and 4,016,043 are referred to by way of example for their disclosure of alternate labeling material and methods.

As used herein, "individual" refers to human subjects as well as non-human subjects. The examples herein are not meant to limit the methodology of the present invention to human subjects only, as the instant methodology is useful in the fields of veterinary

20 medicine, animal sciences and such.

As used herein, "detecting" refers to determining the presence of a gene expression product, for example cDNA, RNA or EST, by any method known to those of skill in the art or taught in numerous texts and laboratory manuals (see for example, Ausubel et al. Short Protocols in Molecular Biology (1995) 3rd Ed. John Wiley & Sons, Inc.). For example,

25 methods of detection include but are not limited to, RNA fingerprinting, Northern blotting, polymerase chain reaction, ligase chain reaction, Qbeta replicase, isothermal amplification method, strand displacement amplification, transcription based amplification systems, nuclease protection (SI nuclease or RNase protection assays) as well as methods disclosed in WO 88/10315, Wo 89/ 06700PCT/US87/00880, PCT/ US89/01025.

As used herein, a disease of the invention includes, but is not limited to, blood disorder, blood lipid disease, autoimmune disease, arthritis (including osteoarthritis, rheumatoid arthritis, lupus, allergies, juvenile rheumatoid arthritis and the like), bone or joint disorder, a cardiovascular disorder, obesity, respiratory disease, lung diseases, hyperlipidemias, endocrine disorder, immune disorder, infectious disease, muscle wasting and whole body wasting disorder, neurological disorders including neurodegenerative and/or neuropsychiatric diseases, mood disorders, skin disorder, kidney disease, scleroderma, stroke, hereditary hemorrhage telangiectasia, diabetes, disorders associated with diabetes (e.g., PVD), hypertension, Gaucher's disease, cystic fibrosis, sickle cell anemia, liver disease, pancreatic disease, eye, ear, nose and/or throat disease, diseases affecting the reproductive organs, gastrointestinal diseases (including diseases of the colon, diseases of the spleen, appendix, gall bladder, and others) and the like. For further discussion of human diseases, see Mendelian Inheritance in Man: A Catalog of Human Genes and Genetic Disorders by Victor A. McKusick (12th Edition (3 volume set) June 1998, Johns Hopkins University Press, ISBN: 0801857422) and Harrison's Principles of Internal Medicine by Braunwald, Fauci, Kasper, Hauser, Longo, & Jameson (15th Edition 2001), the entirety of which is incorporated herein.

In another embodiment of the invention, a disease refers to an immune disorder, such as those associated with overexpression of a gene or expression of a mutant gene (e.g., autoimmune diseases, such as diabetes mellitus, arthritis (including rheumatoid arthritis, juvenile rheumatoid arthritis, osteoarthritis, psoriatic arthritis), multiple sclerosis, encephalomyelitis, myasthenia gravis, systemic lupus erythematosus, autoimmune thyroiditis, dermatitis (including atopic dermatitis and eczematous dermatitis), psoriasis, Sjogren's Syndrome, Crohn's disease, aphthous ulcer, iritis, conjunctivitis, keratoconjunctivitis, ulcerative colitis, asthma, allergic asthma, cutaneous lupus erythematosus, scleroderma, vaginitis, proctitis, drug eruptions, leprosy reversal reactions, erythema nodosum leprosum, autoimmune uveitis, allergic encephalomyelitis, acute necrotizing hemorrhagic encephalopathy, idiopathic bilateral progressive sensorineural hearing loss, aplastic anemia, pure red cell anemia, idiopathic thrombocytopenia, polychondritis, Wegener's granulomatosis, chronic active hepatitis, Stevens-Johnson syndrome, idiopathic sprue, lichen planus, Graves' disease, sarcoidosis, primary biliary

cirrhosis, uveitis posterior, and interstitial lung fibrosis), graft-versus-host disease, cases of transplantation, and allergy.

In another embodiment, a disease of the invention is a cellular proliferative and/or differentiative disorder that includes, but is not limited to, cancer, e.g., carcinoma, sarcoma or other metastatic disorders and the like. As used herein, the term "cancer" refers to cells having the capacity for autonomous growth, i.e., an abnormal state of condition characterized by rapidly proliferating cell growth. "Cancer" is meant to include all types of cancerous growths or oncogenic processes, metastatic tissues or malignantly transformed cells, tissues, or organs, irrespective of histopathologic type or stage of invasiveness.

10 Examples of cancers include but are not limited to solid tumours and leukaemias, including: apudoma, choristoma, branchioma, malignant carcinoid syndrome, carcinoid heart disease, carcinoma (e.g., Walker, basal cell, basosquamous, Brown-Pearce, ductal, Ehrlich tumour, in situ, Krebs 2, Merkel cell, mucinous, non-small cell lung, oat cell, papillary, scirrhous, bronchiolar, bronchogenic, squamous cell, and transitional cell), histiocytic disorders,

15 leukaemia (e.g., B cell, mixed cell, null cell, T cell, T-cell chronic, HTLV-II-associated, lymphocytic acute, lymphocytic chronic, mast cell, and myeloid), histiocytosis malignant, Hodgkin disease, immunoproliferative small, non-Hodgkin lymphoma, plasmacytoma, reticuloendotheliosis, melanoma, chondroblastoma, chondroma, chondrosarcoma, fibroma, fibrosarcoma, giant cell tumours, histiocytoma, lipoma, liposarcoma, mesothelioma,

20 myxoma, myxosarcoma, osteoma, osteosarcoma, Ewing sarcoma, synovioma, adenofibroma, adenolymphoma, carcinosarcoma, chordoma, craniopharyngioma, dysgerminoma, hamartoma, mesenchymoma, mesonephroma, myosarcoma, ameloblastoma, cementoma, odontoma, teratoma, thymoma, trophoblastic tumour, adeno-carcinoma, adenoma, cholangioma, cholesteatoma, cylindroma, cystadenocarcinoma, cystadenoma,

25 granulosa cell tumour, gynandroblastoma, hepatoma, hidradenoma, islet cell tumour, Leydig cell tumour, papilloma, Sertoli cell tumour, theca cell tumour, leiomyoma, leiomyosarcoma, myoblastoma, myoma, myosarcoma, rhabdomyoma, rhabdomyosarcoma, ependymoma, ganglioneuroma, glioma, medulloblastoma, meningioma, neurilemmoma, neuroblastoma, neuroepithelioma, neurofibroma, neuroma, paraganglioma, paraganglioma nonchromaffin,

30 angiokeratoma, angiolymphoid hyperplasia with eosinophilia, angioma sclerosing, angiomatosis, glomangioma, hemangioendothelioma, hemangioma, hemangiopericytoma,

hemangiosarcoma, lymphangioma, lymphangiomyoma; lymphangiosarcoma, pinealoma, carcinosarcoma, chondrosarcoma, cystosarcoma, phyllodes, fibrosarcoma, hemangiosarcoma, leiomyosarcoma, leukosarcoma, liposarcoma, lymphangiosarcoma, myosarcoma, myxosarcoma, ovarian carcinoma, rhabdomyosarcoma, sarcoma (e.g., Ewing, 5 experimental, Kaposi, and mast cell), neoplasms (e.g., bone, breast, digestive system, colorectal, liver, pancreatic, pituitary, testicular, orbital, head and neck, central nervous system, acoustic, pelvic respiratory tract, and urogenital), neurofibromatosis, and cervical dysplasia, and other conditions in which cells have become immortalised or transformed.

As used herein, a gene of the invention is a gene that is expressed in blood and is 10 either upregulated, or downregulated and can be used, either solely or in conjunction with other genes, as a marker for disease as defined herein. The term "gene" includes a region that can be transcribed into RNA, as the invention contemplates detection of RNA or equivalents thereof, i.e., cDNA or EST. A gene of the invention includes but is not limited to genes specific for or involved in a particular biological process, such as apoptosis, 15 differentiation, stress response, aging, proliferation, etc.; cellular mechanism genes, e.g. cell-cycle, signal transduction, metabolism of toxic compounds, and the like; disease associated genes, e.g. genes involved in cancer, schizophrenia, diabetes, high blood pressure, atherosclerosis, viral-host interaction and infection and the like.

For example, the gene of the invention can be an oncogene (Hanahan, D. and R.A. 20 Weinberg, *Cell* (2000) 100:57; and Yokota, J., *Carcinogenesis* (2000) 21(3):497-503) whose expression within a cell induces that cell to become converted from a normal cell into a tumor cell. Further examples of genes of the invention include, but are not limited to, cytokine genes (Rubinstein, M., et al., *Cytokine Growth Factor Rev.* (1998) 9(2):175-81); idiotype (Id) protein genes (Benezra, R., et al., *Oncogene* (2001) 20(58):8334-41; Norton, 25 J.D., *J. Cell Sci.* (2000) 113(22):3897-905); prion genes (Prusiner, S.B., et al., *Cell* (1998) 93(3):337-48; Safar, J., and S.B. Prusiner, *Prog. Brain Res.* (1998) 117:421-34); genes that express molecules that induce angiogenesis (Gould, V.E. and B.M. Wagner, *Hum. Pathol.* (2002) 33(11):1061-3); genes encoding adhesion molecules (Chothia, C. and E.Y. Jones, *Annu. Rev. Biochem.* (1997) 66:823-62; Parise, L.V., et al., *Semin. Cancer Biol.* (2000) 30 10(6):407-14); genes encoding cell surface receptors (Deller, M.C., and Y.E. Jones, *Curr.*

Opin. Struct. Biol. (2000) 10(2):213-9); genes of proteins that are involved in metastasizing and/or invasive processes (Boyd, D., Cancer Metastasis Rev. (1996) 15(1):77-89; Yokota, J., Carcinogenesis (2000) 21(3):497-503); genes of proteases as well as of molecules that regulate apoptosis and the cell cycle (Matrisian, L.M., Curr. Biol. (1999) 9(20):R776-8; 5 Krepela, E., Neoplasia (2001) 48(5):332-49; Basbaum and Werb, Curr. Opin. Cell Biol. (1996) 8:731-738; Birkedal-Hansen, et al., Crit. Rev. Oral Biol. Med. (1993) 4:197-250; Mignatti and Rifkin, Physiol. Rev. (1993) 73:161-195; Stetler-Stevenson, et al., Annu. Rev. Cell Biol. (1993) 9:541-573; Brinkerhoff, E., and L.M. Matrisian, Nature Reviews (2002) 3:207-214; Strasser, A., et al., Annu. Rev. Biochem. (2000) 69:217-45; Chao, D.T. and S.J. 10 Korsmeyer, Annu. Rev. Immunol. (1998) 16:395-419; Mullauer, L., et al., Mutat. Res. (2001) 488(3):211-31; Fotadar, R., et al., Prog. Cell Cycle Res. (1996) 2:147-63; Reed, J.C., Am. J. Pathol. (2000) 157(5):1415-30; D'Ari, R., Bioassays (2001) 23(7):563-5); or multi-drug resistance genes, such as MDR1 gene (Childs, S., and V. Ling, Imp. Adv. Oncol. (1994) 21-36). In another embodiment, a gene of the invention contains a sequence found 15 in Tables 2 or 3 or Figures 22 – 36.

Construction of a Microarray

A nucleic acid microarray (RNA, DNA, cDNA, PCR products or ESTs) according to the invention was constructed as follows.

Nucleic acids (RNA, DNA, cDNA, PCR products or ESTs) (~40 ul) are precipitated 20 with 4 ul (1/10 volume) of 3M sodium acetate (pH 5.2) and 100 ul (2.5 volumes) of ethanol and stored overnight at -20°C. They are then centrifuged at 3,300 rpm at 4°C for 1 hour. The obtained pellets were washed with 50 ul ice-cold 70% ethanol and centrifuged again for 30 minutes. The pellets are then air-dried and resuspended well in 50% dimethylsulfoxide (DMSO) or 20ul 3X SSC overnight. The samples are then deposited either singly or in 25 duplicate onto Gamma Amino Propyl Silane (Corning CMT-GAPS or CMT-GAP2, Catalog No. 40003, 40004) or polylysine-coated slides (Sigma Cat. No. P0425) using a robotic GMS 417 or 427 arrayer (Affymetrix, CA). The boundaries of the DNA spots on the microarray are marked with a diamond scribe. The invention provides for arrays where 10-20,000 different DNAs are spotted onto a solid support to prepare an array, and also may include duplicate or 30 triplicate DNAs.

The arrays are rehydrated by suspending the slides over a dish of warm particle free ddH₂O, for approximately one minute (the spots will swell slightly but not run into each other) and snap-dried on a 70-80°C inverted heating block for 3 seconds. DNA is then UV crosslinked to the slide (Stratagene, Stratalinker, 65 mJ – set display to “650” which is 650 x 100 uJ) or baked at 80°C for two to four hours. The arrays are placed in a slide rack. An empty slide chamber is prepared and filled with the following solution: 3.0 grams of succinic anhydride (Aldrich) is dissolved in 189 ml of 1-methyl-2-pyrrolidinone (rapid addition of reagent is crucial); immediately after the last flake of succinic anhydride dissolved, 21.0 ml of 0.2 M sodium borate is mixed in and the solution is poured into the slide chamber. The slide rack is plunged rapidly and evenly in the slide chamber and vigorously shaken up and down for a few seconds, making sure the slides never leave the solution, and then mixed on an orbital shaker for 15-20 minutes. The slide rack is then gently plunged in 95°C ddH₂O for 2 minutes, followed by plunging five times in 95% ethanol. The slides are then air dried by allowing excess ethanol to drip onto paper towels. The arrays are then stored in the slide box at room temperature until use.

Microarrays

Nucleic acid Microarrays

Any combination of the nucleic acid sequences generated from nucleotides complimentary to regions of DNA expressed in blood are used for the construction of a microarray. In one embodiment, the microarray is chondrocyte-specific and encompasses genes which are important in the osteoarthritis disease process. A microarray according to the invention preferably comprises between 10, 100, 500, 1000, 5000, 10,000 and 15,000 nucleic acid members, and more preferably comprises at least 5000 nucleic acid members. The nucleic acid members are known or novel nucleic acid sequences described herein, or any combination thereof. A microarray according to the invention is used to assay for differential gene expression profiles of genes in blood samples from healthy patients as compared to patients with a disease.

Microarray according to the invention

GENECHIP®

GeneChip® probe arrays are manufactured through a unique and robust process— a combination of photolithography and combinatorial chemistry— that results in many of the arrays' powerful capabilities. With a calculated minimum number of synthesis steps, 5 GeneChip technology produces arrays with hundreds of thousands of different probes packed at an extremely high density. This feature enables researchers to obtain high quality, genome-wide data using small sample volumes. Manufacture is scalable because the length of the probes, not their number, determines the number of synthesis steps required. This robust and automated production process yields arrays with highly reproducible properties, which 10 reduces user set-up time by eliminating the need for individual labs to produce and test their own arrays.

Using technologies adapted from the semiconductor industry, GeneChip manufacturing begins with a 5-inch square quartz wafer. Initially the quartz is washed to ensure uniform hydroxylation across its surface. Because quartz is naturally hydroxylated, it 15 provides an excellent substrate for the attachment of chemicals, such as linker molecules, that are later used to position the probes on the arrays.

The wafer is placed in a bath of silane, which reacts with the hydroxyl groups of the quartz, and forms a matrix of covalently linked molecules. The distance between these silane molecules determines the probes' packing density, allowing arrays to hold over 500,000 probe 20 locations, or features, within a mere 1.28 square centimeters. Each of these features harbors millions of identical DNA molecules. The silane film provides a uniform hydroxyl density to initiate probe assembly. Linker molecules, attached to the silane matrix, provide a surface that may be spatially activated by light.

Probe synthesis occurs in parallel, resulting in the addition of an A, C, T, or G 25 nucleotide to multiple growing chains simultaneously. To define which oligonucleotide chains will receive a nucleotide in each step, photolithographic masks, carrying 18 to 20 square micron windows that correspond to the dimensions of individual features, are placed over the coated wafer. The windows are distributed over the mask based on the desired sequence of each probe. When ultraviolet light is shone over the mask in the first step of synthesis, the

exposed linkers become deprotected and are available for nucleotide coupling. Critical to this step is the precise alignment of the mask with the wafer before each synthesis step. To ensure that this critical step is accurately completed, chrome marks on the wafer and on the mask are perfectly aligned.

- 5 Once the desired features have been activated, a solution containing a single type of deoxynucleotide with a removable protection group is flushed over the wafer's surface. The nucleotide attaches to the activated linkers, initiating the synthesis process.

10 Although the process is highly efficient, some activated molecules fail to attach the new nucleotide. To prevent these "outliers" from becoming probes with missing nucleotides, a capping step is used to truncate them. In addition, the side chains of the nucleotides are protected to prevent the formation of branched oligonucleotides.

In the following synthesis step, another mask is placed over the wafer to allow the next round of deprotection and coupling. The process is repeated until the probes reach their full length, usually 25 nucleotides.

- 15 Although each position in the sequence of an oligonucleotide can be occupied by 1 of 4 nucleotides, resulting in an apparent need for 25×4 , or 100, different masks per wafer, the synthesis process can be designed to significantly reduce this requirement. Algorithms that help minimize mask usage calculate how to best coordinate probe growth by adjusting synthesis rates of individual probes and identifying situations when the same mask can be
20 used multiple times.

Once the synthesis is complete, the wafers are deprotected, diced, and the resulting individual arrays are packaged in flowcell cartridges. Depending on the number of probe features per array, a single wafer can yield between 49 and 400 arrays.

- 25 The manufacturing process ends with a comprehensive series of quality control tests. Additionally, a sampling of arrays from every wafer is used to test the batch by running control hybridizations. A quantitative test of hybridization is also performed using standardized control probes.

After passing these rigorous tests, GeneChip probe arrays are well prepared to help pursue ambitious goals ranging from the discovery of basic biological mechanisms to the development of new disease therapies.

THE HUMAN GENOME U133 SET

5 The Human Genome U133 (HG-U133) Set, consisting of two GeneChip® arrays, contains almost 45,000 probe sets representing more than 39,000 transcripts derived from approximately 33,000 well-substantiated human genes. This set design uses sequences selected from GenBank®, dbEST, and RefSeq.

10 The sequence clusters were created from the UniGene database (Build 133, April 20, 2001). They were then refined by analysis and comparison with a number of other publicly available databases including the Washington University EST trace repository and the University of California, Santa Cruz Golden Path human genome database (April 2001 release).

15 The HG-U133A Array includes representation of the RefSeq database sequences and probe sets related to sequences previously represented on the Human Genome U95Av2 Array. The HG-U133B Array contains primarily probe sets representing EST clusters.

15 K Chondrochip (Version 2b)

20 The Chondrochip version 2b is chondrocyte-specific microarray chip comprising 15000 novel and known EST sequences of the chondrocyte from chondrocyte-specific cDNA libraries.

Controls on the Chondrochip

25 There are two types of controls used on microarrays. First, positive controls are genes whose expression level is invariant between different stages of investigation and are used to monitor:

- a) target DNA binding to the slide,
- b) quality of the spotting and binding processes of the target DNA onto the slide,
- c) quality of the RNA samples, and
- d) efficiency of the reverse transcription and fluorescent labelling of the probes.

5 Second, negative controls are external controls derived from an organism unrelated to and therefore unlikely to cross-hybridize with the sample of interest. These are used to monitor for:

- a) variation in background fluorescence on the slide, and
- b) non-specific hybridization.

10 There are currently 63 controls spots on the ChondroChip™ consisting of:

| <i>Type</i> | <i>No.</i> |
|------------------------|------------|
| Positive Controls: | 2 |
| <i>Alien</i> DNA | 12 |
| <i>A. thaliana</i> DNA | 10 |
| Spotting Buffer | 41 |

Blood Chip

The “Blood chip” is a cDNA microarray slide with 10,368 PCR products derived from peripheral blood cell cDNA libraries as shown in Figure 24.

Target Nucleic acid Preparation and Hybridization

20 *Preparation of Fluorescent DNA Probe from mRNA*

Fluorescently labeled target nucleic acid samples are prepared for analysis with an array of the invention.

2 μ g Oligo-dT primers are annealed to 2 μ g of mRNA isolated from a blood sample of a patient in a total volume of 15 μ l, by heating to 70°C for 10 min, and cooled on ice. The mRNA is reverse transcribed by incubating the sample at 42°C for 1.5-2 hours in a 100 μ l volume containing a final concentration of 50 mM Tris-HCl (pH 8.3), 75 mM KCl, 3 mM MgCl₂, 25 mM DTT, 25 mM unlabeled dNTPs, 400 units of Superscript II (200 U/ μ L, Gibco BRL), and 15 mM of Cy3 or Cy5 (Amersham). RNA is then degraded by addition of 15 μ l of 0.1N NaOH, and incubation at 70°C for 10 min. The reaction mixture is neutralized by addition of 15 μ l of 0.1N HCL, and the volume is brought to 500 μ l with TE (10mM Tris, 1mM EDTA), and 20 μ g of Cot1 human DNA (Gibco-BRL) is added.

10 The labeled target nucleic acid sample is purified by centrifugation in a Centricon-30 micro-concentrator (Amicon). If two different target nucleic acid samples (e.g., two samples derived from a healthy patient vs patient with a disease) are being analyzed and compared by hybridization to the same array, each target nucleic acid sample is labeled with a different fluorescent label (e.g., Cy3 and Cy5) and separately concentrated. The separately
15 concentrated target nucleic acid samples (Cy3 and Cy5 labeled) are combined into a fresh centricon, washed with 500 μ l TE, and concentrated again to a volume of less than 7 μ l. 1 μ L of 10 μ g/ μ l polyA RNA (Sigma, #P9403) and 1 μ l of 10 μ g/ μ l tRNA (Gibco-BRL, #15401-011) is added and the volume is adjusted to 9.5 μ l with distilled water. For final target nucleic acid preparation 2.1 μ l 20XSSC (1.5M NaCl, 150mM NaCitrate (pH8.0)) and 0.35 μ l 10%SDS
20 is added.

Hybridization

Labeled nucleic acid is denatured by heating for 2 min at 100°C, and incubated at 37°C for 20-30 min before being placed on a nucleic acid array under a 22mm x 22mm glass cover slip. Hybridization is carried out at 65°C for 14 to 18 hours in a custom slide chamber
25 with humidity maintained by a small reservoir of 3XSSC. The array is washed by submersion and agitation for 2-5 min in 2X SSC with 0.1%SDS, followed by 1X SSC, and 0.1X SSC. Finally, the array is dried by centrifugation for 2 min in a slide rack in a Beckman GS-6 tabletop centrifuge in Microplus carriers at 650 RPM for 2 min.

Signal Detection And Data Generation

Following hybridization of an array with one or more labeled target nucleic acid samples, arrays are scanned immediately using a GMS Scanner 418 and Scanalyzer software (Michael Eisen, Stanford University), followed by GeneSpring software (Silicon Genetics, CA) analysis. Alternatively, a GMS Scanner 428 and Jaguar software may be used followed by GeneSpring software analysis.

If one target nucleic acid sample is analyzed, the sample is labeled with one fluorescent dye (e.g., Cy3 or Cy5).

After hybridization to a microarray as described herein, fluorescence intensities at the associated nucleic acid members on the microarray are determined from images taken with a custom confocal microscope equipped with laser excitation sources and interference filters appropriate for the Cy3 or Cy5 fluors.

The presence of Cy3 or Cy5 fluorescent dye on the microarray indicates hybridization of a target nucleic acid and a specific nucleic acid member on the microarray. The intensity of Cy3 or Cy5 fluorescence represents the amount of target nucleic acid which is hybridized to the nucleic acid member on the microarray, and is indicative of the expression level of the specific nucleic acid member sequence in the target sample.

After hybridization, fluorescence intensities at the associated nucleic acid members on the microarray are determined from images taken with a custom confocal microscope equipped with laser excitation sources and interference filters appropriate for the Cy3 and Cy5 fluors. Separate scans are taken for each fluor at a resolution of $225 \mu\text{m}^2$ per pixel and 65,536 gray levels. Normalization between the images is used to adjust for the different efficiencies in labeling and detection with the two different fluors. This is achieved by manual matching of the detection sensitivities to bring a set of internal control genes to nearly equal intensity followed by computational calculation of the residual scalar required for optimal intensity matching for this set of genes.

The presence of Cy3 or Cy5 fluorescent dye on the microarray indicates hybridization of a target nucleic acid and a specific nucleic acid member on the microarray. The intensities

of Cy3 or Cy5 fluorescence represent the amount of target nucleic acid which is hybridized to the nucleic acid member on the microarray, and is indicative of the expression level of the specific nucleic acid member sequence in the target sample. If a nucleic acid member on the array shows no color, it indicates that the gene in that element is not expressed in either sample. If a nucleic acid member on the array shows a single color, it indicates that a labeled gene is expressed only in that cell sample. The appearance of both colors indicates that the gene is expressed in both tissue samples. The ratios of Cy3 and Cy5 fluorescence intensities, after normalization, are indicative of differences of expression levels of the associated nucleic acid member sequence in the two samples for comparison. A ratio of expression not equal to 10 is used as an indication of differential gene expression.

The array is scanned in the Cy 3 and Cy5 channels and stored as separate 16-bit TIFF images. The images are incorporated and analysed using Scanalyzer software which includes a gridding process to capture the hybridization intensity data from each spot on the array. The fluorescence intensity and background-subtracted hybridization intensity of each spot is collected and a ratio of measured mean intensities of Cy5 to Cy3 is calculated. A linear regression approach is used for normalization and assumes that a scatter plot of the measured Cy5 versus Cy3 intensities should have a slope of one. The average of the ratios is calculated and used to rescale the data and adjust the slope to one. A post-normalization cutoff of a ratio not equal to 1.0 is used to identify differentially expressed genes.

When comparing two or more samples for differences, results are reported as statistically significant when there is only a small probability that similar results would have been observed if the tested hypothesis (i.e., the genes are not expressed at different levels) were true. A small probability can be defined as the accepted threshold level at which the results being compared are considered significantly different. The accepted lower threshold is set at, but not limited to, 0.05 (i.e., there is a 5% likelihood that the results would be observed between two or more identical populations) such that any values determined by statistical means at or below this threshold are considered significant.

When comparing two or more samples for similarities, results are reported as statistically significant when there is only a small probability that similar results would have been observed if the tested hypothesis (i.e., the genes are not expressed at different levels)

were true. A small probability can be defined as the accepted threshold level at which the results being compared are considered significantly different. The accepted lower threshold is set at, but not limited to, 0.05 (i.e., there is a 5% likelihood that the results would be observed between two or more identical populations) such that any values determined by statistical means above this threshold are not considered significantly different and thus similar.

Identification of genes differentially expressed in blood samples from patients with disease as compared to healthy patients is determined by statistical analysis of the gene expression profiles from healthy patient compared to patients with a disease using the Wilcoxon Mann Whitney rank sum test.

Data Acquisition and Analysis of differentially expressed EST Sequences

The differentially expressed EST sequences are then searched against available databases, including the "nt", "nr", "est", "gss" and "htg" databases available through NCBI to determine putative identities for ESTs matching to known genes or other ESTs. Functional characterization of ESTs with known gene matches are made according to any known method. Preferably, differentially expressed EST sequences are compared to the non-redundant Genbank/EMBL/DDBJ and dbEST databases using the BLAST algorithm (Altschul SF, Gish W, Miller W, Myers EW, Lipman DJ. Basic local alignment search tool. J Mol Biol 1990;215:403-10). A minimum value of $P = 10^{-10}$ and nucleotide sequence identity >95%, where the sequence identity is non-contiguous or scattered, are required for assignments of putative identities for ESTs matching to known genes or to other ESTs. Construction of a non-redundant list of genes represented in the EST set is done with the help of Unigene, Entrez and PubMed at the National Center for Biotechnology Information (NCBI) web site at www.ncbi.nlm.nih.gov.

Genes are identified from ESTs according to known methods. To identify novel genes from an EST sequence, the EST should preferably be at least 100 nucleotides in length, and more preferably 150 nucleotides in length, for annotation. Preferably, the EST exhibits open reading frame characteristics (i.e., can encode a putative polypeptide).

Because of the completion of the Human Genome Project, a specific EST which matches with a genomic sequence can be mapped onto a specific chromosome based on the chromosomal location of the genomic sequence. However, no function may be known for the protein encoded by the sequence and the EST would then be considered "novel" in a functional sense. In one aspect, the invention is used to identify a novel differentially expressed EST, which is part of a larger known sequence for which no function is known, is used to determine the function of a gene comprising the EST. Alternatively, or additionally, the EST can be used to identify an mRNA or polypeptide encoded by the larger sequence as a diagnostic or prognostic marker of a disease.

Having identified an EST corresponding to a larger sequence, other portions of the larger sequence which comprises the EST can be used in assays to elucidate gene function, e.g., to isolate polypeptides encoded by the gene, to generate antibodies specifically reactive with these polypeptides, to identify binding partners of the polypeptides (receptors, ligands, agonists, antagonists and the like) and/or to detect the expression of the gene (or lack thereof) in healthy or diseased individuals.

In another aspect, the invention provides for nucleic acid sequences that do not demonstrate a "significant match" to any of the publicly known sequences in sequence databases at the time a query is done. Longer genomic segments comprising these types of novel EST sequences can be identified by probing genomic libraries, while longer expressed sequences can be identified in cDNA libraries and/or by performing polymerase extension reactions (e.g., RACE) using EST sequences to derive primer sequences as is known in the art. Longer fragments can be mapped to particular chromosomes by FISH and other techniques and their sequences compared to known sequences in genomic and/or expressed sequence databases.

The amino acid sequences encoded by the ESTs can also be used to search databases, such as GenBank, SWISS-PROT, EMBL database, PIR protein database, Vecbase, or GenPept for the amino acid sequences of the corresponding full-length genes according to procedures well known in the art.

Identified genes can be catalogued according to their putative function. Functional characterization of ESTs with known gene matches is preferably made according to the categories described by Hwang et al Compendium of Cardiovascular Genes. Circulation 1997;96:4146-203. The distribution of genes in each of the subcellular categories will provide
5 important insights into the disease process.

Alternative methods for analyzing ESTs are also available. For example, the ESTs may be assembled into contigs with sequence alignment, editing, and assembly programs such as PHRED and PHRAP (Ewing, et al., 1998, *Genome Res.* 3:175, incorporated herein; and the web site at bozeman.genome.washington.edu). Contig redundancy is reduced by clustering
10 nonoverlapping sequence contigs using the EST clone identification number, which is common for the nonoverlapping 5 and 3 sequence reads for a single EST cDNA clone. In one aspect, the consensus sequence from each cluster is compared to the non-redundant Genbank/EMBL/DDBJ and dbEST databases using the BLAST algorithm with the help of unigene, Entrez and PubMed at the NCBI site.

15 *Known Nucleic acid Sequences or ESTs and Novel Nucleic acid Sequences or ESTs*

An EST that exhibits a significant match (> 65%, and preferably 90% or greater, identity) to at least one existing sequence in an existing nucleic acid sequence database is characterized as a "known" sequence according to the invention. Within this category, some known ESTs match to existing sequences which encode polypeptides with known function(s)
20 and are referred to as a "known sequence with a function". Other "known" ESTs exhibit a significant match to existing sequences which encode polypeptides of unknown function(s) and are referred to as a "known sequence with no known function".

EST sequences which have no significant match (less than 65% identity) to any existing sequence in the above cited available databases are categorized as novel ESTs. To
25 identify a novel gene from an EST sequence, the EST is preferably at least 150 nucleotides in length. More preferably, the EST encodes at least part of an open reading frame, that is, a nucleic acid sequence between a translation initiation codon and a termination codon, which is potentially translated into a polypeptide sequence.

The following references were cited herein:

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Description of Tables:

Table 1: Overlap of Genes Expressed in Blood

(Estimated from limited known genes of about 1,800 as derived from the database of 6,297 ESTs from human blood cell library).

Table 2: Comparison of 1,800 Unique Genes Identified in the Blood Cell cDNA

Library to Genes Previously Identified in Specific Tissues

Column 1: List of unique genes derived from 6,283 known ESTs from blood cells. Column 2: Number of genes found in randomly sequenced ESTs from blood cells. Column 3: Accession number. Column 4: "+" indicates the presence of the unique gene in publicly available cDNA libraries of blood (Bl), brain (Br), heart (H), kidney (K), liver (Li) and lung (Lu).

**Comparison to previously identified tissue-specific genes was determined using the GenBank of the National Centre of Biotechnology Information (NCBI) Database.

Table 3: Genes that are differentially expressed in blood samples from patients with different diseases as compared to blood samples from healthy patients.

Table 3A shows the identity of those genes that are differentially expressed in blood samples from patients with osteoarthritis and hypertension as depicted in Figure 8

Table 3B shows the identity of those genes that are differentially expressed in blood samples from patients with osteoarthritis and obesity as depicted in Figure 9.

Table 3C shows the identity of those genes that are differentially expressed in blood samples from patients with osteoarthritis and allergies as depicted in Figure 10.

Table 3D shows the identity of those genes that are differentially expressed in blood samples from patients with osteoarthritis and subject to systemic steroids as depicted in Figure 11.

Table 3E shows the identity of those genes that are differentially expressed in blood samples from patients with hypertension as depicted in Figure 12.

Table 3F shows the identity of those genes that are differentially expressed in blood samples from patients obesity as depicted in Figure 13.

5 Table 3G shows the identity of those genes that are differentially expressed in blood samples from patients with type II diabetes as depicted in Figure 14.

Table 3H shows the identity of those genes that are differentially expressed in blood samples from patients with hyperlipidemia as depicted in Figure 15.

10 Table 3I shows the identity of those genes that are differentially expressed in blood samples from patients with lung disease as depicted in Figure 16.

Table 3J shows the identity of those genes that are differentially expressed in blood samples from patients with bladder cancer as depicted in Figure 17.

Table 3K shows the identity of those genes that are differentially expressed in blood samples from patients with bladder cancer as depicted in Figure 18.

15 Table 3L shows the identity of those genes that are differentially expressed in blood samples from patients with coronary artery disease (CAD) as depicted in Figure 19.

Table 3M shows the identity of those genes that are differentially expressed in blood samples from patients with rheumatoid arthritis as depicted in Figure 20.

20 Table 3N shows the identity of those genes that are differentially expressed in blood samples from patients with depression as depicted in Figure 21.

Table 3O shows the identity of those genes that are differentially expressed in blood samples from patients with various stages of osteoarthritis as depicted in Figure 22.

Table 4 shows 102 EST sequences of Tables 3A-3O with "no-significant match" to known gene sequences.

Table 5 shows a list of genes showing greater than two fold differential expression in CAD peripheral blood cells vs normal blood cells.

The following examples are given for the purpose of illustrating various
5 embodiments of the invention and are not meant to limit the present invention in any fashion.

EXAMPLE 1

Construction of a cDNA library

10 RNA extracted from human tissues (including fetal heart, adult heart, liver, brain, prostate gland and whole blood) were used to construct unidirectional cDNA libraries. The first mammalian heart cDNA library was constructed as early as 1982. Since then, the methodology has been revised and optimal conditions have been developed for construction of human heart and hematopoietic progenitor cDNA libraries (Liew *et al.*, 1984; Liew 1993,
15 Claudio *et al.*, 1998). Most of the novel genes which were identified by sequence annotation can now be obtained as full length transcripts.

EXAMPLE 2

Catalogue of EST database

20 Random partial sequencing of expressed sequence tags (ESTs) of cDNA clones from the blood cell library was carried out to establish an EST database of blood. The known genes as derived from the ESTs were categorized into seven major cellular functions (Hwang, Dempsey *et al.*, 1997). The preparation of the chondrocyte-specific EST database is reported in WO 02/070737, which is hereby incorporated by reference in its entirety.

EXAMPLE 3

Differential screening of cDNA library

cDNA probes generated from transcripts of each tissue were used to hybridize the
5 blood cell cDNA clones or chondrocyte cDNA clones (Liew *et al.*, 1997; WO 02/070737).
The "positive" signals which were hybridized with P-labelled cDNA probes were defined as
genes which shared identity with blood and respective tissues. The "negative" spots which
were not exposed to P-labelled cDNA probes were considered to be blood-cell-enriched or
low frequency transcripts.

EXAMPLE 4

Reverse transcriptase-polymerase chain reaction (RT-PCR) assay

RNA extracted from samples of human tissue was used for RT-PCR analysis (Jin *et al.* 1990). Three pairs of forward and reverse primers were designed for human cardiac
15 beta-myosin heavy chain gene ((MyHC), amyloid precursor protein (APP) gene and
adenomatous polyposis-coli protein (APC) gene. The PCR products were also subjected to
automated DNA sequencing to verify the sequences as derived from the specific transcripts
of blood.

EXAMPLE 5

Detection of tissue specific gene expression in human blood using RT-PCR

The beta-myosin heavy chain gene ((MyHC) transcript (mRNA) is known to be
highly expressed in ventricles of the human heart. This sarcomeric protein is important for
heart muscle contraction and its presence would not be expected in other non-muscle tissues
25 and blood. In 1990, the gene for human cardiac (MyHC) was completely sequenced (Liew
et al. 1990) and was comprised of 41 exons and 42 introns.

The method of reverse transcription polymerase chain reaction (RT-PCR) was used
to determine whether this cardiac specific mRNA is also present in human blood. A pair of
primers was designed; the forward primer (SEQ ID No. 3) was on the boundary of exons 21

and 22, and the reverse primer (SEQ ID No. 4) was on the boundary of exons 24 and 25. This region of mRNA is only present in (MyHC and is not found in the alpha-myosin heavy chain gene ((MyHC).

A blood sample was first treated with lysing buffer and then undergone centrifuge.
5 The resulting pellets were further processed with RT-PCR. RT-PCR was performed using the total blood cell RNA as a template. A nested PCR product was generated and used for sequencing. The sequencing results were subjected to BLAST and the identity of exons 21 to 25 was confirmed to be from (MyHC (Figure 1A).

Using the same method just described, two other tissue specific genes - amyloid
10 precursor protein (APP, forward primer, SEQ ID No. 7; reverse primer, SEQ ID No. 8) found in the brain and associated with Alzheimer's disease, and adenomatous polyposis coli protein (APC) found in the colon and rectum and associated with colorectal cancer (Grodén *et al.* 1991; Santoro and Grodén 1997) - were also detected in the RNA extracted from human blood (Figure 1B).

15

EXAMPLE 6

Multiple RT-PCR analysis on a drop of blood from a normal/diseased individual

A drop of blood was extracted to obtain RNA to carry out quantitative RT-PCR analysis. Specific primers for the insulin gene were designed: forward primer (5'-
20 GCCCTCTGGGGACCTGAC-3', SEQ ID No. 1) of exon 1 and reverse primer (5'-CCCACCTGCAGGTCCTCT-3'', SEQ ID No. 2) of exons 1 and 2 of insulin gene. Such reverse primer was obtained by deleting the intron between the exons 1 and 2. Blood samples of 4 normal subjects were assayed. It was found that the insulin gene is expressed in the blood and the quantitative expression of the insulin gene in a drop of blood is
25 influenced by fasting and non-fasting states of normal healthy subjects (Figure 2). This very low level of expression of the insulin gene reflects the phenotypic status of a person and strongly suggests that there is a physiological and pathological role for its expression, contrary to the basal or illegitimate theory of transcription suggested by Chelly *et al.* (1989) and Kimoto (1998).

Same quantitative RT-PCR analysis was performed using insulin specific primers on RNA samples extracted from a drop of blood from a normal healthy person, a person having late-onset diabetes (Type II) and a person having asymptomatic diabetes. It was found that the insulin gene is expressed differentially amongst subjects that are healthy, diagnosed as type II diabetic, and also in an asymptomatic preclinical patient (Figure 3).

Similarly, specific primers for the atrial natriuretic factor (ANF) gene were designed (forward primer, SEQ ID No. 5; reverse primer, SEQ ID No. 6) and RT-PCR analysis was performed on a drop of blood. ANF is known to be highly expressed in heart tissue biopsies and in the plasma of heart failure patients. However, atrial natriuretic factor was observed to be expressed in the blood and the expression of the atrial natriuretic factor gene is significantly higher in the blood of patients with heart failure as compared to the blood of a normal control patient.

Specific primers for the zinc finger protein gene (ZFP, forward primer, SEQ ID No. 9; reverse primer, SEQ ID No. 10) were also designed and RT-PCR analysis was performed on a drop of blood. ZFP is known to be high in heart tissue biopsies of cardiac hypertrophy and heart failure patients. In the present study, the expression of ZFP was observed in the blood as well as differential expression levels of ZFP amongst the normal, diabetic and asymptomatic preclinical subjects (Figure 4); although neither of the non-normal subjects has been specifically diagnosed as suffering from cardiac hypertrophy and/or heart failure, the higher expression levels of the ZFP gene in their blood may indicate that these subjects are headed in that general direction.

It was hypothesized that a housekeeping gene such as glyceraldehyde dehydrogenase (GADH) which is required and highly expressed in all cells would not be differentially expressed in the blood of normal vs. disease subjects. This hypothesis was confirmed by RT-PCR using GADH specific primers (Figure 4). Thus, GADH is useful as an internal control.

Standardized levels of insulin gene or ZFP gene expressed in a drop of blood were estimated using a housekeeping gene as an internal control relative to insulin or ZFP

expressed (Figures 5A & 5B). The levels of insulin gene expressed in each fractionated cell from whole blood were also standardized and shown in Figure 5C.

EXAMPLE 7

Human blood cell cDNA library

5 In order to further substantiate the present invention, differential screening of the human blood cell cDNA library was conducted. cDNA probes derived from human blood, adult heart or brain were respectively hybridized to the human blood cDNA library clones. As shown in Figure 7, more than 95% of the "positively" identified clones are identical between the blood and other tissue samples.

10 DNA sequencing of randomly selected clones from the human whole blood cell cDNA library was also performed. This allowed information regarding the cellular function of blood to be obtained concurrently with gene identification. More than 20,000 expressed sequence tags (ESTs) have been generated and characterized to date, 17.6% of which did not result in a statistically significant match to entries in the GenBank databases and thus
15 were designated as "Novel" ESTs. These results are summarized in Figure 7 together with the seven cellular functions related to percent distribution of known genes in blood and in the fetal heart.

From 20,000 ESTs, 1,800 have been identified as known genes which may not all appear in the hemopoietic system. For example, the insulin gene and the atrial natriuretic
20 factor gene have not been detected in these 20,000 ESTs but their transcripts were detected in a drop of blood, strongly suggesting that all transcripts of the human genome can be detected by performing RT-PCR analysis on a drop of blood.

In addition, approximately 400 novel genes have been identified from the 20,000 ESTs characterized to date, and these will be subjected to full length sequencing and open
25 reading frame alignment to reduce the actual number of novel ESTs prior to screening for disease markers.

Analysis of the approximately 6,283 ESTs which have known matches in the GenBank databases revealed that this dataset represents over 1,800 unique genes. These genes have been catalogued into seven cellular functions. Comparisons of this set of unique genes with ESTs derived from human brain, heart, lung and kidney demonstrated a greater
5 than 50% overlap in expression (Table 1).

TABLE 1

Overlap of Genes Expressed in Blood *

| | Tissues | ESTs** | Overlap in Blood |
|----|---------|---------|------------------|
| | brain | 134,000 | 60% |
| 10 | heart | 65,000 | 59% |
| | lung | 60,200 | 58% |
| | kidney | 32,300 | 54% |

* Estimated from limited known genes of about 1,800 as derived from the database of 6,297 ESTs from human blood cell library.

15 ** Obtained from the National Centre of Biotechnology Information (NCBI), U.S.A.

EXAMPLE 8

Blood cell ESTs

20 The results from the differential screening clearly indicate that the transcripts expressed in the whole blood are reflective of genes expressed in all cells and tissues of the body. More than 95% of detectable spots were identical from two different tissues. The remaining 5% of spots may represent cell- or tissue-specific transcripts; however, results obtained from partial sequencing to generate ESTs of these clones revealed most of them
25 not to be cell- or tissue-specific transcripts. Therefore, the negative spots are postulated to

be reflective of low abundance transcripts in the tissue from which the cDNA probes were derived.

An alternative approach that was employed to identify transcripts expressed at low levels is the large-scale generation of expressed sequence tags (ESTs). There is substantial evidence regarding the efficiency of this technology to detect previously characterized (known) and uncharacterized (unknown or novel) genes expressed in the cardiovascular system (Hwang & Dempsey *et al.*, 1997). In the present invention, 20,000 ESTs have been produced from a human blood cell cDNA library and resulted in the identification of approximately 1,800 unique known genes (Table 2)

In the most recent GenBank release, analysis of more than 300,000 ESTs in the database (dbESTs) generated more than 48,000 gene clusters which are thought to represent approximately 50% of the genes in the human genome. Only 4,800 of the dbESTs are blood-derived. In the present invention, 20,000 ESTs have been obtained to date from a human blood cDNA library, which provides the world's most informative database with respect to blood cell transcripts. From the limited amount of information generated so far (i.e. 1,800 unique genes), it has already been determined that more than 50% of the transcripts are found in other cells or tissues of the human body (Table 2). Thus, it is expected that by increasing the number of ESTs generated, more genes will be identified that have an overlap in expression between the blood and other tissues. Furthermore, the transcripts for several genes which are known to have tissue-restricted patterns of expression (i.e. (MyHC, APP, APC, ANF, ZFP) have also been demonstrated to be present in blood.

Most recently, a cDNA library of human hematopoietic progenitor stem cells has also been constructed. From the limited set of 1,000 ESTs, there are at least 200 known genes that are shared with other tissue related genes (Claudio *et al.* 1998).

Table 2 demonstrates the expression of known genes of specific tissues in blood cells. Previously, only the presence of "housekeeping" genes would have been expected. Additionally, the presence of at least 25 of the currently known 500 genes corresponding to molecular drug targets was detected. These molecular drug targets are used in the treatment

of a variety of diseases which involve inflammation, renal and cardiovascular function, neoplastic disease, immunomodulation and viral infection (Drews & Ryser, 1997). It is expected that additional novel ESTs will represent future molecular drug targets.

EXAMPLE 9

Blood cDNA chip Microarray Data Analysis of gene expression profiles of blood samples from individuals having coronary artery disease as compared with gene expression profiles from normal individuals

A microarray was constructed using cDNA clones from a human peripheral blood cell cDNA library, as described herein: A total of 10,368 polymerase chain reaction (PCR) products of the clones from the human peripheral blood cell cDNA library were arrayed using GNS 417 arrayer (Affymetrix). RNA for microarray analysis was isolated from whole blood samples obtained from three male and one female patients with coronary heart disease (80 – 90% stenosis) receiving vascular extension drugs and awaiting bypass surgery, and three healthy male controls.

A method of high-fidelity mRNA amplification from 1 pg of total RNA sample was used. Cy5- or Cy3-dUTP was incorporated into cDNA probes by reverse transcription of anti-sense RNA, primed by oligo-dT. Labeled probes were purified and concentrated to the desired volume. Pre- hybridization and hybridization were performed following Hegde's protocol (Hegde P et al. A concise guide to cDNA microarray analysis. Biotechniques 2000;29: 548 – 56). After overnight hybridization and washing, hybridization signals were detected with a GMS 418 scanner at 635-nm (Cy5) and 532-nm (Cy3) wave lengths (see Figure 24). Two RNA pools were labeled alternatively with Cy5- and Cy3-dUTP, and each experiment was repeated twice. Cluster analysis using GeneSpring 4.1.5 (Silicon Genetics) revealed two distinct groups consisting of four CAD and three normal control samples. Two images scanned at different wavelengths were super- imposed. Individual spots were identified on a customized grid. Of 10,368 spots, 10,012 (96.6%) were selected after the removal of spots with irregular shapes. Data quality was assessed with values of ChlGTB2 and Ch2GTB2 provided by ScanAlyze. Only spots with ChlGTB2 and Ch2GTB2 over 0.50

were selected. After evaluation of signal intensities, 8750 (84.4%) spots were left. Signal intensities were normalized using a scatter-plot of the signal intensities of the two channels. After normalization, the expression ratios of β -actin were 1.00 ± 0.21 , 1.11 ± 0.22 , 1.14 ± 0.20 and 1.30 ± 0.18 (24 samples of β -actin were spotted on this slide as the positive control) in the four images. Gene differential expression was assessed as the ratio of two wave-length signal intensities. Spots showing a differential expression more than twofold in all four experiments were identified as peripheral blood cell, differentially expressed candidate genes in CAD. 108 genes are differentially expressed in CAD peripheral blood cells, 43 genes are downregulated in CAD blood cells and 65 are upregulated (see Table 5).

Functional characterization of these genes shows that differential expression takes place in every gene functional category, indicating that profound changes occur in CAD blood cells.

The differential expression of three genes, pro-platelet basic protein (PBP), platelet factor 4 (PF4) and coagulation factor XIII A1 (F13A), initially identified in the microarray data analysis, was further examined by reverse transcriptase-PCR (RT-PCR) using the Titan One-tube RT-PCR kit (Boehringer Mannheim). Reaction solution contains 0.2 mM each dNTP, 5 mM DTT, 1.5 mM MgCl₂ 0.1 μ g of total RNA from each sample and 20 pmol each of left and right primers of PBP (5'-GGTGCTGCTGCTTCTGTCAT-3' and 5'-GGCAGATTTT CCTCCCATCC-3'), F13A (5'-AGTCCACCGTGCTAACCATC-3' and 5'-AGGGAGTCACTGCTCATGCT-3') and PF4 (5' GTTGCTGCTCCTGCCACTT 3' and 5' GTGGCTATCAGTTGGGCAGT-3'). RT-PCR steps are as follows: 1. reverse-transcription: 30 min at 60 °C; 2. PCR: 2 min at 94 °C, followed by 30 – 35 cycles (as optimized for each gene) for 30 s at 94 °C, 30 s at optimized annealing temperature and 2 min at 68 °C; 3. final extension: 7 min at 68 °C. PCR products were electrophoresed on 1.5% agarose gels. Human (β -actin primers (5'-GCGAGAAGATGACCCAGATCAT-3' and 5'-GCTCAGGAGGAGCAATGATCTT-3') were used as the internal control. The RT-PCR analysis confirmed that the expression of the three secreted proteins: PBP, PF4 and F13A were all upregulated in CAD blood cells (see Figure 23).

TABLE 5

| | Accession number | Fold (average) | Functional category | Protein Accession Number |
|---|------------------|-------------------|-----------------------|-----------------------------|
| <i>Upregulated gene in CAD</i> | | | | |
| REV3-like, catalytic subunit of DNA polymerase zeta | AF035537 | 2.3 | Cell cycle | NP_002903 |
| TGFB1-induced anti-apoptotic factor 1 | D86970 | 2.2 | Cell cycle | NP_510880 |
| A disintegrin and metalloproteinase domain 10 | AA044656 | 2.7 | Cell signaling | NP_001101 |
| Centaurin, delta 2 | AA351412 | 2 | Cell signaling | NP_631920 |
| Chloride intracellular channel 4 | AA411940 | 2.2 | Cell signaling | NP_039234 |
| Endothelin receptor type A | D90348 | 2.1 | Cell signaling | NP_001948 |
| Glutamate receptor, ionotropic | N33821 | 2.4 | Cell signaling | NP_777567 |
| Mitogen-activated protein kinase 7 | L38486 | 3.7 | Cell signaling | NP_002395 |
| Mitogen-activated protein kinase kinase 7 | AB009356 | 4.5 | Cell signaling | NP_663306 |
| Myristoylated alanine-rich protein kinase C substrate | D10522 | 2.5 | Cell signaling | NP_002347 |
| NIMA-related kinase 7 | AA093324 | 3.5 | Cell signaling | NP_598001 |
| PAK2 | AA262968 | 3.5 | Cell signaling | Q13177 |
| Phospholipid scramblase 1 | AA054476 | 3.3 | Cell signaling | NP_066928 |
| Serum deprivation response | Z30112 | 4.5 | Cell signaling | NP_004648 |
| Adducin 3 | AA029158 | 2.9 | Cell structure | NP_063968 |
| Desmin | AF167579 | 4.4 | Cell structure | NP_001918 |
| Fibromodulin | W23613 | 2.9 | Cell structure | NP_002014 |
| Laminin, beta 2 | S77512 | 2.2 | Cell structure | NP_002283 |
| Laminin, beta 3 | L25541 | 2.4 | Cell structure | NP_000219 |
| Osteonectin | Y00755 | 3.1 | Cell structure | NP_003109 |
| CD59 antigen p18-20 | W01111 | 2.4 | Cell/organism defense | NP_000602 |
| Clusterin | M64722 | 3.5 | Cell/organism defense | NP_001822 |
| F13A | M14539 | 2.1 | Cell/organism defense | NP_000120 |

| | | | | |
|--|----------|-----|-----------------------|-------------|
| Defensin, alpha 1 | M26602 | 4.2 | Cell/organism defense | NP_004075 |
| PF4 | M25897 | 2.1 | Cell/organism defense | NP_002610 |
| PBP | M54995 | 5.5 | Cell/organism defense | NP_002695 |
| E2F transcription factor 3 | D38550 | 2.1 | Gene expression | NP_001940 |
| Early growth response 1 | M62829 | 2.7 | Gene expression | NP_001955 |
| Eukaryotic translation elongation factor 1 alpha 1 | N86030 | 2.3 | Gene expression | NP_001393 |
| Eukaryotic translation initiation factor 4E | M15353 | 2.1 | Gene expression | NP_001959 |
| F-box and WD-40 domain protein 1B | AB014596 | 2.7 | Gene expression | NP_387449 |
| Makorin, ring finger protein, 2 | AA331966 | 2.1 | Gene expression | NP_054879 |
| Non-canonical ubiquitin-conjugating enzyme 1 | N92776 | 2.5 | Gene expression | NP_057420 |
| Nuclear receptor subfamily 1, group I, member 3 | Z30425 | 4.7 | Gene expression | NP_005113 |
| Ring finger protein 11 | T08927 | 3 | Gene expression | NP_055187 |
| Transducin-like enhancer of split 1 | M99435 | 3.3 | Gene expression | NP_005068 |
| Alkaline phosphatase, liver/bone/kidney | AB011406 | 2.2 | Metabolism | NP_000469 |
| Annexin A3 | M63310 | 3.4 | Metabolism | NP_005130 |
| Branched chain aminotransferase 1, cytosolic | AA336265 | 4.8 | Metabolism | NP_005495.1 |
| Cytochrome b | AF042500 | 2.5 | Metabolism | |
| Glutaminase | D30931 | 2.6 | Metabolism | NP_055720 |
| Lysophospholipase I | AF035293 | 2.8 | Metabolism | NP_006321 |
| NADH dehydrogenase 1, subcomplex unknown 1, 6 kDa | AA056111 | 2.5 | Metabolism | NP_002485 |
| Phosphofructokinase | M26066 | 2.2 | Metabolism | NP_000280 |
| Ubiquinol-cytochrome c reductase binding protein | M22348 | 2.5 | Metabolism | NP_006285 |
| CGI-110 protein | AA341061 | 2.4 | Unclassified | NP_057131 |
| Dactylidin | H95397 | 2.7 | Unclassified | NP_112225 |
| Deleted in split-hand/split-foot 1 region | T24503 | 2.4 | Unclassified | NP_006295 |
| Follistatin-like 1 | R14219 | 2.7 | Unclassified | NP_009016 |
| FUS-interacting protein 1 | W37945 | 2.8 | Unclassified | NP_473357 |
| Hypothetical protein FLJ12619 | W47233 | 7 | Unclassified | NP_112201 |

| | | | | |
|--|----------|------|----------------|-------------|
| Hypothetical protein from EUROIMAGE 588495 | N68247 | 2.7 | Unclassified | |
| Hypothetical protein LOC51315 | AA251423 | 2.2 | Unclassified | NP_057702 |
| KIAA1705 protein | T80569 | 2.7 | Unclassified | NP_009121.1 |
| Mesoderm induction early response 1 | AI650409 | 2.2 | Unclassified | NP_065999 |
| Phosphodiesterase 4D-interacting protein | AA740661 | 2.5 | Unclassified | NP_055459 |
| Preimplantation protein 3 | D59087 | 2.5 | Unclassified | NP_056202 |
| Putative nuclear protein ORF1-FL49 | W33098 | 2.8 | Unclassified | NP_115788 |
| Similar to rat nuclear ubiquitous casein kinase 2 | H09434 | 2.2 | Unclassified | Q9H1E3 |
| Similar to RIKEN | AA297412 | 2.5 | Unclassified | T02670 |
| Spectrin, beta | AI334431 | 2.5 | Unclassified | Q01082 |
| Stromal cell-derived factor receptor 1 | H71558 | 4.1 | Unclassified | NP_816929 |
| Thioredoxin-related protein | AA421549 | 2.8 | Unclassified | NP_110437 |
| Transmembrane 4 superfamily member 2 | D29808 | 2.4 | Unclassified | NP_004606 |
| Tumor endothelial marker 8 | D79964 | 2.5 | Unclassified | NP_444262 |
| <i>Downregulated gene in CAD</i> | | | | |
| CASP8 and FADD-like apoptosis regulator | AF015450 | 0.45 | Cell cycle | NP_003870 |
| CD81 antigen | M33680 | 0.41 | Cell cycle | NP_004347 |
| Cell division cycle 25B | M81934 | 0.4 | Cell cycle | NP_068660 |
| DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 27 | AA985699 | 0.42 | Cell cycle | NP_694705 |
| F-box and leucine-rich repeat protein 11 | R98291 | 0.27 | Cell cycle | NP_036440 |
| Minichromosome maintenance deficient 3 associated protein | H10286 | 0.43 | Cell cycle | NP_003897 |
| Protein phosphatase 2, regulatory subunit A, alpha isoform | J02902 | 0.48 | Cell cycle | NP_055040 |
| Thyroid autoantigen 70 kDa | J04607 | 0.25 | Cell cycle | NP_001460 |
| A disintegrin and metalloproteinase domain 17 | R32760 | 0.37 | Cell signaling | |
| A kinase anchor protein 13 | M90360 | 0.31 | Cell signaling | NP_658913 |
| Calpastatin | AF037194 | 0.39 | Cell signaling | NP_006471 |

| | | | | |
|--|----------|------|-----------------------|-----------|
| Diacylglycerol kinase, alpha 80 kDa | AF064770 | 0.44 | Cell signaling | NP_001336 |
| gamma-aminobutyric acid B receptor, 1 | AJ012187 | 0.42 | Cell signaling | NP_068705 |
| Inositol polyphosphate-5-phosphatase, 145 kDa | U84400 | 0.41 | Cell signaling | NP_005532 |
| Lymphocyte-specific protein tyrosine kinase | X05027 | 0.45 | Cell signaling | NP_005347 |
| RAP1B, member of RAS oncogene family | P09526 | 0.4 | Cell signaling | P09526 |
| Ras association (RalGDS/AF-6) domain family 1 | AF061836 | 0.43 | Cell signaling | NP_733835 |
| CDC42-effector protein 3 | AF104857 | 0.28 | Cell signaling | NP_006440 |
| Leupaxin | AF062075 | 0.31 | Cell signaling | NP_004802 |
| Annexin A6 | D00510 | 0.45 | Cell structure | NP_004024 |
| RAN-binding protein 9 | AB008515 | 0.41 | Cell structure | NP_005484 |
| Thymosin, beta 10 | M20259 | 0.26 | Cell structure | NP_066926 |
| GranzymeA | M18737 | 0.17 | Cell/organism defense | NP_006135 |
| ThromboxaneA synthase 1 | M80646 | 0.44 | Cell/organism defense | NP_112246 |
| Coatamer protein complex, subunit beta | AA357332 | 0.39 | Gene expression | NP_057535 |
| Cold-inducible RNA-binding protein | H39820 | 0.27 | Gene expression | NP_001271 |
| Leucine-rich repeat interacting protein 1 | U69609 | 0.44 | Gene expression | NP_004726 |
| Proteasome subunit, alpha type, 3 | D00762 | 0.31 | Gene expression | NP_687033 |
| Proteasome subunit, alpha type, 7 | AF022815 | 0.35 | Gene expression | NP_689468 |
| Protein phosphatase 1G, gamma isoform | A1417405 | 0.5 | Gene expression | NP_817092 |
| Ribonuclease/angiogenin inhibitor | M36717 | 0.44 | Gene expression | NP_002930 |
| RNA-binding protein-regulatory subunit | AF021819 | 0.3 | Gene expression | NP_009193 |
| Signal transducer and activator of transcription 6 | U16031 | 0.45 | Gene expression | NP_003144 |
| Transcription factor A, mitochondrial | M62810 | 0.41 | Gene expression | NP_036383 |
| Ubiquitin-specific protease 4 | AF017306 | 0.31 | Gene expression | NP_003354 |
| Dehydrogenase/reductase SDR family member 1 | AA100046 | 0.46 | Metabolism | NP_612461 |
| Solute carrier family 25, member 6 | J03592 | 0.3 | Metabolism | NP_001627 |
| Amplified in osteosarcoma | U41635 | 0.45 | Unclassified | NP_006803 |

| | | | | |
|--|----------|------|--------------|-----------|
| Expressed in activated T/LAK lymphocytes | C00577 | 0.45 | Unclassified | NP_009198 |
| Integral inner nuclear membrane protein | W00460 | 0.4 | Unclassified | NP_055134 |
| Phosphodiesterase 4D-interacting protein | T95969 | 0.45 | Unclassified | NP_055459 |
| Tumor endothelial marker 7 precursor | N93789 | 0.45 | Unclassified | NP_065138 |
| Wiskott-Aldrich syndrome protein interacting protein | AF031588 | 0.22 | Unclassified | NP_003378 |

EXAMPLE 10

ChondroChip Microarray Data Analysis of gene expression profiles of blood samples from individuals having osteoarthritis and hypertension as compared with gene expression profiles from normal individuals

This example demonstrates the use of the claimed invention to detect differential gene expression in blood samples taken from patients with osteoarthritis and hypertension on as compared to blood samples taken from healthy patients.

As used herein, the term "hypertension" is defined as high blood pressure or elevated arterial pressure. Patients identified with hypertension herein include persons who have an increased risk of developing a morbid cardiovascular event and/or persons who benefit from medical therapy designed to treat hypertension. Patients identified with hypertension also can include persons having systolic blood pressure of >130 mm Hg or a diastolic blood pressure of >90 mm Hg or a person takes antihypertensive medication.

Osteoarthritis (OA), as used herein also known as "degenerative joint disease", represents failure of a diarthrodial (movable, synovial-lined) joint. It is a condition, which affects joint cartilage, and or subsequently underlying bone and supporting tissues leading to pain, stiffness, movement problems and activity limitations. It most often affects the hip, knee, foot, and hand, but can affect other joints as well.

OA severity can be graded according to the system described by Marshall (Marshall KW. J Rheumatol, 1996;23(4) 582-85). Briefly, each of the six knee articular surfaces was assigned a cartilage grade with points based on the worst lesion seen on each particular

surface. Grade 0 is normal (0 points), Grade I cartilage is soft or swollen but the articular surface is intact (1 point). In Grade II lesions, the cartilage surface is not intact but the lesion does not extend down to subchondral bone (2 points). Grade III damage extends to subchondral bone but the bone is neither eroded nor eburnated (3 points). In Grade IV lesions, there is eburnation of or erosion into bone (4 points). A global OA score is calculated by summing the points from all six cartilage surfaces. If there is any associated pathology, such as meniscus tear, an extra point will be added to the global score. Based on the total score, each patient is then categorized into one of four OA groups: mild (1-6), moderate (7-12), marked (13-18), and severe (>18). As used herein, patients identified with OA may be categorized in any of the four OA groupings as described above.

Blood samples were taken from patients who were diagnosed with osteoarthritis and hypertension as defined herein. Gene expression profiles were then analyzed and compared to profiles from patients unaffected by any disease. In each case, the diagnosis of osteoarthritis and hypertension was corroborated by a skilled Board certified physician.

Total mRNA from a drop of peripheral whole blood taken from each patient was isolated using TRIzol® reagent (GIBCO) and fluorescently labeled probes for each blood sample were generated as described above. Each probe was denatured and hybridized to a 15K ChondroGene Microarray Chip (Chondrochip) as described herein. Identification of genes differentially expressed in blood samples from patients with disease as compared to healthy patients was determined by statistical analysis using the Wilcoxon Mann Whitney rank sum test (Glantz SA. Primer of Biostatistics. 5th ed. New York, USA: McGraw-Hill Medical Publishing Division, 2002).

Figure 8 shows a diagrammatic representation of gene expression profiles of blood samples from individuals having hypertension as compared with gene expression profiles from normal individuals. Expression profiles were generated using GeneSpring software analysis as described herein. Each column represents the hybridization pattern resulting from a single individual. In this example, hypertensive patients also presented with OA, as described herein. Normal individuals have no known medical conditions and were not taking any known medication. Hybridizations to create said gene expression profiles were done using the ChondroChip (version 2). A dendrogram analysis is shown above. Samples are

clustered and marked as representing patients who are hypertensive or normal. The “*” indicates those patients who abnormally clustered as either hypertensive, or normal despite presenting with the reverse. The number of hybridizations profiles determined for either hypertensive patients or normal individuals are shown. 861 differentially expressed genes were identified as being differentially expressed with a p value of < 0.05 as between the hypertensive patients and normal individuals. The identity of the differentially expressed genes is shown in Table 3A.

EXAMPLE 11

ChondroChip Microarray Data Analysis of gene expression profiles of blood samples from individuals having osteoarthritis and obesity as compared with gene expression profiles from normal individuals.

This example demonstrates the use of the claimed invention to detect differential gene expression in blood samples taken from patients with obesity as compared to blood samples taken from healthy patients.

As used herein, “obesity” is defined as an excess of adipose tissue that imparts a health risk. Obesity is assessed in terms of height and weight in the relevance of age. Patients who are considered obese include, but are not limited to, patients having a body mass index or BMI ((defined as body weight in kg divided by (height in meters)²) greater than or equal to 30.0. Patients having obesity as defined herein are those with a BMI of greater than or equal to 30.0.

Blood samples were taken from patients who were diagnosed with osteoarthritis and obesity as defined herein. Gene expression profiles were then analyzed and compared to profiles from patients unaffected by any disease. In each case, the diagnosis of the disease was corroborated by a skilled Board certified physician. Total mRNA from a drop of peripheral whole blood taken from each patient was isolated using TRIzol® reagent (GIBCO) and fluorescently labeled probes for each blood sample were generated as described above. Each probe was denatured and hybridized to a 15K ChondroGene Microarray Chip (ChondroChip) as described herein. Identification of genes differentially expressed in blood samples from patients with disease as compared to healthy patients was determined by statistical analysis

using the Wilcoxon Mann Whitney rank sum test (Glantz SA. Primer of Biostatistics. 5th ed. New York, USA: McGraw-Hill Medical Publishing Division, 2002).

Figure 9 shows a diagrammatic representation of gene expression profiles of blood samples from individuals who were identified as obese as described herein as compared with gene expression profiles from normal individuals. Expression profiles were generated using GeneSpring software analysis as described herein. Each column represents the hybridization pattern resulting from a single individual. In this example, obese patients also presented with OA, as described herein. Normal individuals have no known medical conditions and were not taking any known medication. Hybridizations to create said gene expression profiles were done using the ChondroChip (version 2). A dendrogram analysis is shown above. Samples are clustered and marked as representing patients who are obese or normal. The "*" indicates those patients who abnormally clustered as either obese or normal despite presenting with the reverse. The number of hybridization profiles determined for obese patients and normal individuals are shown. 913 genes were identified as being differentially expressed with a p value of < 0.05 as between the obese patients and normal individuals is noted. The identity of the differentially expressed genes is shown in Table 3B.

EXAMPLE 12

ChondroChip Microarray Data Analysis of gene expression profiles of blood samples from individuals having osteoarthritis and allergies as compared with gene expression profiles from normal individuals

This example demonstrates the use of the claimed invention to detect differential gene expression in blood samples taken from patients with allergies as compared to blood samples taken from healthy patients.

As used herein, "allergies" encompasses diseases and conditions wherein a patient demonstrates a hypersensitive or allergic reaction to one or more substances or stimuli such as drugs, food stuffs, plants, animals etc. and as a result has an increased immune response. Such immune responses can include anaphylaxis, allergic rhinitis, asthma, skin sensitivity such as urticaria, eczema, and allergic contact dermatitis and ocular allergies such as allergic

conjunctivitis and contact allergy. Patients identified as having allergies includes patients having one or more of the above noted conditions.

Blood samples were taken from patients who were diagnosed with osteoarthritis and allergies as defined herein. Gene expression profiles were then analyzed and compared to profiles from patients unaffected by any disease. In each case, the diagnosis of osteoarthritis and allergies was corroborated by a skilled Board certified physician.

Total mRNA from a drop of peripheral whole blood taken from each patient was isolated using TRIzol® reagent (GIBCO) and fluorescently labeled probes for each blood sample were generated as described above. Each probe was denatured and hybridized to a 15K ChondroGene Microarray Chip (Chondrochip) as described herein. Identification of genes differentially expressed in blood samples from patients with osteoarthritis and allergies as compared to healthy patients was determined by statistical analysis using the Wilcoxon Mann Whitney rank sum test (Glantz SA. Primer of Biostatistics. 5th ed. New York, USA: McGraw-Hill Medical Publishing Division, 2002).

Figure 10 shows a diagrammatic representation of gene expression profiles of blood samples from individuals who were identified as having allergies as described herein as compared with gene expression profiles from normal individuals. Expression profiles were generated using GeneSpring software analysis as described herein. Each column represents the hybridization pattern resulting from a single individual. In this example, patients with allergies also presented with OA, as described herein. Normal individuals have no known medical conditions and were not taking any known medication. Hybridizations to create said gene expression profiles were done using the ChondroChip (version 2). A dendrogram analysis is shown above. Samples are clustered and marked as representing patients who are obese or normal. The "*" indicates those patients who abnormally clustered as either having allergies or being normal despite presenting with the reverse. The number of hybridizations profiles determined for patients with allergies and normal individuals are shown. 633 genes were identified as being differentially expressed with a p value of < 0.05 as between patients with allergies and normal individuals is noted. The identity of the differentially expressed genes is shown in Table 3C.

EXAMPLE 13

ChondroChip Microarray Data Analysis of gene expression profiles of blood samples from individuals having osteoarthritis and subject to systemic steroids as compared with gene
5 expression profiles from normal individuals

This example demonstrates the use of the claimed invention to detect differential gene expression in blood samples taken from patients subject to systemic steroids as compared to blood samples taken from healthy patients.

As used herein, "systemic steroids" indicates a person subjected to artificial levels of
10 steroids as a result of medical intervention. Such systemic steroids include birth control pills, prednisone, and hormones as a result of hormone replacement treatment. A person identified as having systemic steroids is one who is on one or more of the following treatment regimes.

Blood samples were taken from patients who were diagnosed with osteoarthritis and subject to systemic steroids as defined herein. Gene expression profiles were then analyzed
15 and compared to profiles from patients unaffected by any disease. In each case, the diagnosis of osteoarthritis and systemic steroids was corroborated by a skilled Board certified physician.

Total mRNA from a drop of peripheral whole blood taken from each patient was isolated using TRIzol® reagent (GIBCO) and fluorescently labeled probes for each blood
20 sample were generated as described above. Each probe was denatured and hybridized to the 15K ChondroGene Microarray Chip (Chondrochip) as described herein. Identification of genes differentially expressed in blood samples from patients with osteoarthritis and subject to systemic steroids as compared to healthy patients was determined by statistical analysis using the Wilcoxon Mann Whitney rank sum test (Glantz SA. Primer of Biostatistics. 5th ed.
25 New York, USA: McGraw-Hill Medical Publishing Division, 2002).

Figure 11 shows a diagrammatic representation of gene expression profiles of blood samples from individuals who were subject to systemic steroids as described herein as

compared with gene expression profiles from normal individuals. Expression profiles were generated using GeneSpring software analysis as described herein. Each column represents the hybridization pattern resulting from a single individual. In this example, patients taking systemic steroids also presented with OA, as described herein. Normal individuals have no known medical conditions and were not taking any known medication. Hybridizations to create said gene expression profiles were done using the ChondroChip (version 2). A dendrogram analysis is shown above. Samples are clustered and marked as representing patients who are taking systemic steroids or normal. The "*" indicates those patients who abnormally clustered as either systemic steroids or normal despite presenting with the reverse. The number of hybridizations profiles determined for patients with systemic steroids and normal individuals are shown. 605 genes were identified as being differentially expressed with a p value of < 0.05 as between patients with systemic steroids and normal individuals is noted. The identity of the differentially expressed genes is shown in Table 3D.

EXAMPLE 14

ChondroChip Microarray Data Analysis of gene expression profiles of blood samples from individuals having hypertension as compared with gene expression profiles from normal individuals

This example demonstrates the use of the claimed invention to detect differential gene expression in blood samples taken from patients with hypertension but without osteoarthritis as compared to blood samples taken from healthy patients.

As used herein, the term "hypertension" is defined as high blood pressure or elevated arterial pressure. Patients identified with hypertension herein include persons who have an increased risk of developing a morbid cardiovascular event and/or persons who benefit from medical therapy designed to treat hypertension. Patients identified with hypertension also can include persons having systolic blood pressure of >130 mm Hg or a diastolic blood pressure of >90 mm Hg or a person takes antihypertensive medication.

Blood samples were taken from patients who were diagnosed with hypertension as defined herein. Gene expression profiles were then analyzed and compared to profiles from

patients unaffected by any disease. In each case, the diagnosis of hypertension was corroborated by a skilled Board certified physician.

Total mRNA from a drop of peripheral whole blood taken from each patient was isolated using TRIzol® reagent (GIBCO) and fluorescently labeled probes for each blood sample were generated as described above. Each probe was denatured and hybridized to a 15K ChondroGene Microarray Chip (ChondroChip) as described herein. Identification of genes differentially expressed in blood samples from patients with hypertension as compared to healthy patients was determined by statistical analysis using the Wilcoxon Mann Whitney rank sum test (Glantz SA, Primer of Biostatistics, 5th ed. New York, USA: McGraw-Hill Medical Publishing Division, 2002).

Figure 12 shows a diagrammatic representation of gene expression profiles of blood samples from individuals having hypertension as compared with gene expression profiles from samples of both non-hypertensive and normal individuals. Expression profiles were generated using GeneSpring software analysis as described herein. Each column represents the hybridization pattern resulting from a single individual. Non-hypertensive individuals presented without hypertension, but may have presented with other medical conditions and may be under various treatment regimes. Normal individuals have no known medical conditions and were not taking any known medication. Hybridizations to create said gene expression profiles were done using the ChondroChip (version 2). A dendrogram analysis is shown above. Samples are clustered and marked as representing patients who are hypertensive, normal or non-hypertensive. The “*” indicates those patients who abnormally clustered as either hypertensive, non-hypertensive or normal despite actual presentation. The number of hybridizations profiles determined for hypertensive patients, non-hypertensive patients and normal individuals are shown. 1,993 genes identified as being differentially expressed with a p value of < 0.05 as between the hypertensive patients and the combined normal and non-hypertensive individuals is noted. The identity of the differentially expressed genes are shown in Table 3E.

EXAMPLE 15

Chondrochip Microarray Data Analysis of gene expression profiles of blood samples from individuals having obesity as compared with gene expression profiles from normal individuals

This example demonstrates the use of the claimed invention to detect differential gene
5 expression in blood samples taken from patients with obesity but without osteoarthritis as compared to blood samples taken from healthy patients.

As used herein, "obesity" is defined as an excess of adipose tissue that imparts a health risk. Obesity is assessed in terms of height and weight in the relevance of age. Patients who are considered obese include, but are not limited to, patients having a body mass
10 index or BMI ((defined as body weight in kg divided by (height in meters)²) greater than or equal to 30.0. Patients having obesity as defined herein are those with a BMI of greater than or equal to 30.0.

Blood samples were taken from patients who were diagnosed with hypertension as defined herein. Gene expression profiles were then analyzed and compared to profiles from
15 patients unaffected by any disease. In each case, the diagnosis of obesity was corroborated by a skilled Board certified physician.

Total mRNA from a drop of peripheral whole blood taken from each patient was isolated using TRIzol® reagent (GIBCO) and fluorescently labeled probes for each blood sample were generated as described above. Each probe was denatured and hybridized to a
20 (Chondrochip) as described herein. Identification of genes differentially expressed in blood samples from patients with obesity as compared to healthy patients was determined by statistical analysis using the Wilcoxon Mann Whitney rank sum test (Glantz SA. Primer of Biostatistics. 5th ed. New York, USA: McGraw-Hill Medical Publishing Division, 2002).

Figure 13 shows a diagrammatic representation of gene expression profiles of blood
25 samples from individuals who were identified as obese as described herein as compared with gene expression profiles from normal and non-obese individuals. Expression profiles were generated using GeneSpring software analysis as described herein. Each column represents the hybridization pattern resulting from a single individual. Normal individuals

have no known medical conditions and were not taking any known medication. Non-obese individuals presented without obesity, but may have presented with other medical conditions and may be under various treatment regimes. Hybridizations to create said gene expression profiles were done using the ChondroChip (version 2). A dendrogram analysis is shown above. Samples are clustered and marked as representing patients who are obese, normal or non-obese. The "*" indicates those patients who abnormally clustered as either obese, normal or non-obese despite actual presentation. The number of hybridizations profiles determined for obese patients, non-obese patients and normal individuals are shown. 1,147 genes were identified as being differentially expressed with a p value of < 0.05 as between the obese patients and the combination of normal and non-obese individuals is noted. The identity of the differentially expressed genes is shown in Table 3F.

EXAMPLE 16

Chondrochip Microarray Data Analysis of gene expression profiles of blood samples from individuals having type 2 diabetes as compared with gene expression profiles from normal individuals

This example demonstrates the use of the claimed invention to detect differential gene expression in blood samples taken from patients with type 2 diabetes but without osteoarthritis as compared to blood samples taken from healthy patients.

As used herein, "diabetes", or "diabetes mellitus" includes both "type 1 diabetes" (insulin-dependent diabetes (IDDM)) and "type 2 diabetes" (insulin-independent diabetes (NIDDM)). Both type 1 and type 2 diabetes characterized in accordance with Harrison's Principles of Internal Medicine 14th edition, as a person having a venous plasma glucose concentration $\geq 140\text{mg/dL}$ on at least two separate occasions after overnight fasting and venous plasma glucose concentration $\geq 200\text{mg/dL}$ at 2 h and on at least one other occasion during the 2-h test following ingestion of 75g of glucose. Patients identified as having type 2 diabetes as described herein are those demonstrating insulin-independent diabetes as determined by the methods described above.

Blood samples were taken from patients who were diagnosed with type II diabetes as defined herein. Gene expression profiles were then analyzed and compared to profiles from patients unaffected by any disease. In each case, the diagnosis of type II diabetes was corroborated by a skilled Board certified physician.

5 Total mRNA from a drop of peripheral whole blood taken from each patient was isolated using TRIzol® reagent (GIBCO) and fluorescently labeled probes for each blood sample were generated as described above. Each probe was denatured and hybridized to a 15K ChondroGene Microarray Chip (Chondrochip) as described herein. Identification of genes differentially expressed in blood samples from patients with type 2 diabetes as
10 compared to healthy patients was determined by statistical analysis using the Wilcoxon Mann Whitney rank sum test (Glantz SA. Primer of Biostatistics. 5th ed. New York, USA: McGraw-Hill Medical Publishing Division, 2002).

Figure 14 shows a diagrammatic representation of gene expression profiles of blood samples from individuals who were identified as having type 2 diabetes as described herein
15 as compared with gene expression profiles from normal and non-type 2 diabetes individuals. Expression profiles were generated using GeneSpring software analysis as described herein. Each column represents the hybridization pattern resulting from a single individual. Normal individuals have no known medical conditions and were not taking any known medication. Non-type 2 diabetes individuals presented without type 2 diabetes, but may have presented
20 with other medical conditions and may be under various treatment regimes. Hybridizations to create said gene expression profiles were done using the ChondroChip (version 2). A dendrogram analysis is shown above. Samples are clustered and marked as representing patients who have type 2 diabetes, are normal or do not have type 2 diabetes. The “*” indicates those patients who abnormally clustered despite actual presentation. The number
25 of hybridizations profiles determined for type 2 diabetes, non-type 2 diabetes and normal individuals are shown. 915 were identified as being differentially expressed with a p value of < 0.05 as between the type 2 diabetes patients and the combination of normal and non type 2 diabetes individuals is noted. The identity of the differentially expressed genes is shown in Table 3G.

EXAMPLE 17

Chondrochip Microarray Data Analysis of gene expression profiles of blood samples from individuals having hyperlipidemia as compared with gene expression profiles from normal individuals

5 This example demonstrates the use of the claimed invention to detect differential gene expression in blood samples taken from patients with hyperlipidemia but without osteoarthritis as compared to blood samples taken from healthy patients.

As used herein, "hyperlipidemia" is defined as an elevation of lipid protein profiles and includes the elevation of chylomicrons, very low-density lipoproteins (VLDL),
10 intermediate-density lipoproteins (IDL), low-density lipoproteins (LDL), and/or high-density lipoproteins (HDL) as compared with the general population. Hyperlipidemia includes hypercholesterolemia and/or hypertriglyceridemia. By hypercholesterolemia, it is meant elevated fasting plasma total cholesterol level of >200mg/dL, and/or LDL-cholesterol levels of >130mg/dL. A desirable level of HDL-cholesterol is > 60mg/dL. By
15 hypertriglyceridemia it is meant plasma triglyceride (TG) concentrations of greater than the 90th or 95th percentile for age and sex and can include, for example, TG > 160mg/dL as determined after an overnight fast.

Blood samples were taken from patients who were diagnosed with hyperlipidemia as defined herein. Gene expression profiles were then analyzed and compared to profiles from
20 patients unaffected by any disease. In each case, the diagnosis of hyperlipidemia was corroborated by a skilled Board certified physician.

Total mRNA from a drop of peripheral whole blood taken from each patient was isolated using TRIzol® reagent (GIBCO) and fluorescently labeled probes for each blood sample were generated as described above. Each probe was denatured and hybridized to a
25 15K Chondrogene Microarray Chip (Chondrochip) as described herein. Identification of genes differentially expressed in blood samples from patients with hyperlipidemia as compared to healthy patients was determined by statistical analysis using the Wilcoxon Mann

Whitney rank sum test (Glantz SA. Primer of Biostatistics. 5th ed. New York, USA: McGraw-Hill Medical Publishing Division, 2002).

Figure 15 shows a diagrammatic representation of gene expression profiles of blood samples from individuals who were identified as having hyperlipidemia as described herein as compared with gene expression profiles from normal and non-hyperlipidemia patients. Expression profiles were generated using GeneSpring software analysis as described herein. Each column represents the hybridization pattern resulting from a single individual. Normal individuals have no known medical conditions and were not taking any known medication. Non hyperlipidemia individuals presented without elevated cholesterol or elevated triglycerides but may have presented with other medical conditions and may be under various treatment regimes. Hybridizations to create said gene expression profiles were done using the ChondroChip (version2). A dendrogram analysis is shown above. Samples are clustered and marked as representing patients who have elevated lipids and/or cholesterol, are normal or do not have elevated lipids or cholesterol. The "*" indicates those patients who abnormally clustered as having either hyperlipidemia, normal or non-hyperlipidemia despite actual presentation. The number of hybridizations profiles determined for hyperlipidemia patients, non-hyperlipidemia patients and normal individuals are shown. 1,022 genes were identified as being differentially expressed with a p value of < 0.05 as between the patients with hyperlipidemia and the combination of normal and non hyperlipidemia individuals. The identity of the differentially expressed genes is shown in Table 3H.

EXAMPLE 18

Chondrochip Microarray Data Analysis of gene expression profiles of blood samples from individuals having lung disease as compared with gene expression profiles from normal individuals

This example demonstrates the use of the claimed invention to detect differential gene expression in blood samples taken from patients with lung disease but without osteoarthritis as compared to blood samples taken from healthy patients.

As used herein, "lung disease" encompasses any disease that affects the respiratory system and includes bronchitis, chronic obstructive lung disease, emphysema, asthma, lung cancer. Patients identified as having lung disease includes patients having one or more of the above noted conditions.

5 Blood samples were taken from patients who were diagnosed with lung disease as defined herein. Gene expression profiles were then analyzed and compared to profiles from patients unaffected by any disease. In each case, the diagnosis of lung disease was corroborated by a skilled Board certified physician.

Total mRNA from a drop of peripheral whole blood taken from each patient was
10 isolated using TRIzol® reagent (GIBCO) and fluorescently labeled probes for each blood sample were generated as described above. Each probe was denatured and hybridized to a 15K ChondroGene Microarray Chip (Chondrochip) as described herein. Identification of genes differentially expressed in blood samples from patients with lung disease as compared to healthy patients was determined by statistical analysis using the Wilcoxon Mann Whitney
15 rank sum test (Glantz SA. Primer of Biostatistics. 5th ed. New York, USA: McGraw-Hill Medical Publishing Division, 2002).

Figure 16 shows a diagrammatic representation of gene expression profiles of blood samples from individuals who were identified as having lung disease as described herein as compared with gene expression profiles from normal and non lung disease individuals.
20 Expression profiles were generated using GeneSpring software analysis as described herein. Each column represents the hybridization pattern resulting from a single individual. Normal individuals have no known medical conditions and were not taking any known medication. Non-lung disease individuals presented without lung disease, but may have presented with other medical conditions and may be under various treatment regimes. Hybridizations to
25 create said gene expression profiles were done using the ChondroChip (version 2). A dendrogram analysis is shown above. Samples are clustered and marked as representing patients who have lung disease, are normal or do not have lung disease. The "*" indicates those patients who abnormally clustered despite actual presentation. The number of hybridizations profiles determined for either the lung disease patients, non-lung disease
30 patients and normal individuals are shown. 596 genes were identified as being differentially

expressed with a p value of < 0.05 as between the lung disease patients and the combination of normal and non lung disease individuals is noted. The identity of the differentially expressed genes is shown in Table 3I.

EXAMPLE 19

- 5 Affymetrix U133A Chip Microarray Data Analysis of gene expression profiles of blood samples from individuals having bladder cancer as compared with gene expression profiles from normal individuals

This example demonstrates the use of the claimed invention to detect differential gene expression in blood samples taken from patients with bladder cancer but without osteoarthritis
10 as compared to blood samples taken from healthy patients.

As used herein, the term "cancer" or "carcinoma" is defined as a disease in which cells behave abnormally and includes; (i) cancers which originate from a single cell proliferating to form a clone of malignant cells, (ii) cancers wherein the growth of the cell is not regulated by normal biological and physical influences of the environment, (iii) anaplastic cancer, wherein
15 the cells lack normal coordinated cell differentiation and (iv) metastasis cancer, wherein the cells have the capacity for discontinuous growth and dissemination to other parts of the body. The diagnosis of cancer can include careful clinical assessment and/or diagnostic investigations including endoscopy, imaging, histopathology, cytology and laboratory studies.

As used herein, "bladder cancer" includes carcinomas that occur in the transitional
20 epithelium lining the urinary tract, starting at the renal pelvis and extending through the ureter, the urinary bladder, and the proximal two-thirds of the urethra. As used herein, patients diagnosed with bladder cancer include patients diagnosed utilizing any of the following methods or a combination thereof: urinary cytologic evaluation, endoscopic evaluation for the presence of malignant cells, CT (computed tomography), MRI (magnetic
25 resonance imaging) for metastasis status.

Blood samples were taken from patients who were diagnosed with bladder cancer as defined herein. Gene expression profiles were then analyzed and compared to profiles from

patients unaffected by any disease. In each case, the diagnosis of bladder cancer was corroborated by a skilled Board certified physician.

Total mRNA from a drop of peripheral whole blood taken from each patient was isolated using TRIzol® reagent (GIBCO) and fluorescently labeled probes for each blood sample were generated as described above. Each probe was denatured and hybridized to a Affymetrix U133A Chip as described herein. Identification of genes differentially expressed in blood samples from patients with bladder cancer as compared to healthy patients was determined by statistical analysis using the Wilcox Mann Whitney rank sum test (Glantz SA. Primer of Biostatistics. 5th ed. New York, USA: McGraw-Hill Medical Publishing Division, 2002).

Figure 17 shows a diagrammatic representation of gene expression profiles of blood samples from individuals who were identified as having bladder cancer as described herein as compared with gene expression profiles from non bladder cancer individuals. Expression profiles were generated using GeneSpring software analysis as described herein. Each column represents the hybridization pattern resulting from a single individual. Non bladder cancer individuals presented without bladder cancer, but may have presented with other medical conditions and may be under various treatment regimes. Hybridizations to create said gene expression profiles were done using the Affymetrix U1338 chip. A dendogram analysis is shown above. Samples are clustered and marked as representing patients who have bladder cancer, or do not have bladder cancer. The “*” indicates those patients who abnormally clustered as either bladder cancer, or non bladder cancer despite actual presentation. The number of hybridizations profiles determined for patients with bladder cancer and without bladder cancer are shown. 4,228 genes were identified as being differentially expressed with a p value of < 0.05 as between the bladder cancer patients and the non bladder cancer individuals is noted. The identity of the differentially expressed genes is shown in Table 3J.

EXAMPLE 20

Affymetrix U133A Chip Microarray Data Analysis of gene expression profiles of blood samples from individuals having early or advanced bladder cancer as compared with gene expression profiles from normal individuals

5 This example demonstrates the use of the claimed invention to detect differential gene expression in blood samples taken from patients with early or advanced late stage bladder cancer but without osteoarthritis as compared to blood samples taken from healthy patients.

As used herein, "early stage bladder cancer" includes bladder cancer wherein the detection of the anatomic extent of the tumor, both in its primary location and in metastatic
10 sites, as defined by the TNM staging system in accordance with Harrison's Principles of Internal Medicine 14th edition can be considered early stage. More specifically, early stage bladder cancer can include those instances wherein the carcinoma is mainly superficial.

As used herein, "advanced stage bladder cancer" is defined as bladder cancer wherein the detection of the anatomic extent of the tumor, both in its primary location and in
15 metastatic sites, as defined by the TNM staging system in accordance with Harrison's Principles of Internal Medicine 14th edition, can be considered as advanced stage. More specifically, advanced stage carcinomas can involve instances wherein the cancer has infiltrated the muscle and wherein metastasis has occurred.

Blood samples were taken from patients who were diagnosed with early or advanced
20 late stage bladder cancer as defined herein. Gene expression profiles were then analyzed and compared to profiles from patients unaffected by any disease. In each case, the diagnosis of early or advanced late stage bladder cancer was corroborated by a skilled Board certified physician.

Total mRNA from a drop of peripheral whole blood taken from each patient was
25 isolated using TRIzol® reagent (GIBCO) and fluorescently labeled probes for each blood sample were generated as described above. Each probe was denatured and hybridized to a Affymetrix U133A Chip as described herein. Identification of genes differentially expressed in blood samples from patients with early or advanced late stage bladder cancer as compared

to healthy patients was determined by statistical analysis using the Wilcoxon Mann Whitney rank sum test (Glantz SA. Primer of Biostatistics. 5th ed. New York, USA: McGraw-Hill Medical Publishing Division, 2002).

Figure 18 shows a diagrammatic representation of gene expression profiles of blood samples from individuals who were identified as having advanced stage bladder cancer or early stage bladder cancer as described herein as compared with gene expression profiles from non bladder cancer individuals. Expression profiles were generated using GeneSpring software analysis as described herein. Each column represents the hybridization pattern resulting from a single individual. Non bladder cancer individuals presented without bladder cancer, but may have presented with other medical conditions and may be under various treatment regimes. Hybridizations to create said gene expression profiles were done using the Affymetrix U1338 chip. A dendrogram analysis is shown above. Samples are clustered and marked as representing patients who have early stage bladder cancer, advanced stage bladder cancer, or do not have bladder cancer. The "*" indicates those patients who abnormally clustered despite actual presentation. The number of hybridizations profiles determined for either early stage bladder cancer, advanced bladder cancer or non-bladder cancer are shown. 3,518 genes were identified as being differentially expressed with a p value of < 0.05 as between the bladder cancer patients and the non bladder cancer individuals is noted. The identity of the differentially expressed genes is shown in Table 3K.

20

EXAMPLE 21

Affymetrix U133A Chip Microarray Data Analysis of gene expression profiles of blood samples from individuals having coronary artery disease as compared with gene expression profiles from normal individuals

This example demonstrates the use of the claimed invention to detect differential gene expression in blood samples taken from patients with coronary artery disease but without osteoarthritis as compared to blood samples taken from healthy patients

As used herein, "Coronary artery disease" (CAD) is defined as a condition wherein at least one coronary artery has $>50\%$ luminal diameter stenosis, as diagnosed by coronary

angiography and includes conditions in which there is atheromatous narrowing and subsequent occlusion of the vessel. CAD includes those conditions which manifest as angina, silent ischaemia, unstable angina, myocardial infarction, arrhythmias, heart failure, and sudden death. Patients identified as having CAD herein Coronary artery disease is defined

5 Blood samples were taken from patients who were diagnosed with Coronary artery disease as defined herein. Gene expression profiles were then analyzed and compared to profiles from patients unaffected by any disease. In each case, the diagnosis of Coronary artery disease was corroborated by a skilled Board certified physician .

Total mRNA from a drop of peripheral whole blood taken from each patient was
10 isolated using TRIzol® reagent (GIBCO) and fluorescently labeled probes for each blood sample were generated as described above. Each probe was denatured and hybridized to a Affymetrix U133A Chip as described herein. Identification of genes differentially expressed in blood samples from patients with Coronary artery disease as compared to healthy patients was determined by statistical analysis using the Wilcoxon Mann Whitney rank sum test (Glantz
15 SA. Primer of Biostatistics. 5th ed. New York, USA: McGraw-Hill Medical Publishing Division, 2002).

Figure 19 shows a diagrammatic representation of gene expression profiles of blood samples from individuals who were identified as having coronary artery disease (CAD) as described herein as compared with gene expression profiles from non-coronary artery disease
20 individuals. Expression profiles were generated using GeneSpring software analysis as described herein. Each column represents the hybridization pattern resulting from a single individual. Non coronary artery disease individuals presented without coronary artery disease, but may have presented with other medical conditions and may be under various treatment regimes. Hybridizations to create said gene expression profiles were done using the
25 Affimetrix™ U1338 chip. A dendrogram analysis is shown above. Samples are clustered and marked as representing patients who have coronary artery disease or do not have coronary artery disease. The “*” indicates those patients who abnormally clustered despite actual presentation. The number of hybridizations profiles determined for patients with CAD or without CAD are shown. 967 genes were identified as being differentially expressed with a p

value of < 0.05 as between the coronary artery disease patients and those individuals without coronary artery disease is noted. The identity of the differentially expressed genes is shown in Table 3L.

EXAMPLE 22

- 5 Affymetrix U133A Chip Microarray Data Analysis of gene expression profiles of blood samples from individuals having Rheumatoid arthritis as compared with gene expression profiles from normal individuals

This example demonstrates the use of the claimed invention to detect differential gene expression in blood samples taken from patients with Rheumatoid arthritis but without
10 osteoarthritis as compared to blood samples taken from healthy patients

Rheumatoid arthritis (RA) is defined as a chronic, multisystem disease of unknown etiology with the characteristic feature of persistent inflammatory synovitis. Said inflammatory synovitis usually involves peripheral joints in a systemic distribution. Patients having RA as defined herein were identified as having one or more of the following;
15 (i) cartilage destruction, (ii) bone erosions and/or (iii) joint deformities.

Blood samples were taken from patients who were diagnosed Rheumatoid arthritis as defined herein. Gene expression profiles were then analyzed and compared to profiles from patients unaffected by any disease. In each case, the diagnosis of Rheumatoid arthritis was corroborated by a skilled Board certified physician .

20 Total mRNA from a drop of peripheral whole blood taken from each patient was isolated using TRIzol® reagent (GIBCO) and fluorescently labeled probes for each blood sample were generated as described above. Each probe was denatured and hybridized to a Affymetrix U133A Chip as described herein. Identification of genes differentially expressed in blood samples from patients with Rheumatoid arthritis as compared to healthy patients was
25 determined by statistical analysis using the Wilcoxon Mann Whitney rank sum test (Glantz SA. Primer of Biostatistics. 5th ed. New York, USA: McGraw-Hill Medical Publishing Division, 2002).

Figure 20 shows a diagrammatic representation of gene expression profiles of blood samples from individuals who were identified as having rheumatoid arthritis as described herein as compared with gene expression profiles from non-rheumatoid arthritis individuals. Expression profiles were generated using GeneSpring software analysis as described herein.

5 Each column represents the hybridization pattern resulting from a single individual. Normal individuals have no known medical conditions and were not taking any known medication. Non rheumatoid arthritis individuals presented without rheumatoid arthritis, but may have presented with other medical conditions and may be under various treatment regimes. Hybridizations to create said gene expression profiles were done using ChondroChip
10 (version2). A dendogram analysis is shown above. Samples are clustered and marked as representing patients who have rheumatoid arthritis or do not have rheumatoid arthritis. The “*” indicates those patients who abnormally clustered despite actual presentation. The number of hybridizations profiles determined for patients with rheumatoid arthritis and without rheumatoid arthritis are shown: 2,068 genes were identified as being differentially expressed
15 with a p value of < 0.05 as between the rheumatoid arthritis patients and a combination of those individuals without rheumatoid arthritis and normal is noted. The identity of the differentially expressed genes is shown in Table 3M.

EXAMPLE 23

20 Affymetrix U133A Chip Microarray Data Analysis of gene expression profiles of blood samples from individuals having depression as compared with gene expression profiles from normal individuals

This example demonstrates the use of the claimed invention to detect differential gene expression in blood samples taken from patients with depression but without osteoarthritis as
25 compared to blood samples taken from healthy patients

As used herein “mood disorders” are conditions characterized by a disturbance in the regulation of mood, behaviour, and affect. “Mood disorders” can include depression, anxiety, schizophrenia, bipolar disorder, manic depression and the like.

As used herein "depression" includes depressive disorders or depression in association with medical illness or substance abuse in addition to depression as a result of sociological situations. Patients defined as having depression were diagnosed mainly on the basis of clinical symptoms including a depressed mood episode wherein a person displays a depressed mood on a daily basis for a period of greater than 2 weeks. A depressed mood episode may be characterized by sadness, indifference, apathy, or irritability and is usually associated with changes in a number of neurovegetative functions, including sleep patterns, appetite and weight, fatigue, impairment in concentration and decision making.

Blood samples were taken from patients who were diagnosed with depression as defined herein. Gene expression profiles were then analyzed and compared to profiles from patients unaffected by any disease. In each case, the diagnosis of depression was corroborated by a skilled Board certified physician.

Total mRNA from a drop of peripheral whole blood taken from each patient was isolated using TRIzol® reagent (GIBCO) and fluorescently labeled probes for each blood sample were generated as described above. Each probe was denatured and hybridized to a Affymetrix U133A Chip as described herein. Identification of genes differentially expressed in blood samples from patients with depression as compared to healthy patients was determined by statistical analysis using the Wilcoxon Mann Whitney rank sum test (Glantz SA. Primer of Biostatistics. 5th ed. New York, USA: McGraw-Hill Medical Publishing Division, 2002).

Figure 21 shows a diagrammatic representation of gene expression profiles of blood samples from individuals who were identified as having depression as described herein as compared with gene expression profiles from non-depression individuals. Expression profiles were generated using GeneSpring software analysis as described herein. Each column represents the hybridization pattern resulting from a single individual. Normal individuals have no known medical conditions and were not taking any known medication. Non depression individuals presented without depression, but may have presented with other medical conditions and may be under various treatment regimes. Hybridizations to create said gene expression profiles were done using ChondroChip (version2). A dendrogram analysis is shown above. Samples are clustered and marked as representing patients who have

depression, having non-depression or normal. The "*" indicates those patients who abnormally clustered despite actual presentation. The number of hybridizations profiles determined for patients with depression, non-depression and normal are shown. 941 genes were identified as being differentially expressed with a p value of < 0.05 as between the patients with depression and a combination of those individuals without depression and normal is noted. The identity of the differentially expressed genes is shown in Table 3N.

EXAMPLE 24

ChondroChip Microarray Data Analysis of gene expression profiles of blood samples from individuals having osteoarthritis as compared with gene expression profiles from normal individuals.

This example demonstrates the use of the claimed invention to detect differential gene expression in blood samples taken from patients who were identified as having various stages of osteoarthritis as compared to blood samples taken from healthy patients.

Osteoarthritis (OA), as used herein also known as "degenerative joint disease", represents failure of a diarthrodial (movable, synovial-lined) joint. It is a condition, which affects joint cartilage, and or subsequently underlying bone and supporting tissues leading to pain, stiffness, movement problems and activity limitations. It most often affects the hip, knee, foot, and hand, but can affect other joints as well.

OA severity can be graded according to the system described by Marshall (Marshall KW. J Rheumatol, 1996;23(4):582-85). Briefly, each of the six knee articular surfaces was assigned a cartilage grade with points based on the worst lesion seen on each particular surface. Grade 0 is normal (0 points), Grade I cartilage is soft or swollen but the articular surface is intact (1 point). In Grade II lesions, the cartilage surface is not intact but the lesion does not extend down to subchondral bone (2 points). Grade III damage extends to subchondral bone but the bone is neither eroded nor eburnated (3 points). In Grade IV lesions, there is eburnation of or erosion into bone (4 points). A global OA score is calculated by summing the points from all six cartilage surfaces. If there is any associated pathology, such as meniscus tear, an extra point will be added to the global score. Based on the total

score, each patient is then categorized into one of four OA groups: mild (1-6), moderate (7-12), marked (13-18), and severe (>18). As used herein, patients identified with OA may be categorized in any of the four OA groupings as described above.

5 Blood samples were taken from patients who were diagnosed with osteoarthritis as defined herein. Gene expression profiles were then analyzed and compared to profiles from patients unaffected by any disease. In each case, the diagnosis of osteoarthritis was corroborated by a skilled Board certified physician.

10 Total mRNA from a drop of peripheral whole blood taken from each patient was isolated using TRIzol® reagent (GIBCO) and fluorescently labeled probes for each blood sample were generated as described above. Each probe was denatured and hybridized to a 15K ChondroGene Microarray Chip (Chondrochip) as described herein. Identification of genes differentially expressed in blood samples from patients with disease as compared to healthy patients was determined by statistical analysis using the Wilcoxon Mann Whitney rank sum test (Glantz SA. Primer of Biostatistics. 5th ed. New York, USA: McGraw-Hill Medical
15 Publishing Division, 2002).

Figure 22 shows a diagrammatic representation of gene expression profiles of blood samples from individuals having osteoarthritis as compared with gene expression profiles from normal individuals. Expression profiles were generated using GeneSpring software analysis as described herein. Each column represents the hybridization pattern resulting from
20 a single individual. Normal individuals have no known medical conditions and were not taking any known medication. Hybridizations to create said gene expression profiles were done using the ChondroChip (version 2). A dendrogram analysis is shown above. Samples are clustered and marked as representing patients who presented with different stages of osteoarthritis or normal. The “*” indicates those patients who abnormally clustered despite
25 actual presentation. The number of hybridizations profiles determined for either osteoarthritis patients or normal individuals are shown. 300 differentially expressed genes were identified as being differentially expressed with a p value of < 0.05 as between the osteoarthritis patients and normal individuals. The identity of the differentially expressed genes is shown in Table 30.

EXAMPLE 25

Microarray Data Analysis of gene expression profiles of blood samples from individuals undergoing therapeutic treatment as compared with gene expression profiles from individuals not undergoing treatment

5 This example demonstrates the use of the claimed invention to detect differential gene expression in blood samples taken from individuals undergoing therapeutic treatment as compared with gene expression profiles from individuals not undergoing treatment.

 Blood samples are taken from patients who are undergoing therapeutic treatment. Gene expression profiles are then analyzed and compared to profiles from patients not
10 undergoing treatment.

 Total mRNA from a drop of peripheral whole blood taken from each patient is isolated using TRIzol® reagent (GIBCO) and fluorescently labeled probes for each blood sample are generated as described above. Each probe is denatured and hybridized to a microarray for example the 15K Chondrogene Microarray Chip (Chondrochip), Affymetrix Genechip or
15 Blood chip as described herein. Identification of genes differentially expressed in blood samples from patients undergoing therapeutic treatment as compared to patients not undergoing treatment is determined by statistical analysis using the Wilcoxon Mann Whitney rank sum test (Glantz SA. Primer of Biostatistics. 5th ed. New York, USA: McGraw-Hill Medical Publishing Division, 2002). Expression profiles are generated using GeneSpring
20 software analysis as described herein. The number of differentially expressed genes are then identified as being differentially expressed with a p value of < 0.05 .

 All patents, patent applications, and published references cited herein are hereby incorporated by reference in their entirety. While this invention has been particularly shown and described with references to preferred embodiments thereof, it will be understood by
25 those skilled in the art that various changes in form and details may be made therein without departing from the scope of the invention encompassed by the appended claims.

 One skilled in the art will appreciate readily that the present invention is well adapted to carry out the objects and obtain the ends and advantages mentioned, as well as those

objects, ends and advantages inherent herein. The present examples, along with the methods, procedures, treatments, molecules, and specific compounds described herein are presently representative of preferred embodiments, are exemplary, and are not intended as limitations on the scope of the invention. Changes therein and other uses will occur to those skilled in the art which are encompassed within the spirit of the invention as defined by the scope of the claims.

TABLE 2

Comparison of 1,800 Unique Genes Identified in the Blood Cell cDNA Library to Genes Previously Identified in Specific Tissues

| Gene Identification | No. of ESTs | Accession No. | Tissue Distribution | | | | | |
|---|-------------|---------------|---------------------|----|---|---|----|----|
| | | | Bl | Br | H | K | Li | Lu |
| 100 kDa coactivator | 2 | U22055 | | + | | | | + |
| 10kD protein (BC10) | 2 | AF053470 | | + | + | | + | + |
| 14-3-3 epsilon | 2 | U54778 | | + | + | | | + |
| 14-3-3 protein | 11 | U28964 | | + | + | | + | |
| 15 kDa selenoprotein (SEP15) | 1 | AF051894 | | + | + | | | + |
| 1-phosphatidylinositol-4-phosphate 5-kinase isoform C | 1 | S78798 | | | | | | |
| 23 kD highly basic protein | 21 | X56932 | + | + | + | + | + | + |
| 2-5A-dependent RNase | 1 | L10381 | | | | | | |
| 2'-5'oligoadenylate synthetase 2 (OAS2) | 4 | M87284 | B | | | | | |
| 26S proteasome subunit 11 | 1 | AF086708 | | | | | | |
| 36 kDa phosphotyrosine protein | 2 | AJ223280 | T | | + | | | |
| 3-7 gene product (non-exact 86%aa) | 1 | D64159 | | | | | | |
| 3-phosphoglycerate dehydrogenase (PGAD) | 1 | AF006043 | T | + | + | | | + |
| 3-prime-phosphoadenosine 5-prime-phosphosulfate synthase 1 (PAPSS1) | 2 | U53447 | + | + | + | + | | + |
| 46kd mannose 6-phosphate receptor (MPR46) (low match) | 1 | X56257 | | | | | | |
| 5-aminoimidazole-4-carboxamide ribonucleotide | 1 | D89976 | | | | | | |

| | | | | | | | | | |
|---|----|----------|----------------|---|---|---|---|---|---|
| transformylase | | | | | | | | | |
| 5'-nucleotidase | 3 | D38524 | T | + | | | | + | |
| 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4 (PFKFB4) | 1 | D49818 | | + | | | | | |
| 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (PF2K) | 1 | AF041829 | | | | | | | |
| 71 kd heat shock cognate protein hsc70 | 23 | Y00371 | | | | | | | |
| 76 kDa membrane protein (P76) | 2 | U81006 | | + | + | + | + | + | |
| 8-oxoguanine DNA glycosylase (OGG1) | 1 | U96710 | B | | | | | + | + |
| a disintegrin and metalloprotease domain 10 (ADAM10) | 1 | AF009615 | T | | | | | + | |
| a disintegrin and metalloprotease domain 8 (ADAM8) | 1 | D26579 | B | + | | | | | |
| A kinase anchor protein 95 (AKAP95) | 2 | Y11997 | B, T activated | | + | | | | + |
| A kinase anchor protein, 149kD (AKAP149) | 2 | X97335 | | + | + | + | | | + |
| A4 differentiation-dependent protein (A4), triple LIM domain protein (LMO6), and synaptophysin (SYP); calcium channel alpha-1 subunit (CACNA1F) | 1 | U93305 | | | | | | | |
| ABL and putative M8604 Met protein | 1 | U07561 | | | | | | | |
| Absent in melanoma 1 (AIM1) | 1 | U83115 | + | + | | | | | + |
| accessory proteins BAP31/BAP29 (DXS1357E) | 2 | Z31696 | | + | + | | | | |
| acetyl-Coenzyme A acyltransferase (peroxisomal 3-oxoacyl-Coenzyme A thiolase) | 2 | X12966 | + | + | + | + | + | + | |

| | | | | | | | | | | |
|--|-----|----------|------------|---|---|---|---|---|---|------------------------|
| (ACAA) | | | | | | | | | | |
| acetyl-Coenzyme A transporter (ACATN) | 1 | D88152 | T lymphoma | + | + | | | | | |
| acidic 82 kDa protein | 4 | U15552 | | | | | | | | |
| acidic protein rich in leucines (SSP29) | 1 | Y07969 | B | + | + | | + | + | | |
| Aconitase 2, mitochondrial (ACO2) | 1 | U80040 | + | + | + | + | | + | | |
| actin binding protein MAYVEN | 1 | AF059569 | | | | | | | | |
| actin, beta (ACTB) | 158 | X04098 | T, B | + | + | | + | | | |
| actin, beta (ACTB) (non-exact, low match 73%) | 1 | M10277 | | | | | | | | |
| actin, gamma (low score) | 1 | K00791 | | | | | | | | |
| actin, gamma 1 (ACTG1) | 4 | X04098 | + | + | + | + | + | + | | high in many libraries |
| actin-binding LIM protein (ABLIM) | 4 | D31883 | | + | + | + | | + | | |
| Actinin, alpha 1 (ACTN1) | 8 | M95178 | | + | + | + | | + | | |
| actinin, alpha 4 (ACTN4) | 1 | D89980 | | + | + | | + | | | |
| activated p21cdc42Hs kinase (ACK) | 1 | L13738 | B | + | | | | + | | |
| activated RNA polymerase II transcription cofactor 4 (PC4) | 1 | X79805 | + | + | + | + | | + | | |
| activating transcription factor 1 (ATF1) | 1 | X55544 | | | + | | | | | |
| activating transcription factor 2 (ATF2) | 1 | X15875 | | + | + | | + | | | |
| activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4) | 2 | M86842 | | | | | | + | + | |
| active BCR-related gene (ABR) | 1 | U01147 | + | + | + | + | | + | | |
| acyl-CoA oxidase (AOX) | 1 | U03254 | | | | | | | | |

| | | | | | | | | | |
|--|---|----------|------|---|---|---|---|---|--|
| acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain (ACADM) | 2 | M16827 | | | | | | | |
| acyl-Coenzyme A dehydrogenase, very long chain (ACADVL) | 3 | D43682 | + | + | + | + | + | + | |
| acyloxyacyl hydrolase (neutrophil) (AOAH) | 3 | M62840 | T | | + | | + | + | |
| adaptin, delta (ADTD) | 2 | U91930 | | + | + | | + | | |
| adaptin, delta (ADTD) (non-exact 59%) | 1 | AC005328 | | | | | | | |
| adaptin, gamma (ADTG) | 1 | Y12226 | | + | + | + | | + | |
| adaptor complex sigma3B (AP3S3) | 2 | X99459 | | + | | + | | + | |
| adaptor protein p150 | 1 | Y08991 | | | | | | | |
| adducin 1 (alpha) (ADD1) | 2 | L07261 | | + | + | | + | | |
| adducin 1 (alpha) (add1) | 3 | L29296 | + | + | + | + | | + | |
| adducin 3 (gamma) (ADD3) | 3 | U37122 | B, W | + | + | | + | + | |
| adenine nucleotide translocator 2 (fibroblast) (ANT2) | 2 | M57424 | | + | + | | + | | |
| adenine nucleotide translocator 2 (fibroblast) (ANT2) (non-exact 81%) | 1 | J02683 | | | | | | | |
| adenine nucleotide translocator 2 (fibroblast) (ANT2) (non-exact, 79%) | 1 | J02683 | | | | | | | |
| adenine nucleotide translocator 2 (fibroblast) (ANT2) (non-exact, 86%) | 1 | J02683 | | | | | | | |
| adenine nucleotide translocator 3 (liver) (ANT3) | 3 | J03592 | | + | + | | + | + | |
| adenosine deaminase, RNA-specific (ADAR) | 6 | U18121 | | + | + | | + | | |
| adenylate cyclase 3 (ADCY3) | 2 | AF033861 | | + | + | + | + | + | |

| | | | | | | | | | |
|--|----|----------|------------|---|---|---|---|---|--|
| adenylate cyclase 7 (ADCY7) | 1 | D25538 | | | | | | | |
| adenylate kinase 2 (AK2) | 2 | U39945 | | + | + | | + | + | |
| adenylate kinase 3 (AK3) (non-exact, 67%) | 1 | X60673 | | | | | | | |
| adenylyl cyclase-associated protein (CAP) | 28 | M98474 | T | | + | | + | | |
| adipose differentiation-related protein; adipophilin (ADFP) | 1 | X97324 | | | + | | + | + | |
| ADP-ribosylation factor 1 (ARF1) | 13 | M84326 | | + | + | | + | + | |
| ADP-ribosylation factor 3 (ARF3) | 2 | M33384 | | + | + | | + | | |
| ADP-ribosylation factor 4 (ARF4) | 1 | M36341 | T lymphoma | + | + | | | + | |
| ADP-ribosylation factor 5 (ARF5) | 1 | M57567 | | | + | + | + | + | |
| ADP-ribosylation factor domain protein 1, 64kD (ARFD1) | 1 | L04510 | | + | | | | | |
| ADP-ribosyltransferase (NAD ⁺ ; poly (ADP-ribose) polymerase) (ADPRT) | 4 | M32721 | + | + | + | + | + | + | |
| adrenergic, beta, receptor kinase 1 (ADRBK1) | 2 | X61157 | B | + | | | + | | |
| adrenoleukodystrophy-like 1 (ALDL1) | 1 | AJ000327 | | | | | | | |
| AE-binding protein 1 (AEBP1) (non-exact, 62%) | 1 | D86479 | | | | | | | |
| AF-17 | 1 | U07932 | | | | | | | |
| A-gamma-globin | 1 | V00514 | | | | | | | |
| A-gamma-globin (chromosome 11 allele) | 1 | J00176 | | | | | | | |
| agammaglobulinaemia tyrosine kinase (ATK) | 1 | U78027 | | | | | | | |
| AHNAK nucleoprotein | 4 | M80899 | + | + | + | + | | + | |

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|--|---|----------|---|---|---|---|---|---|--|
| (desmoyokin) (AHNAK) | | | | | | | | | |
| alanyl (membrane) aminopeptidase (aminopeptidase N, aminopeptidase M, microsomal aminopeptidase, CD13, p150) (ANPEP) | 1 | X13276 | | | + | | + | | |
| alcohol dehydrogenase 5 (class III), chi polypeptide (ADH5) | 1 | M29872 | | | | | | | |
| aldehyde dehydrogenase 1, soluble (ALDH1) | 1 | AF003341 | | + | | | + | + | |
| aldehyde dehydrogenase 10 (fatty aldehyde dehydrogenase) (ALDH10) | 2 | U75286 | | | | | | | |
| aldehyde reductase 1 (low Km aldose reductase) (ALDR1) | 3 | J04795 | B | + | + | + | + | | |
| aldo-keto reductase family 1, member A1 (aldehyde reductase) (AKR1A1) | 2 | J04794 | B | + | + | | + | | |
| aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, type II) (AKR1C3) | 1 | D17793 | | + | + | + | | + | |
| aldo-keto reductase family 7, member A2 (aflatoxin aldehyde reductase) (AKR7A2) | 1 | Y16675 | | + | + | | + | + | |
| aldolase A, fructose-bisphosphate (ALDOA) | 7 | X12447 | | + | + | | + | | |
| aldolase C, fructose-bisphosphate (ALDOC) | 2 | X05196 | | + | + | | + | | |
| alkaline phosphatase, liver/bone/kidney (ALPL) | 1 | 4502062 | | | | | | | |
| ALL-1 (=L04731;L04284 HRX) | 4 | Z69780 | | | | | | | |
| alpha mannosidase II isozyme | 1 | D55649 | | + | | | + | | |
| alpha thalassemia/mental retardation syndrome X- | 3 | U75653 | + | + | + | + | | + | |

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|---|---|----------|---|---|---|---|---|---|--|
| linked (ATRX) | | | | | | | | | |
| alpha-2-macroglobulin | 1 | Z11711 | | | | | | | |
| alpha-2-globin | 2 | V00516 | | | | | | | |
| alpha-2-macroglobulin receptor/lipoprotein receptor protein (A2MR/LRP) | 1 | U06985 | | | | | | | |
| alpha-polypeptide of N-acetyl-alpha-glucosaminidase (HEXA) | 1 | M13520 | | | | | | | |
| alpha-spectrin | 1 | X86901 | | | | | | | |
| alpha-subunit of Gi2 a (GTP-binding signal transduction protein) | 1 | X07854 | | | | | | | |
| aminin receptor 1 (67kD); Ribosomal protein SA (LAMR1) | 2 | J03799 | T | + | + | | + | + | |
| aminolevulinatase, delta-, dehydratase (ALAD) | 1 | X64467 | | + | | | | | |
| amino-terminal enhancer of split (AES) | 2 | X73358 | + | + | + | + | | + | |
| amino-terminal enhancer of split (AES) | 3 | U04241 | B | + | + | | + | + | |
| AMP deaminase isoform L (AMPD2) | 8 | M91029 | | + | | | | + | |
| amphiphysin (Stiff-Mann syndrome with breast cancer 128kD autoantigen) (AMPH) | 1 | U07616 | B | + | | | | + | |
| amphiphysin (Stiff-Mann syndrome with breast cancer 128kD autoantigen) (AMPH)(non-exact, 68%) | 1 | U07616 | | | | | | | |
| amphiphysin (Stiff-Mann syndrome with breast cancer 128kD autoantigen) (AMPH)(non-exact, 68%) | 1 | U07616 | | | | | | | |
| amphiphysin II | 4 | U87558 | | + | + | | + | | |
| amphiphysin II (67%aa amphiphysin?) | 1 | AF068915 | | | | | | | |

| | | | | | | | | | |
|---|---|----------|------------|---|---|---|---|---|-------------------------|
| amphiphysin II (non-exact 69% aa) | 1 | AF001383 | | | | | | | |
| amphiphysin-like (AMPHL) | 1 | U68485 | | + | + | | | | |
| amphiphysin-like (AMPHL) (low match) | 1 | AF068918 | | | | | | | |
| AMY-1 | 1 | D50692 | B, T | | | | + | | |
| amyloid beta (A4) precursor protein-binding, family B, member 1 (Fe65) (APBB1) | 1 | L77864 | | + | + | + | | + | |
| amyloid beta (A4) precursor-like protein 2 (APLP2) | 6 | L27631 | T lymphoma | + | + | | + | + | |
| ankyrin 3, node of Ranvier (ankyrin G) (ANK) (non-exact, 50%) | 1 | U43965 | | | | | | | |
| annexin I (lipocortin I) (ANX1) | 1 | X05908 | | + | + | + | | + | |
| annexin II | 1 | D28364 | | | | | | | |
| annexin II (lipocortin II; calpactin I, heavy polypeptide) (ANX2) | 7 | D00017 | + | + | + | + | + | + | high in many libraries. |
| annexin IV (placental anticoagulant protein II) (ANX4) | 1 | M19383 | | + | + | + | + | + | |
| annexin V (endonexin II) (ANX5) | 2 | M21731 | | + | + | + | | + | |
| annexin V (endonexin II) (ANXV) | 1 | M19384 | | + | + | + | | + | |
| annexin VI (p68) (ANX6) | 6 | Y00097 | | + | + | + | | + | |
| annexin VII (synexin) (ANX7) | 1 | J04543 | | + | + | + | | + | |
| antigen identified by monoclonal antibodies 12E7, F21 and O13 (MIC2) | 2 | M16279 | | + | + | + | | + | |
| antigen identified by monoclonal antibodies 4F2, TRA1.10, TROP4, and T43 (MDU1) | 3 | J02939 | | + | + | + | + | + | |

| | | | | | | | | | |
|--|---|----------|-------------|---|---|---|---|---|--|
| antigen TQ1 | 1 | | | | | | | | |
| anti-oxidant protein 2 (non-selenium glutathione peroxidase, acidic calcium-independent phospholipase A2) (KIAA0106) | 1 | D14662 | | + | + | + | + | + | |
| APEX nuclease (multifunctional DNA repair enzyme) (APEX) | 5 | X66133 | | + | + | | + | + | |
| Apolipoprotein L (APOL) (59%aa) | 1 | Z82215 | | | | | | | |
| apoptosis inhibitor 1 (API1) | 1 | L49431 | | + | + | + | + | + | |
| apoptosis inhibitor 4 (survivin) (API4) | 1 | U75285 | B, W | + | + | | + | | |
| apoptosis inhibitor 5 (API5) | 1 | U83857 | T lymphoma | + | | | + | | |
| apoptosis specific protein (ASP) | 1 | Y11588 | B | + | | | + | + | |
| apoptotic protease activating factor (APAF1) | 1 | AF013263 | B | + | + | | + | | |
| aquaporin 3 (AQP3) | 1 | AB001325 | T | | | | + | | |
| aquaporin 9 (AQP9) | 7 | AB008775 | T activated | | | | + | | |
| arachidonate 12-lipoxygenase (ALOX12) | 1 | M58704 | T | | | | + | + | |
| arachidonate 5-lipoxygenase-activating protein (ALOX5AP) | 3 | X52195 | + | + | | + | | + | |
| ariadne homolog (ARI) | 1 | AJ009771 | + | + | + | + | | + | |
| ariadne-2 (D. melanogaster) homolog (all-trans retinoic acid inducible RING finger) (ARI2) | 1 | AF099149 | + | + | + | + | | + | |
| ARP1 (actin-related protein 1, yeast) homolog A (centractin alpha) (ACTR1A) | 1 | X82206 | | + | | | + | | |
| ARP2 (actin-related protein 2, yeast) homolog (ACTR2) | 9 | AF006082 | | + | + | | + | + | |

| | | | | | | | | | |
|--|----|----------|---------------------|---|---|---|---|---|--|
| ARP2/3 protein complex subunit 34 (ARC34) | 5 | AF006085 | T activated, W | + | + | | + | | |
| Arp2/3 protein complex subunit p41 (ARC41) | 6 | AF006084 | monocyte stimulated | + | + | | + | | |
| Arp2/3 protein complex subunit p41 (ARC41)) (low match) | 1 | AF006084 | | | | | | | |
| Arp2/3 protein complex subunit p16 (ARC16) | 20 | AF017807 | | + | + | | + | + | |
| Arp2/3 protein complex subunit p20 (ARC20) | 2 | AF006087 | | + | + | | + | + | |
| Arp2/3 protein complex subunit p21 (ARC21) | 3 | AF006086 | W | | | | + | + | |
| ARP3 (actin-related protein 3, yeast) homolog (ACTR3) | 11 | AF006083 | W | | + | | + | + | |
| arrestin, beta 2 (ARRB2) | 1 | AF106941 | B, T, W | + | + | | + | | |
| arsA (bacterial) arsenite transporter, ATP-binding, homolog 1 (ASNA1) | 1 | AF047469 | B, T | + | | | + | | |
| aryl hydrocarbon receptor nuclear translocator-like (ARNTL) | 2 | AF044288 | B | + | + | | + | | |
| aryl hydrocarbon receptor-interacting protein (AIP) | 1 | U31913 | + | + | + | + | | + | |
| arylsulfatase A (ARSA) | 1 | X52151 | T activated | + | | | + | | |
| asialoglycoprotein receptor 2 (ASGR2) | 1 | M11025 | | | | | + | + | |
| asparaginyl-tRNA synthetase (NARS) | 3 | D84273 | | + | + | | + | | |
| aspartyl-tRNA synthetase (DARS) | 1 | J05032 | B | + | + | | + | | |
| ataxia telangiectasia mutated (includes complementation groups A, C and D) (ATM) | 1 | U82828 | B, T | | + | | + | | |
| ataxin-2-like protein A2LP (A2LG) | 1 | AF034373 | B, T activated | + | + | | | + | |
| ATF6 | 1 | AF005887 | | + | | | + | | |

| | | | | | | | | | |
|--|---|----------|-------------|---|---|---|---|---|--|
| ATP binding cassette transporter (ABCR) (non-exact 80%) | 1 | U88667 | | | | | | | |
| ATP synthase (F1-ATPase) alpha subunit, mitochondrial | 1 | X59066 | | | | | | | |
| ATP synthase beta subunit gene | 1 | M19482 | | | | | | | |
| ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit b, isoform 1 (ATP5F1) | 1 | X60221 | + | + | + | + | | + | |
| ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 1 (ATP5G1) | 1 | X69907 | T activated | + | + | | + | + | |
| ATP synthase, H ⁺ transporting, mitochondrial F1 complex, alpha subunit, isoform 1, cardiac muscle (ATP5A1) | 3 | D14710 | | | | | | | |
| ATP synthase, H ⁺ transporting, mitochondrial F1 complex, alpha subunit, isoform 1, cardiac muscle (ATP5A1) (low match) | 1 | D14710 | | | | | | | |
| ATP synthase, H ⁺ transporting, mitochondrial F1 complex, beta polypeptide (ATP5B) | 2 | M27132 | | | | | | | |
| ATP synthase, H ⁺ transporting, mitochondrial F1 complex, gamma polypeptide 1 (ATP5C1) | 1 | D16563 | W | + | + | + | + | | |
| ATP synthase, H ⁺ transporting, mitochondrial F1F0, subunit g (ATP5JG) | 1 | AF092124 | + | + | + | + | + | + | |
| ATP/GTP-binding protein (HEAB) | 2 | U73524 | + | + | + | + | | + | |
| ATPase, Ca ⁺⁺ transporting, ubiquitous (ATP2A3) | 5 | Z69881 | | + | | | | | |
| ATPase, H ⁺ transporting, lysosomal (vacuolar proton | 2 | D89052 | + | + | + | + | | + | |

| | | | | | | | | | |
|--|---|----------|-------------|---|---|---|---|---|----------------|
| pump) 21kD (ATP6F) | | | | | | | | | |
| ATPase, H ⁺ transporting, lysosomal (vacuolar proton pump) 31kD (ATP6E) | 1 | X76228 | | + | + | + | | + | |
| ATPase, H ⁺ transporting, lysosomal (vacuolar proton pump) 42kD; Vacuolar proton-ATPase, subunit C; V-ATPase, subunit C (ATP6D) | 5 | X69151 | | + | + | + | | + | |
| ATPase, H ⁺ transporting, lysosomal (vacuolar proton pump), alpha polypeptide, 70kD, isoform 1 (ATP6A1) | 3 | L09235 | | + | | + | | | |
| ATPase, H ⁺ transporting, lysosomal (vacuolar proton pump), beta polypeptide, 56/58kD, isoform 2 (ATP6B2) | 6 | X62949 | + | + | + | + | | + | |
| ATPase, H ⁺ transporting, lysosomal (vacuolar proton pump), member J (ATP6J) | 2 | AF038954 | + | + | + | + | | + | high in testis |
| ATPase, H ⁺ transporting, lysosomal (vacuolar proton pump), subunit 1 (ATP6S1) | 1 | D16469 | | + | + | + | | + | |
| ATP-binding cassette 50 (TNF-alpha stimulated) (ABC50) | 1 | AF027302 | + | + | + | + | | + | |
| ATP-binding cassette protein M-ABC1 (mitochondrial) | 1 | AF047690 | | | | | | | |
| ATP-dependent RNA helicase | 1 | AJ010840 | T lymphoma | | + | | + | | |
| autoantigen (Hs.75528) | 2 | L05425 | T activated | | + | | | | |
| autoantigen (Hs.75528) (non-exact 84%) | 1 | L05425 | | | | | | | |
| autoantigen (Hs.75682) | 1 | U17474 | B | + | | | | + | |
| autoantigen La/SS-B | 1 | Z35127 | | | | | | | |
| axin (AXIN1) | 1 | AF009674 | T | + | | | | | |
| axonemal dynein heavy | 1 | AJ000522 | | | | | | + | |

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|--|----|----------|---|---|---|---|---|---|---|---------------------------------|
| chain (DNAH17) | | | | | | | | | | |
| BAI1-associated protein 3 (BAIAP3) (non-exact 54%) | 1 | AB017111 | | | | | | | | |
| basement membrane-induced gene (ICB1) | 1 | AF044896 | | | | | | | | |
| basic leucine zipper nuclear factor 1 (JEM-1) (BLZF1) | 2 | U79751 | | | | | | | | |
| basic transcription factor 3 (BTF3) | 5 | X74070 | + | + | + | + | + | + | | |
| basigin (BSG) | 1 | L10240 | | + | | | | + | | |
| BC-2 | 1 | AF042384 | B | | + | + | + | | | |
| B-cell CLL/lymphoma 6 (zinc finger protein 51) (BCL6) | 1 | U00115 | | + | + | | | | | |
| B-cell translocation gene 1, anti-proliferative (BTG) | 1 | X61123 | | | + | | | | + | |
| BCL2/adenovirus E1B 19kD-interacting protein 2 (BNIP2) | 1 | U15173 | B | + | | | | + | + | |
| BCL2/adenovirus E1B 19kD-interacting protein 3-like (BNIP3L) | 2 | AF067396 | | + | + | + | | | + | |
| beclin 1 (coiled-coil, myosin-like BCL2-interacting protein) (BECN1) | 1 | AF077301 | B | + | + | | | + | | |
| beta-1,2-N-acetylglucosaminyltransferase II (MGAT2) | 2 | U15128 | | | | | | | | |
| beta-2-microglobulin (B2M) | 63 | S82297 | + | + | + | + | + | + | | high in invasive prostate tumor |
| beta-hexosaminidase alpha chain (HEXA) | 1 | M16411 | | | | | | | | |
| beta-tubulin | 7 | V00599 | + | + | + | + | + | + | | high in many libraries |
| beta-tubulin (non-exact, 76%) | 1 | AF070561 | | | | | | | | |
| beta-tubulin, pseudogene | 1 | J00315 | | | | | | | | |

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|--|---|----------|---|---|---|---|---|---|--|
| BING4 | 1 | Z97184 | | | | | | | |
| biotinidase (BTD) (non-exact 62%) | 1 | U03274 | | | | | | | |
| biotinidase (BTD) (non-exact 70%) | 1 | U03274 | | | | | | | |
| biotinidase (BTD) (non-exact, 56%) | 1 | U03274 | | | | | | | |
| BIOTINIDASE PRECURSOR | 1 | P43251 | | | | | | | |
| biphenyl hydrolase-like (serine hydrolase) (BPHL) | 1 | X81372 | | + | | | + | | |
| bone marrow stromal cell antigen 1 (BST1) | 1 | D21878 | | | | | + | | |
| box-dependent myc-interacting protein isoform BIN1-10 (BIN1) | 1 | AF043900 | | | | | | | |
| box-dependent myc-interacting protein isoform BIN1-10 (BIN1) (non-exact, 64%) | 1 | AF043900 | | | | | | | |
| brain my047 protein | 1 | AF063605 | T | + | + | | + | | |
| branched chain keto acid dehydrogenase E1, alpha polypeptide (maple syrup urine disease) (BCKDHA) | 3 | Z14093 | T | + | + | | + | | |
| BRCA1 associated protein-1 (ubiquitin carboxy-terminal hydrolase) (BAP1) | 1 | D87462 | + | + | + | + | | | |
| BRCA1, Rho7 and vatl genes, and ipf35 | 1 | L78833 | | | | | | | |
| breakpoint cluster region protein, uterine leiomyoma, 1; barrier to autointegration factor (BCRP1) | 2 | AF044773 | | + | + | | | | |
| breakpoint cluster region protein, uterine leiomyoma, 2 (BCRP2) | 2 | AF044774 | | + | + | | + | + | |
| breast cancer anti-estrogen resistance 3 (BCAR3) (non-exact 73%) | 1 | U92715 | | | | | | | |

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|--|---|------------|---|---|---|---|--|---|---|--|
| bromodomain-containing protein, 140kD (peregrin) (BR140) | 2 | M91585 | | + | | | | | | |
| Bruton's agammaglobulinemia tyrosine kinase (Btk) | 1 | U13424 | | | | | | | | |
| Bruton's tyrosine kinase (BTK) | 1 | U78027 | | | | | | | | |
| Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) | 1 | U78027 | | | | | | | | |
| BS4 | 1 | AF108083 | | | | | | | | |
| BTG2 (BTG2) | 6 | Y09943 | + | + | + | + | | | + | |
| BTK region clone ftp | 1 | U78027 | + | + | + | + | | | + | |
| BTK region clone ftp-3 | 1 | U01923 | | + | + | | | + | | |
| BUB3 (budding uninhibited by benzimidazoles 3, yeast) homolog (BUB3) | 4 | AF053304 | + | + | + | + | | | + | |
| butyrate response factor 1 (EGF-response factor 1) (BRF1) | 4 | X79067 | + | + | + | + | | | + | |
| butyrophilin (BTF1) | 7 | U90543 | | + | + | | | + | | |
| butyrophilin like receptor | 1 | AB020625.1 | | | | | | | | |
| CAG repeat containing (CTG4A) | 2 | U80744 | | + | + | | | | | |
| CAGH32 | 2 | U80743 | | + | + | | | + | | |
| calcium channel, voltage-dependent, L type, alpha 1D subunit (CACNA1D) (low match) | 1 | M83566 | | | | | | | | |
| calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma (CAMK2G) | 1 | AF069765 | | + | + | + | | | + | |
| calcium/calmodulin-dependent protein kinase kinase (KIAA0787) | 1 | AF101264 | B | + | + | | | + | | |

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|--|---|----------|------|---|---|---|---|---|--|
| calmodulin (=M19311) | 7 | D45887 | | | | | | | |
| calmodulin 1 (phosphorylase kinase, delta) (CALM1) | 6 | M27319 | B | + | + | | + | + | |
| calnexin (CANX) | 3 | M94859 | T | + | | | + | + | |
| calpain, large polypeptide L1 (CAPN1) | 5 | X04366 | | + | + | | + | + | |
| calpain, large polypeptide L2 (CANP2) | 5 | M23254 | | + | + | | | | |
| calpain, small polypeptide (CAPN4) | 1 | X04106 | | + | + | | + | + | |
| calpastatin (CAST) | 3 | D16217 | | | | | + | | |
| Calponin 2 | 2 | D83735 | | + | | + | | + | |
| calponin 2 (CNN2) | 1 | D83735 | B, T | + | | | + | | |
| calponin 2 (CNN2) (low score) | 1 | D83735 | | | | | | | |
| calumenin (CALU) | 3 | AF013759 | B | | + | | + | + | |
| cAMP response element- binding protein CRE-Bpa (H_GS165L15.1) | 4 | L05912 | | | | | | | |
| cAMP-dependent protein kinase type II (Ht31) | 1 | M90360 | | | | | | | |
| canicular multispecific organic anion transporter (CMOAT2) | 1 | AF009670 | | | | + | + | + | |
| capping protein (actin filament) muscle Z-line, alpha 1 (CAPZA1) | 6 | U56637 | B, T | | + | | | + | |
| capping protein (actin filament) muscle Z-line, alpha 2 (CAPZA2) | 2 | U03269 | B | + | + | | | | |
| capping protein (actin filament) muscle Z-line, beta (CAPZB) | 1 | U03271 | + | + | + | + | | + | |
| capping protein (actin filament), gelsolin-like (CAPG) | 8 | M94345 | + | + | | + | | + | |

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|--|---|------------|----------------------------|---|---|---|---|---|--|
| carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase (CAD) | 1 | D78586 | + | + | + | + | | + | |
| carbonic anhydrase V, mitochondrial (CA5) | 1 | L19297 | | + | | | + | | |
| carboxypeptidase D (CPD) | 3 | U65090 | B | + | + | | | | |
| carnitine/acylcarnitine translocase (CACT) | 1 | Y10319 | | + | + | | + | | |
| Cas-Br-M (murine) ecotropic retroviral transforming sequence (cbl) | 2 | X57110 | | | | | + | | |
| casein kinase 1, alpha 1 (CSNK1A1) | 1 | L37042 | + | + | + | + | | + | |
| casein kinase 2, alpha 1 polypeptide (CSNK2A1) | 2 | M55265 | B | + | | | + | + | |
| casein kinase I gamma 3L (CSNK1G3L) | 1 | AF049090.1 | | | | | | | |
| casein kinase II alpha subunit(=S72393) | 1 | X69951 | | | | | | | |
| CASP8 and FADD-like apoptosis regulator (CFLAR) | 4 | AF015450 | | + | + | + | + | + | |
| caspase 1, apoptosis-related cysteine protease (interleukin 1, beta, convertase) (CASP1) | 7 | U13697 | + | | | + | | | |
| caspase 10, apoptosis-related cysteine protease (CASP10) | 1 | U60519 | B, T activated, T lymphoma | | | | + | | |
| caspase 3, apoptosis-related cysteine protease (CASP3) | 3 | U13737 | B, T | + | + | + | + | | |
| caspase 4, apoptosis-related cysteine protease (CASP4) | 6 | U25804 | + | + | + | + | | + | |
| caspase 5, apoptosis-related cysteine protease (CASP5) | 1 | U28015 | | | + | | | | |
| caspase 8, apoptosis-related cysteine protease | 2 | X98173 | | + | | + | | + | |

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|---|----|----------|------------------------------------|---|---|---|---|---|--|--|
| (CASP8) | | | | | | | | | | |
| caspase 9, apoptosis-related cysteine protease (CASP9) | 1 | U56390 | B | | | + | + | | | |
| catalase (CAT) | 5 | X04076 | B | + | + | | + | | | |
| catechol-O-methyltransferase (COMT) | 1 | M65213 | | + | + | | + | | | |
| catenin (cadherin-associated protein), alpha 1 (102kD) (CTNNA1) | 6 | D14705 | | + | + | | | | | |
| cathelicidin antimicrobial peptide (CAMP) | 1 | X89658 | B | | | | | | | |
| cathepsin B (CTSB) | 4 | L16510 | | | + | | + | + | | |
| cathepsin C (CTSC) | 3 | U79415 | | + | + | + | | + | | |
| cathepsin D (lysosomal aspartyl protease) (CTSD) | 4 | M11233 | | + | + | | + | | | |
| cathepsin E (CTSE) | 1 | J05036 | | | | | + | | | |
| cathepsin G (CTSG) | 1 | M16117 | T, W | | + | | | | | |
| cathepsin S (CTSS) | 34 | M86553 | B, Monocyte stimulated, T lymphoma | | | | + | + | | |
| cathepsin W (lymphopain) (CTSW) | 4 | AF013611 | | | | | | + | | |
| CBF1 interacting corepressor CIR (=U03644 recepin) | 1 | AF098297 | | | | | | | | |
| CCAAT/enhancer binding protein (C/EBP), alpha (CEBPA) | 3 | X87248 | | + | + | + | | + | | |
| CCAAT/enhancer binding protein (C/EBP), delta (CEBPB) | 1 | S63168 | | | + | | + | + | | |
| CCAAT-box-binding transcription factor (CBF2) | 2 | M37197 | T lymphoma | | | + | + | | | |
| CCR5 receptor (CCR5) (non-exact?) | 1 | AF011504 | | | | | | | | |
| CD14 antigen (CD14) | 11 | M86511 | + | + | + | + | | + | | |

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|---|---|----------|------------|---|---|---|---|---|--|
| CD18 (=M95293) | 4 | X64071 | | | | | | | |
| CD1C antigen, c polypeptide (CD1C) | 2 | M28827 | | | | | | + | |
| CD2 antigen (cytoplasmic tail)-binding protein 2 (CD2BP2) | 1 | AF104222 | | | | | | | |
| CD2 antigen (p50), sheep red blood cell receptor (CD2) | 4 | M14362 | + | | + | + | | + | |
| CD2 cytoplasmic tail-binding protein 1 (CD2BP1) | 2 | AF038602 | | | | | + | | |
| CD20 antigen (CD20) | 1 | X12530 | | | | | | | |
| CD20 receptor (S7) | 1 | X07203 | | | | | | | |
| CD22 antigen (CD22) | 1 | U62631 | B | | | | | | |
| CD24 signal transducer | 1 | M58664 | | | | | | | |
| CD33 antigen (gp67) (CD33) | 1 | M23197 | | | | | + | | |
| CD33 antigen-like 2; OB binding protein-2 (CD33L2) (non-exact, 68%) | 1 | U71383 | | | | | | | |
| CD33L2 (61% aa) | 1 | D86359 | | | | | | | |
| CD36 antigen (collagen type I receptor, thrombospondin receptor) (CD36) | 7 | M98398 | T lymphoma | | + | | + | + | |
| CD37 antigen (CD37) | 5 | X14046 | + | + | | + | | + | |
| CD38 alt | 1 | D84277 | | | | | | | |
| CD39 antigen (CD39) | 1 | U87967 | B | + | | | + | + | |
| CD3D antigen, delta polypeptide (TIT3 complex) (CD3D) | 1 | X03934 | | | + | + | | + | |
| CD3E antigen, epsilon polypeptide (TIT3 complex) (CD3E) | 1 | X03884 | + | | | + | | | |
| CD3G antigen, gamma polypeptide (TIT3 complex) (CD3G) | 2 | X06026 | W | | | | + | | |

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|--|----|--------|---|---|---|---|---|---|------------------------|
| CD3Z antigen, zeta polypeptide (TiT3 complex) (CD3Z) | 2 | J04132 | + | | | + | | | |
| CD3-zeta (clone pBS NK1) | 1 | X55510 | | | | | | | |
| CD4 (low match) | 1 | S68043 | | | | | | | |
| CD4 antigen (p55) (CD4) | 4 | M12807 | | + | + | | + | | |
| CD44 antigen (homing function and Indian blood group system) (CD44) | 6 | X56794 | W | | | | + | + | |
| CD48 antigen (B-cell membrane protein) (CD48) | 3 | X06341 | + | + | + | + | | + | |
| CD53 antigen (CD53) | 10 | L11670 | + | + | | + | | + | |
| CD53 antigen (CD53) (low match) | 1 | M60871 | | | | | | | |
| CD63 antigen (melanoma 1 antigen) (CD63) | 3 | M59907 | | | | | | | |
| CD68 antigen (CD68) | 2 | S57235 | | + | + | | + | + | |
| CD74 antigen (invariant polypeptide of major histocompatibility complex, class II antigen-associated) (CD74) | 72 | K01144 | + | + | + | + | + | + | high in many libraries |
| CD79A antigen (immunoglobulin-associated alpha) (CD79A) | 2 | M80462 | | | + | | | | |
| CD79B antigen (immunoglobulin-associated beta) (CD79B) | 2 | M89957 | + | | | | | | |
| CD8 antigen, alpha polypeptide (p32) (CD8A) | 2 | M27161 | + | | | + | | + | |
| CD8 antigen, beta polypeptide 1 (p37) (CD8B1) | 1 | X13445 | W | | | | | | |
| CD81 antigen (target of antiproliferative antibody 1) (CD81) | 1 | M33680 | | + | + | | | + | |
| CD83 antigen (activated B lymphocytes, immunoglobulin superfamily) (CD83) | 1 | Q01151 | B | + | + | | | + | |

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|---|----|----------|-------------|---|---|---|---|---|--|
| CD84 antigen (leukocyte antigen) (CD84) | 1 | U82988 | | + | + | | | + | |
| CD86 antigen | 1 | L25259 | | + | | | | | |
| CD9 antigen (p24) (CD9) | 2 | M38690 | | | + | | + | + | |
| CD97 antigen (CD97) | 12 | X84700 | + | + | | + | | | |
| CD97 antigen (CD97) (non-exact 59%) | 1 | P48960 | | | | | | | |
| CD97 antigen (CD97) (non-exact 62%) | 1 | X94630 | + | + | | + | | | |
| CDC23 (cell division cycle 23, yeast, homolog) (CDC23) | 1 | AF053977 | | + | | | + | + | |
| CDC37 homolog | 1 | U63131 | B | + | + | | + | + | |
| Cdc42 effector protein 3 (CEP3) | 2 | AF104857 | B | + | + | | + | | |
| CDC-like kinase (CLK) | 1 | L29219 | | + | + | + | | + | |
| CDC-like kinase 2 (CLK2) | 1 | AF023268 | B | + | + | | | | |
| CDW52 antigen (CAMPATH-1 antigen) (CDW52) | 13 | X15183 | T activated | + | + | | + | | |
| cell cycle progression restoration 8 protein(CPR8) | 1 | AF011794 | | | | | | | |
| cell division cycle 10 (homologous to CDC10 of <i>S. cerevisiae</i>) (CDC10) | 4 | S72008 | + | + | + | + | | + | |
| cell division cycle 20, <i>S. cerevisiae</i> homolog (CDC20) | 1 | U05340 | | + | + | + | | | |
| cell division cycle 25B (CDC25B) | 6 | Z68092 | + | + | + | + | | + | |
| cell division cycle 2-like 1 (PITSLRE proteins) (CDC2L1) (non-exact 42%) | 1 | AF067514 | | | | | | | |
| cell division cycle 42 (GTP-binding protein, 25kD) (CDC42) | 5 | M35543 | + | + | + | + | | + | |
| cell division protein (non-) | 1 | AF063015 | | | | | | | |

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|---|---|------------|------------------|---|---|---|---|---|--------------|
| exact 68%) | | | | | | | | | |
| CELL-CYCLE NUCLEAR AUTOANTIGEN SG2NA (S/G2 NUCLEAR ANTIGEN) | 1 | Q13033 | | | | | | | |
| centromere protein B (80kD) (CENPB) | 1 | X55039 | | + | | | + | | |
| cep250 centrosome associated protein | 3 | AF022655 | B | + | | | + | | |
| ceroid-lipofuscinosis, neuronal 2, late infantile (Jansky-Bielschowsky disease) (CLN2) | 7 | AF017456 | + | + | + | + | + | + | high in bone |
| c-fgr (=M63877 nonreceptor protein- tyrosine kinase (fgr)) | 6 | X52206 | | | | | | | |
| CGI-19 protein | 3 | AF132953.1 | | | | | | | |
| chaperonin containing TCP1, subunit 3 (gamma) (CCT3) | 1 | X74801 | | + | + | | | + | |
| chaperonin containing TCP1, subunit 4 (delta) (CCT4) | 1 | AF026291 | | + | + | | + | + | |
| chaperonin containing TCP1, subunit 6A (zeta 1) (CCT6A) | 4 | L27706 | B | + | + | | | | |
| chaperonin containing TCP1, subunit 7 (eta) (CCT7) | 4 | AF026292 | B | + | | | | + | |
| Chediak-Higashi syndrome 1 (CHS1) | 1 | U67615 | B, T lymphoma | + | + | | + | | |
| Chediak-Higashi syndrome 1 (CHS1) (low score) | 1 | U67615 | | | | | | | |
| chemokine (C-C motif) receptor 2 (CCR2) | 4 | U03905 | | | | | | | |
| chemokine (C-C motif) receptor 4 (CCR4) (low match) (may contain repeat) | 1 | X85740 | | | | | | | |
| chemokine (C-C motif) receptor 7 (CCR7) | 6 | L31581 | | | | | | | |

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|--|---|----------|---|---|---|---|---|---|--|
| chemokine (C-X3-C) receptor 1 (CX3CR1) | 5 | U20350 | | + | | | | | |
| chemokine (C-X-C motif), receptor 4 (fusin) (CXCR4) | 5 | M99293 | + | + | + | + | | + | |
| chitinase 3-like 1 (cartilage glycoprotein-39) (CHI3L1) | 2 | M80927 | | + | | + | | + | |
| chitinase 3-like 2 (CHI3L2) | 2 | U49835 | | + | | + | | + | |
| chloride channel 1, skeletal muscle (CLCN1) | 1 | G18280 | | | | | | | |
| chloride channel 6 (CLCN6) | 1 | D28475 | | + | + | | | | |
| Chloride intracellular channel 1 (CLIC1) | 1 | U93205 | + | + | + | + | | + | |
| chondroitin sulfate proteoglycan 2 (versican) (CSPG2) | 5 | X15998 | | | + | | | | |
| chondroitin sulfate proteoglycan core protein | 2 | J02814 | | | + | | | + | |
| chromatin assembly factor 1 p48 subunit (CAF-1 P48 subunit) (retinoblastoma binding protein p48) (retinoblastoma-binding protein 4) (MSI1 protein homolog) | 1 | Q09028 | | | | | | | |
| chromodomain helicase DNA binding protein 1 (CHD1) | 2 | AF006513 | | | | | | | |
| chromodomain helicase DNA binding protein 1-like (CHD1L) | 1 | AF054177 | | | | | | | |
| chromodomain helicase DNA binding protein 2 (CHD2) | 1 | AF006514 | B | + | + | | + | | |
| chromodomain helicase DNA binding protein 3 (CHD3) | 1 | AF006515 | | | | | | | |
| chromodomain helicase DNA binding protein 4 (CHD4) | 5 | X86691 | + | + | + | + | | + | |
| chromosome 1 open | 1 | AF054176 | | | | | | | |

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|---|---|----------|---|---|---|---|---|---|--|
| reading frame 7 (C1ORF7) | | | | | | | | | |
| chromosome 1 specific transcript KIAA0493 | 1 | AB007962 | | | | | | | |
| chromosome 17 open reading frame 1B (C17ORF1B) | 1 | AJ008112 | T | + | | | | | |
| chromosome 4 open reading frame 1 (C4ORF1) | 1 | AF006621 | | + | + | + | | + | |
| chromosome condensation 1-like (CHC1L) | 2 | AF060219 | | + | + | + | | + | |
| chromosome X open reading frame 5 (CXORF5) | 1 | Y15164 | B | + | + | | + | | |
| chromosome-associated polypeptide C(CAP-C) | 2 | AF092564 | B | + | + | | + | + | |
| cig42 | 1 | AF026944 | | | | | | | |
| cig5 | 3 | AF026941 | | | | | | | |
| citrate synthase (CS) | 2 | AF047042 | B | + | + | | + | + | |
| class I major histocompatibility antigen (HLA-Cw3) | 2 | U31372 | | | | | | | |
| class I major histocompatibility antigen (HLA-Cw3) (low match) | 1 | U31372 | | | | | | | |
| clathrin assembly protein lymphoid myeloid leukemia (CALM) | 3 | U45976 | B | + | + | | | + | |
| clathrin heavy chain | 1 | X55878 | | | | | | | |
| clathrin, heavy polypeptide-like 2 (CLTCL2) | 1 | D21260 | | | | | | | |
| clathrin, light polypeptide (Lca) (CLTA) (low match) | 1 | M20472 | | | | | | | |
| clathrin-associated/assembly/adapt or protein, medium 1 (CLAPM1) | 3 | D63475 | | + | + | + | + | + | |
| cleavage stimulation factor, 3' pre-RNA, subunit 2 64kD (CSTF2) (non-exact 82%) | 1 | M85085 | | | | | | | |

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|--|----|--------|---|---|---|---|---|---|---------------------|
| cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kD (CSTF3) | 1 | U15782 | B | + | + | | + | | |
| clk3 | 1 | L29220 | B | + | + | | | | |
| clone 23815 (Hs.82845) | 1 | U90916 | | + | + | | | + | |
| clone 24592 mRNA sequence | 1 | D88378 | + | + | + | + | | + | |
| Clq/MBL/SPA receptor C1qR(p) () | 1 | U94333 | | | | | | | |
| clusterin (complement lysis inhibitor, SP-40,40, sulfated glycoprotein 2, testosterone-repressed prostate message 2, apolipoprotein J) (CLU) | 1 | M64722 | + | + | + | + | + | + | |
| CMP-sialic acid transporter (CMPST) | 1 | D87969 | B | + | + | | | | |
| CMRF35 | 3 | X66171 | | | | | | | |
| c-myc oncogene containing coxIII | 1 | X54629 | | | | | | | |
| coagulation factor II (thrombin) receptor (F2R) | 1 | M62424 | | + | + | | | + | |
| coagulation factor V (proaccelerin, labile factor) (F5) | 1 | M14335 | | + | | + | + | | |
| coagulation factor XIII a subunit | 3 | M21998 | | | | | | | |
| coagulation factor XIII, A1 polypeptide (F13A1) | 6 | M14354 | | + | + | + | | + | |
| coated vesicle membrane protein (RNP24) | 1 | X92098 | + | + | + | + | + | + | |
| coatamer protein complex, subunit alpha (COPA) | 5 | U24105 | T | + | | | + | | |
| Cofilin 1 (non-muscle) (CFL1) | 13 | X95404 | + | + | + | + | + | + | high in fetal brain |
| cold inducible RNA-binding protein (CIRBP) | 7 | D78134 | | + | + | | | + | |

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|--|----|----------|---|---|---|---|---|---|--|
| cold shock domain protein A (CSDA) | 3 | X95325 | | + | + | | | | |
| collagen, type IX, alpha 2 (COL9A2) | 3 | AF019406 | B | | | | | | |
| colony stimulating factor 1 receptor, formerly McDonough feline sarcoma viral (v-fms) oncogene homolog (CSF1R) | 3 | X03663 | | + | | | + | + | |
| colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage) (CSF2RB) | 5 | M59941 | | | | | | | |
| colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage) (CSF2RB) (low match) | 1 | M59941 | | | | | | | |
| colony stimulating factor 3 receptor (granulocyte) (CSF3R) | 16 | X55720 | | + | | | | | |
| complement component 5 receptor 1 (C5a ligand) (C5R1) | 1 | M62505 | L | | | | | | |
| conserved gene amplified in osteosarcoma (OS4) | 2 | AF000152 | | + | + | + | | + | |
| COP9 (constitutive photomorphogenic, Arabidopsis, homolog) subunit 3 (COPS3) | 2 | AF031647 | | + | + | | | + | |
| COP9 homolog (HCOP9) | 2 | U51205 | B | + | + | + | + | + | |
| COP11 protein, homolog of s. cerevisiae SEC23p (SEC23A) | 4 | X97064 | | + | + | | | | |
| copine I (CPNE1) | 2 | U83246 | B | + | + | | + | | |
| copine I (CPNE1) (low score) | 1 | U83246 | | | | | | | |
| coproporphyrinogen oxidase (coproporphyrin, harderoporphyrin) (CPO) | 1 | D16611 | | | + | | + | + | |
| core-binding factor, beta subunit (CBFB) | 1 | L20298 | | + | | | | | |

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|--|----|----------|------------------|---|---|---|---|---|--|
| coronin | 22 | X89109 | T, W | + | + | | + | | |
| coronin (low match) | 1 | U34690 | | | | | | | |
| coronin (non-exact, 71%) | 1 | X89109 | | | | | | | |
| cot (cancer Osaka thyroid) oncogene (COT) | 1 | D14497 | + | + | + | + | | + | |
| cryptochrome 1 (photolyase-like) (CRY1) | 1 | D84657 | | + | + | | | + | |
| CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) phosphatase, subunit 1 (CTDP1) | 1 | AF081287 | | + | + | + | | + | |
| C-terminal binding protein 1 (CTBP1) | 1 | U37408 | B | + | + | | + | | |
| C-terminal binding protein 2 (CTBP2) | 2 | AF016507 | | + | + | | + | | |
| CUG triplet repeat, RNA- binding protein 1 (CUGBP1) | 3 | U63289 | | + | + | + | | + | |
| cullin 1 (CUL1) | 3 | U58087 | | + | + | + | | + | |
| cullin 3 (CUL3) | 2 | U58089 | | + | + | + | | + | |
| cut (Drosophila)-like 1 (CCAAT displacement protein) (CUTL1) | 1 | M74099 | B | + | | | | | |
| cyclin D2 (CCND2) | 2 | D13639 | | + | + | + | | + | |
| cyclin D3 (CCND3) | 5 | M92287 | B, T lymphoma | | + | | + | | |
| cyclin G1 (CNNG1) | 1 | D78341 | B | + | + | | | + | |
| cyclin I | 3 | D50310 | B | + | | | + | | |
| cyclin T2 (CNNT2) | 1 | AF048732 | B, T lymphoma | B | | | | | |
| cyclin-dependent kinase 2 (CDK2) | 1 | X62071 | | | | | | | |
| cyclin-dependent kinase inhibitor (p27Kip1) | 1 | S76986 | | | | | | | |
| cyclin-dependent kinase inhibitor 1A (p21, Cip1) | 2 | S67388 | + | + | + | + | + | + | |

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|--|---|----------|------------|---|---|---|---|---|--|
| (CDKN1A) | | | | | | | | | |
| CYP2D7-CYP2D6 intergenic region (partial) | 1 | X90926 | | | | | | | |
| cystatin B (stefin B) (CSTB) | 1 | L03558 | | | + | | + | + | |
| cysteine and glycine-rich protein 3 (cardiac LIM protein) (CSR3P3) | 5 | L54057 | | | + | | | | |
| cytidine deaminase (CDA) | 2 | L27943 | | | | | + | | |
| cytochrome b | 1 | AF042500 | | | | | | | |
| cytochrome b (CYTB) (isolate Aus5) | 1 | AF042518 | | | | | | | |
| cytochrome b(-245) beta chain N-terminal region (X- linked granulomatous disease gene) | 2 | X05895 | | | | | | | |
| cytochrome b-245, beta polypeptide (chronic granulomatous disease) (CYBB) | 2 | X04011 | + | | | + | | + | |
| cytochrome C | 1 | P00001 | | | | | | | |
| cytochrome c oxidase subunit IV (COX4) | 1 | U90915 | T | + | + | | + | + | |
| cytochrome c oxidase subunit Vb (COX5B) | 2 | M59250 | | | | | + | | |
| cytochrome c oxidase subunit VII-related protein (COX7RP) | 6 | AB007618 | + | + | + | + | | + | |
| cytokine suppressive anti- inflammatory drug binding protein 1 (p38 MAP kinase) (CSBP1) | 1 | L35263 | lymphocyte | + | + | | + | | |
| Cytoplasmic antiproteinase=38 kda intracellular serine proteinase inhibitor | 1 | S69272 | | | + | | | | |
| cytotoxic granule- associated RNA-binding protein p40-TIA-1 | 1 | S70114 | | | | | | | |
| D123 (D123) | 1 | D14878 | + | + | | + | | + | |

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|--|----|----------|---|---|---|---|---|---|--|
| D2-2 | 1 | AF019226 | | | | | | | |
| D38 | 1 | X74802 | | | | | | | |
| damage-specific DNA binding protein 1 (127kD) (DDB1) | 2 | AJ002955 | + | + | + | + | + | + | |
| DCHT (low match) | 1 | AF017635 | | | | | | | |
| DEAD/H (Asp-Glu-Ala-Asp/His) box binding protein 1 (DDXBP1) | 1 | U78524 | | + | + | + | + | + | |
| DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide (72kD) (P72) | 2 | U59321 | T | + | + | | + | + | |
| DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) | 1 | X70649 | | + | + | | | + | |
| DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 15 (DDX15) | 2 | AB001636 | | | | | | | |
| DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 16 (DDX16) | 2 | AB011149 | + | + | + | + | | + | |
| DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3 (DDX3) | 3 | U50553 | + | + | + | + | | + | |
| DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 5 (RNA helicase, 68kD) (DDX5) | 37 | X15729 | + | + | + | + | | + | |
| DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 5 (RNA helicase, 68kD) (DDX5) (low match) | 1 | AF015812 | | | | | | | |
| DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 6 (RNA helicase, 54kD) (DDX6) | 2 | D17532 | + | + | | | | | |
| DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 8 (RNA helicase, 54kD) (DDX8) | 1 | D50487 | | + | + | + | | + | |
| DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 9 (RNA helicase A, nuclear DNA helicase II; | 3 | L13848 | + | + | + | + | | + | |

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|--|---|----------|------------------------|---|---|---|---|---|--|
| leukophysin) (DDX9) | | | | | | | | | |
| DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide, Y chromosome (DBY) | 1 | AF000985 | | + | + | | + | | |
| Death associated protein 3 (DAP3) | 2 | X83544 | + | + | + | + | + | + | |
| death effector domain-containing protein (DEDD) | 1 | AF083236 | | + | + | + | | + | |
| death-associated protein 6 (DAXX) | 2 | AF039136 | | + | + | + | | + | |
| dedicator of cyto-kinesis 2 (DOCK2) | 4 | D86964 | + | + | | + | | + | |
| defender against cell death 1 (DAD1) | 1 | D15057 | | | + | | + | + | |
| Defensin, alpha 1, myeloid-related sequence (DEFA1) | 4 | L12690 | | | | + | + | + | |
| DEK gene (D6S231E) | 1 | X64229 | B | | + | | + | | |
| delta sleep inducing peptide, immunoreactor (DSIP) | 4 | Z50781 | + | + | + | + | | + | |
| dendritic cell protein (GA17) | 3 | AF064603 | + | + | + | + | | + | |
| deoxycytidine kinase (DCK) | 1 | M60527 | | | | | | | |
| deoxyribonuclease II, lysosomal (DNASE2) | 3 | AB004574 | | | | | | | |
| DGS-I | 2 | L77566 | | + | | | | | |
| diacylglycerol kinase | 3 | D16440 | | | | | | | |
| diacylglycerol kinase alpha (DAGK1) (clone 24) | 3 | AF064771 | | + | | | | | |
| diacylglycerol kinase alpha (DAGK1) (clone 24) (low match) | 1 | AF064771 | | | | | | | |
| diaphanous (Drosophila, homolog) 1 (DIAPH1) | 1 | AF051782 | B, monocyte stimulated | + | + | | + | + | |
| diaphorase (NADH) (cytochrome b-5 reductase) (DIA1) | 1 | Y09501 | + | + | + | + | + | + | |

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|--|---|----------|-----------------------|---|---|---|---|---|--|
| differentiated Embryo Chondrocyte expressed gene 1 (DEC1) | 1 | AB004066 | | + | | | + | + | |
| differentiated Embryo Chondrocyte expressed gene 1 (DEC1) (low match) | 1 | AB004066 | | | | | | | |
| differentiation antigen CD20 | 1 | L23415 | | | | | | | |
| DiGeorge syndrome critical region gene 2 (DGCR2) | 1 | X84076 | | + | + | | | + | |
| dihydrolipoamide dehydrogenase (E3 component of pyruvate dehydrogenase complex, 2-oxo-glutarate complex, branched chain keto acid dehydrogenase complex) (DLD) | 2 | J03620 | | + | | | + | + | |
| dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex) (DLAT) | 1 | Y00978 | B | + | | | + | | |
| dihydropyrimidinase-like 2 (DPYSL2) | 1 | D78013 | | + | + | | + | + | |
| dinG gene | 1 | Y10571 | | | | | | | |
| diphtheria toxin resistance protein required for diphthamide biosynthesis (Saccharomyces)-like 2 (DPH2L2) | 3 | AF053003 | B | + | + | | + | + | |
| disintegrin-protease (non-exact 72%) | 1 | Y13323 | | | | | | | |
| DJ-1 protein | 2 | AF021819 | + | + | + | + | | + | |
| Dmx-like 1 (DMXL1) | 1 | AJ005821 | + | | + | + | | | |
| DNA (cytosine-5)-methyltransferase 1 (DNMT1) | 3 | X63692 | T activated, lymphoma | + | | | + | + | |
| DNA fragmentation factor, 40 kD, beta subunit (DFFB) | 1 | AF064019 | | | | | | | |
| DNA fragmentation factor, 45 kD, alpha subunit | 2 | U91985 | T | + | + | | | + | |

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|---|---|----------|-------------|---|---|---|---|---|---|------------------------|
| (DFFA) | | | | | | | | | | |
| DNA mismatch repair protein (hMLH1) | 1 | U17840 | | | | | | | | |
| DNA segment on chromosome X (unique) 648 expressed sequence | 3 | M64241 | + | + | + | + | + | + | + | high in many libraries |
| DNA segment, single copy probe LNS-CAI/LNS-CAII (deleted in polyposis (D5S346)) | 3 | M73547 | | + | + | + | | | + | |
| DNA-damage-inducible transcript 1 (DDIT1) (low match) | 1 | L24498 | | | | | | | | |
| DnaJ protein | 1 | AJ001309 | | | | | | | | |
| DnaJ protein | 1 | AJ001309 | | | | | | | | |
| docking protein 2, 56kD (DOK2) | 1 | AF034970 | | | | | | | | |
| dolichyl-diphosphooligosaccharide-protein glycosyltransferase (DDOST) | 1 | D89060 | + | + | + | + | + | + | + | activated T cell |
| dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit (DPM1) | 1 | D86198 | T activated | + | + | | | + | | |
| down-regulated by activation (immunoglobulin superfamily) (DORA) | 1 | AJ223183 | | | | | | + | | |
| down-regulated in adenoma DRA (low match) | 1 | P40879 | | | | | | | | |
| D-type cyclin-interacting protein 1 (DIP1) | 1 | AF082569 | B | | | | | + | + | |
| dual specificity phosphatase 1 (DUSP1) | 4 | X68277 | + | + | + | + | + | + | + | |
| dual specificity phosphatase 11 (RNA/RNP complex 1-interacting) (dusp11) | 1 | AF023917 | + | + | + | + | | | + | |
| dual specificity phosphatase 3 (vaccinia virus phosphatase VH1- | 1 | L05147 | | + | + | | | + | + | |

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|---|---|----------|---|---|---|---|---|---|--|
| related) (DUSP3) | | | | | | | | | |
| dual specificity phosphatase 6 (DUSP6) | 6 | X93920 | + | + | + | + | + | + | |
| dynactin 1 (p150, Glued (Drosophila) homolog) (DYTN1) | 3 | X98801 | | | | | | | |
| dynactin 1 (p150, Glued (Drosophila) homolog) (DYTN1) (low match) | 1 | X98801 | B | + | + | | | | |
| dynamitin 2 (DNM2) | 1 | L36983 | | | | | | | |
| dynamitin (dynactin complex 50 kD subunit) (DCTN-50) (non-exact 88%) | 1 | U50733 | | | | | | | |
| dynein, axonemal, heavy polypeptide 17-like (non-exact, 57%aa) | 1 | X99947 | | | | | | | |
| dynein, cytoplasmic, light intermediate polypeptide 2 (DNCL12) | 1 | AF035812 | B | + | + | | | + | |
| dynein, cytoplasmic, light intermediate polypeptide 2 (DNCL12) (non-exact, 69%) | 1 | AF035812 | | | | | | | |
| dyskeratosis congenita 1, dyskerin (DKC1) | 1 | U59151 | B | + | | | + | + | |
| dystonia 1, torsion (autosomal dominant) (DYT1) | 1 | AF007871 | | + | + | + | | + | |
| dystrobrevin, beta (DTNB) | 1 | AF022728 | | + | | | | | |
| dystrophia myotonica-containing WD repeat motif (DMWD) | 1 | L19267 | | + | + | | + | + | |
| dystrophia myotonica-protein kinase (DMPK) | 1 | L08835 | + | + | + | | | + | |
| dystrophin (muscular dystrophy, Duchenne and Becker types) (DMD) (low match, 59%aa) | 1 | X14298 | | | | | | | |
| E1B-55kDa-associated protein | 1 | AJ007509 | W | + | + | | + | + | |

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|---|---|----------|---|---|---|---|---|---|--|
| E2F transcription factor 3 (E2F3) | 2 | D38550 | | + | + | + | + | + | |
| E2F transcription factor 4, p107/p130-binding (E2F4) | 1 | X86096 | B | + | | | + | | |
| E2F transcription factor 5, p130-binding (E2F5) | 2 | U15642 | + | + | | + | | + | |
| E74-like factor 1 (ets domain transcription factor) (ELF1) | 1 | M82882 | B | | + | | + | + | |
| E74-like factor 4 (ets domain transcription factor) (ELF4) | 3 | U32645 | | + | + | | | + | |
| E74-like factor 4 (ets domain transcription factor) (ELF4) (non-exact, 71%) | 1 | U32645 | | | | | | | |
| early development regulator 2 (homolog of polyhomeotic 2) (EDR2) | 4 | U89278 | + | + | + | + | | + | |
| EBV induced G-protein coupled receptor (EBI2) | 1 | L08177 | W | | | | | | |
| ecotropic viral integration site 2B (EVI2B) | 3 | M60830 | | + | | + | | | |
| ectin, galactoside-binding, soluble, 1 (galectin 1) (LGALS1) | 1 | J04456 | | | | | | + | |
| EGF-like-domain, multiple 4 (EGFL4) | 1 | AB011541 | | | | | | | |
| eIF-2-associated p67 homolog | 3 | U13261 | B | + | | | | + | |
| elastin (supravalvular aortic stenosis, Williams-Beuren syndrome) (ELN) (low match) | 1 | M24782 | | + | + | | | | |
| elav-type RNA-binding protein (ETR-3) | 3 | U69546 | | | | | | | |
| electron-transfer-flavoprotein, alpha polypeptide (glutaric aciduria II) (ETFA) | 2 | J04058 | | + | | | | | |
| ELK3, ETS-domain protein (SRF accessory protein 2) | 2 | Z36715 | | | + | | | + | |

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|---|----|------------|---|---|---|---|---|---|--|
| (ELK3) | | | | | | | | | |
| elongation factor 1-beta | 1 | L26404 | | | | | | | |
| elongation factor Ts (mitochondrial protein) | 1 | AF110399 | | | | | | | |
| elongation factor Tu- nuclear encoded mitochondrial | 1 | X84694 | | | | | | | |
| eMDC II protein | 1 | AJ242015.1 | | | | | | | |
| ems1 sequence (mammary tumor and squamous cell carcinoma-associated (p80/85 src substrate) (EMS1) | 1 | M98343 | | + | + | | + | + | |
| endogenous retroviral element HC2 | 1 | Z70664 | | | | | | | |
| endosulfine alpha (ENSA) | 1 | X99906 | T | + | | | | | |
| endothelial differentiation, sphingolipid G-protein- coupled receptor, 1 (EDG1) | 2 | M31210 | | + | + | + | | + | |
| endothelial differentiation, sphingolipid G-protein- coupled receptor, 1 (EDG1) (low match 66%) | 1 | M31210 | | | | | | | |
| endothelial monocyte- activating polypeptide (EMAPII) | 1 | U10117 | + | + | + | + | | + | |
| enolase 1, (alpha) (ENO1) | 12 | M14328 | + | + | + | + | + | + | |
| enolase 2, (gamma, neuronal) (ENO2) | 1 | X51956 | | + | | | | | |
| enolase-alpha | 1 | D28437 | | | | | | | |
| enoyl Coenzyme A hydratase 1, peroxisomal (ECH1) | 2 | U16660 | | | | | | | |
| enoyl Coenzyme A hydratase, short chain, 1, mitochondrial (ECHS1) | 1 | D13900 | + | + | + | + | + | + | |
| ENOYL-COA HYDRATASE, MITOCHONDRIAL PRECURSOR (SHORT CHAIN ENOYL-COA | 1 | P30084 | | | | | | | |

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|--|-----|--------|------|---|---|---|--|---|----------------------|
| HYDRATASE) (SCEH) (ENOYL-COA HYDRATASE 1) (low match, non-exact 56%) | | | | | | | | | |
| epidermal growth factor receptor pathway substrate 15 (EPS15) | 2 | U07707 | | + | | + | | + | |
| EPIDIDYMAL SECRETORY PROTEIN E1 PRECURSOR (EPI-1) (HE1) (EPIDIDYMAL SECRETORY PROTEIN 14.6) (ESP14.6) | 2 | Q15668 | | | | | | | |
| epithelial membrane protein 3 (EMP3) | 1 | U87947 | + | + | + | + | | + | |
| Epoxide hydrolase 1, microsomal (xenobiotic) (EPHX1) | 1 | L29766 | | | | | | + | only |
| ERCC2 (=L47234) | 1 | X52221 | | | | | | | |
| ERF-2 | 3 | U07802 | + | + | + | + | | + | high in gall bladder |
| ERp28 protein | 1 | X94910 | + | + | + | + | | + | |
| erythrocyte membrane protein | 2 | M81635 | | | | | | | |
| erythroleukemic cells K562 | 2 | L25343 | | | | | | | |
| EST (Hs.189509) | 2 | U24166 | | | | | | | |
| estrogen receptor-related protein (hERRa1) | 1 | L38487 | | | | | | | |
| ESTs, Highly similar to ADENYLOSUCCINATE SYNTHETASE | 1 | X66503 | B, T | + | + | | | | |
| ESTs, Moderately similar to cysteine-rich fibroblast growth factor receptor | 1 | U28811 | + | + | + | + | | + | |
| ET binding factor 1 (SBF1) | 1 | U93181 | + | + | | | | + | |
| ets domain protein ERF | 1 | U15655 | + | + | + | + | | + | |
| eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) | 326 | X03558 | T | + | + | | | + | |

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|--|----|----------|---|---|---|---|---|---|---------------------------|
| eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) (low match) | 1 | X03558 | | | | | | | |
| eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) (low match) | 1 | X03558 | | | | | | | |
| eukaryotic translation elongation factor 1 beta 2 (EEF1B2) | 5 | X60489 | + | + | + | + | | + | |
| eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein) (EEF1D) | 1 | Z21507 | + | + | + | + | + | + | |
| eukaryotic translation elongation factor 1 gamma (EEF1G) | 31 | Z11531 | | | | | | | |
| eukaryotic translation elongation factor 2 (EEF2) | 2 | X51466 | | + | | | | + | |
| eukaryotic translation initiation factor 2, subunit 1 (alpha, 35kD) (EIF2S1) | 1 | J02645 | | | | | | | |
| eukaryotic translation initiation factor 2, subunit 2 (beta, 38kD) (EIF2S2) | 1 | M29536 | | | | | | | |
| eukaryotic translation initiation factor 2, subunit 3 (gamma, 52kD) (EIF2S3) | 3 | L19161 | | + | + | | | | |
| eukaryotic translation initiation factor 3, subunit 10 (theta, 150/170kD) (EIF3S10) | 2 | U78311 | | | | | | | |
| eukaryotic translation initiation factor 3, subunit 2 (beta, 36kD) (EIF3S2) | 3 | U36764 | + | + | + | + | + | + | high in white blood cells |
| eukaryotic translation initiation factor 3, subunit 3 (gamma, 40kD) (EIF3S3) | 6 | U54559 | + | + | + | + | | + | high in spleen |
| eukaryotic translation initiation factor 3, subunit 4 (delta, 44kD) (EIF3S4) | 9 | AF020833 | | + | + | + | | + | |
| eukaryotic translation initiation factor 3, subunit 6 (48kD) (EIF3S6) | 4 | U94175 | + | + | + | + | | + | high in bladder |

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|--|----|----------|------|---|---|---|---|---|--|
| eukaryotic translation initiation factor 3, subunit 6 (EIF3S6) | 1 | U62962 | | + | + | + | | + | Highly represented (1.4833 pct) in library 36 human gall bladder |
| eukaryotic translation initiation factor 3, subunit 7 (zeta, 66/67kD) (EIF3S7) | 3 | U54558 | + | + | + | + | | + | |
| eukaryotic translation initiation factor 3, subunit 8, 110kD (EIF3S8) | 5 | U46025 | + | + | + | + | + | + | high in testis |
| eukaryotic translation initiation factor 4 gamma, 1 (EIF4G) | 1 | AF012088 | | | | | | | |
| eukaryotic translation initiation factor 4 gamma, 1 (EIF4G) (low match) | 1 | AF012088 | | | | | | | |
| eukaryotic translation initiation factor 4 gamma, 1 (EIF4G1) | 2 | D12686 | | | | | | | |
| eukaryotic translation initiation factor 4 gamma, 2 (EIF4G2) | 6 | U73824 | + | + | + | + | + | + | |
| eukaryotic translation initiation factor 4 gamma, 2 (EIFG2) | 2 | U76111 | + | + | + | + | + | + | |
| eukaryotic translation initiation factor 4A, isoform 1 (EIF4A1) | 29 | D13748 | | | | | | | |
| eukaryotic translation initiation factor 4A, isoform 2 (EIF4A2) | 11 | D30655 | + | + | + | + | + | + | |
| eukaryotic translation initiation factor 4B (EIF4B) | 18 | X55733 | + | + | + | + | | + | |
| eukaryotic translation initiation factor 4E (EIF4E) | 1 | P06730 | | | | | | | |
| Eukaryotic translation initiation factor 4E binding protein 2 (EIF4EBP2) | 3 | L36056 | T, B | + | | | | + | + |
| eukaryotic translation initiation factor 4H (EIF4H) | 2 | Q15056 | | | | | | | |
| eukaryotic translation initiation factor 5 (EIF5) | 2 | U49436 | + | + | + | + | + | + | |

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|--|---|----------|---|---|---|---|--|---|--|
| eukaryotic translation termination factor 1 (ETF1) | 2 | U90176 | + | + | + | + | | + | |
| EV12 protein | 1 | M55266 | | + | | | | | |
| Ewing sarcoma breakpoint region 1 (EWSR1) | 1 | X66899 | + | + | + | + | | + | |
| EWS/FLI1 activated transcript 2 homolog (EAT-2) | 2 | AF020264 | | | | | | | |
| EWS-E1A-F chimeric protein | 1 | U35622 | | | | | | | |
| excision repair cross-complementing rodent repair deficiency, complementation group 1 (includes overlapping antisense sequence) (ERCC1) | 1 | M28650 | + | + | + | + | | + | |
| excision repair cross-complementing rodent repair deficiency, complementation group 5 (xeroderma pigmentosum, complementation group G (Cockayne syndrome)) (ERCC5) | 1 | X69978 | | + | + | + | | + | |
| exostoses (multiple)-like 3 (EXTL3) | 1 | AF001690 | | + | + | + | | + | |
| F11 | 1 | X77744 | | | | + | | | |
| F1-ATPase beta subunit (F-1 beta) | 2 | X03559 | | | | | | | |
| Fanconi anaemia group A | 2 | Z83095 | | | | | | | |
| Fanconi anemia, complementation group A (FANCA) | 1 | X99226 | + | + | + | + | | | |
| far upstream element (FUSE) binding protein 1 (FUBP1) | 2 | U05040 | + | | + | | | + | |
| farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltransferase, geranyltransferase) (FDPS) | 1 | J05262 | + | + | + | + | | + | |

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|---|----|----------|---|---|---|---|---|---|------------------------|
| farnesyl-diphosphate farnesyltransferase 1 (FDFT1) | 2 | X69141 | + | + | + | + | + | + | |
| farnesyltransferase, CAAX box, beta (FNTB) | 2 | L00635 | | + | + | | | | |
| Fas ligand (gene and promoter region) | 1 | AF044583 | | | | | | | |
| Fas-ligand associated factor 1 | 1 | U70667 | | | | | | | |
| fatty-acid-Coenzyme A ligase, long-chain 1 (FACL1) | 4 | D10040 | + | + | + | + | + | + | |
| Fc fragment of IgA, receptor for (FCAR) | 1 | X54150 | | | | | | | |
| Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide (FCER1G) | 1 | M33195 | + | + | + | + | | + | |
| Fc fragment of IgE, low affinity II, receptor for (CD23A) (FCER2) | 2 | X04772 | + | + | | | | | |
| Fc fragment of IgG, low affinity IIa, receptor for (CD32) | 6 | M31932 | + | + | + | + | + | + | |
| Fc fragment of IgG, low affinity IIa, receptor for (CD32) (FCGR2A) | 1 | X62572 | + | + | + | + | + | + | |
| Fc fragment of IgG, low affinity IIIa, receptor for (CD16) (FCGR3A) | 34 | X07934 | + | + | + | + | | + | |
| Fc fragment of IgG, receptor, transporter, alpha (FCGRT) | 3 | U12255 | | + | + | + | + | + | high in many libraries |
| fc-fgr | 1 | Z13983 | | | | | | | |
| Fc-gamma-receptorIIIB (FCGR3B) | 2 | M90746 | | | | | | | |
| feline sarcoma (Snyder- Theilen) viral (v- fes)/Fujinami avian sarcoma (PRCII) viral (v- fps) oncogene homolog(FES) c-fes/fps) | 3 | X06292 | | | | | | | |

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|---|----|----------|---|---|---|---|---|---|---|
| female sterile homeotic-related gene 1 (mouse homolog) (FSRG1) | 2 | X96670 | + | + | + | + | | + | |
| ferritin L-chain | 9 | Y09188 | | | | | | | |
| ferritin, heavy polypeptide 1 (FTH1) | 4 | M11146 | + | + | + | + | + | + | |
| fertilin alpha pseudogene | 1 | Y09232 | | | | | | | |
| fetal Alzheimer antigen (FALZ) | 2 | U05237 | | + | | | | | |
| fetal Ig heavy chain variable region | 1 | M34024 | | | | | | | |
| fibrillarin (FBL) | 1 | X56597 | + | + | + | + | + | + | |
| fibrinogen-like protein 2 (T49) | 3 | Z36531 | | | | + | | | |
| fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1; Crouzon syndrome) syndrome, Pfeiffer syndrome, Jackson-Weiss) (FGFR2) | 1 | M35718 | + | + | + | + | + | + | |
| ficolin (collagen/fibrinogen domain-containing) 1 (FCN1) | 19 | D83920 | | | | + | | + | |
| filamin A, alpha (actin-binding protein-280) (FLNA) | 2 | X53416 | | | | | | | |
| filamin B, beta (actin-binding protein-278) (FLNB) | 1 | AF043045 | | + | + | | + | | |
| Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed (fox derived); ribosomal protein S30 (FAU) | 2 | X65923 | + | + | + | + | + | + | Highly represented in intraepithelial neoplasia and invasive prostate tumor |
| FK-506 binding protein | 1 | M80199 | + | + | + | + | | + | |
| FK506-binding protein 1A (12kD) (FKBP1A) | 2 | M34539 | | | | | | | |
| FK506-binding protein 1B | 1 | M92423 | | + | | + | | + | |

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|---|---|----------|---|---|---|---|---|---|---------------------------------------|
| (12.6 kD) (FKBP1B) | | | | | | | | | |
| FK506-binding protein 5 (FKBP5) | 4 | U71321 | | + | + | + | | + | |
| Flightless I (Drosophila) homolog (FLII) | 3 | U80184 | | + | | | | | |
| Flightless I (Drosophila) homolog (FLII) (low match) | 1 | U80184 | | | | | | | |
| FLN29 (FLN29) | 2 | AB007447 | | + | | + | | + | |
| flotillin 2 (FLOT2) | 5 | M60922 | + | + | + | + | + | + | |
| folate receptor 2 (fetal) (FOLR2) | 1 | AF000380 | | + | + | + | | + | |
| forkhead, (Drosophila) homolog (rhabdomyosarcoma) like 1 (FKHRL1) | 1 | AF032886 | + | + | | + | | + | |
| Formyl peptide receptor 1 (FPR1) | 9 | M60627 | + | + | + | + | | + | |
| formyl peptide receptor-like 1 (FPRL1) | 1 | M84562 | | | | | | | Found only in libraries from placenta |
| formyl peptide receptor-like 1 (FPRL1) (low score) | 1 | M84562 | | | | | | | |
| fragile X mental retardation 1 (FMR1) | 1 | L29074 | + | + | | + | | + | |
| fragile X mental retardation, autosomal homolog 1 (FXR1) | 1 | U25165 | + | + | + | + | | | |
| Friend leukemia virus integration 1 (FLI1) | 3 | M93255 | + | + | | | | | |
| fructose-bisphosphatase 1 (FBP1) | 1 | D26054 | | | | + | | + | |
| FSHD-associated repeat DNA, proximal region | 1 | U85056 | | | | | | | |
| fucose-1-phosphate guanylyltransferase (FPGT) | 1 | AF017445 | | + | + | + | | | |
| full length insert cDNA clone ZA78A09 | 1 | AF086122 | | | | | | | |

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|---|----|----------|---|---|---|---|---|---|--|
| full length insert cDNA YP07G10 | 1 | AF075061 | | | | | | | |
| fumarate hydratase (FH) | 1 | U59309 | | + | + | + | | + | |
| FUS (low match) | 1 | X99006 | | | | | | | |
| FYN-binding protein (FYB- 120/130) (FYB) | 16 | U93049 | | + | | + | | | |
| G alpha interacting protein. (GAIP) (low score) | 1 | X91809 | | | | | | | |
| G protein beta subunit-like protein 12.3 | 2 | D28398 | | | | | | | |
| G protein-coupled receptor 64 (HE6) (non-exact 59%) | 1 | X81892 | | | | + | | | |
| G protein-coupled receptor kinase 6 (GPRK6) | 2 | L16862 | + | + | + | | | + | |
| G1 to S phase transition 1 (GSPT1) | 2 | X17644 | | + | + | + | + | + | |
| GA-binding protein transcription factor, beta subunit 2 (47kD) (GABPB2) | 1 | D13316 | | + | + | + | + | + | |
| galactose-1-phosphate uridylyltransferase (GALT) | 2 | M60091 | | | | | | | |
| galactosidase, beta 1 (GLB1) | 3 | M27508 | | + | | | + | + | |
| galactosyltransferase (=X13223 N- acetylglucosamide-(beta 1- 4)-galactosyltransferase) | 1 | M13701 | | | | | | | |
| galectin-9 isoform | 1 | AB006782 | + | | | + | | + | |
| gamma2-adaptin (G2AD) | 1 | AF068706 | + | + | | + | | + | |
| gamma-actin | 2 | M37130 | | | | | | | |
| gamma-aminobutyric acid (GABA) B receptor 1 (GABBR1) | 2 | AJ012187 | | + | + | | | + | |
| GATA-binding protein 2 (GATA2) | 1 | M68891 | | | | + | | + | |
| GATA-binding protein 3 (GATA3) | 1 | M69106 | | | + | + | | + | |

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|--|---|----------|------|---|---|---|---|---|---------------------|
| GCN5 (general control of amino-acid synthesis, yeast, homolog)-like 1 (GCN5L1) | 3 | D64007 | + | + | + | + | | + | |
| GDP dissociation inhibitor 1 (GDI1) | 1 | D45021 | + | + | + | + | | + | high in adult brain |
| GDP dissociation inhibitor 2 (GDI2) | 4 | Y13286 | | | | | | | |
| GDS-related protein (HKE1.5) | 4 | U68142 | + | + | + | + | | + | |
| gelsolin (amyloidosis, Finnish type) (GSN) | 3 | X04412 | | + | + | + | + | + | |
| general transcription factor II, I (GTF2I) | 4 | Y14946 | + | + | + | + | + | + | |
| general transcription factor II, i, pseudogene 1 (GTF2IP1) | 1 | AF038968 | + | + | + | + | + | + | high in fetal brain |
| general transcription factor IIF, polypeptide 1 (74kD subunit) (GTF2F1) | 4 | X64037 | + | + | + | + | | + | |
| general transcription factor IIH, polypeptide 3 (34kD subunit) (GTF2H3) | 2 | Z30093 | B, T | | | | | | |
| general transcription factor IIH, polypeptide 4 (52kD subunit) (GTF2H4) | 3 | Y07595 | | + | | + | | + | |
| general transcription factor IIIA (GTF3A) | 1 | U14134 | + | + | | + | | + | |
| general transcription factor IIIC, polypeptide 1 (alpha subunit, 220kD) (GTF3C1) | 1 | U02619 | | + | | + | | | |
| general transcription factor IIIC, polypeptide 2 (beta subunit, 110kD) (GTF3C2) | 3 | D13636 | + | + | + | + | + | + | |
| germline immunoglobulin heavy chain (IGHV@) | 1 | L06612 | | | | | | | |
| germline immunoglobulin heavy chain, variable region | 1 | X92236 | | | | | | | |
| germline immunoglobulin heavy chain, variable region, (21-2) | 1 | X92343 | | | | | | | |

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|--|---|----------|---|---|---|---|---|---|---|--|
| GLE1 (yeast homolog)-like, RNA export mediator (GLE1L) | 1 | AF058922 | | + | + | | | | | |
| glia maturation factor, beta (GMFB) | 1 | AB001106 | + | + | | + | | | + | |
| glioma-associated oncogene homolog (zinc finger protein) (GLI) | 1 | X07384 | | | | | | | | |
| glioma-associated oncogene homolog (zinc finger protein) (GLI) (low score) | 1 | X07384 | | | | | | | | |
| globin, alpha 2 | 1 | V00516 | | | | | | | | |
| glucocorticoid receptor (=M69104) | 1 | M32284 | | | | | | | | |
| glucocorticoid receptor (GRL) | 2 | U80947 | + | + | + | + | | | + | |
| glucos phosphate isomerase (CONTAINS LARGE REPEAT) | 1 | L09105 | | | | | | | | |
| glucosamine (N-acetyl)-6-sulfatase (Sanfilippo disease IIID) (GNS) | 1 | Z12173 | + | | | | | | | |
| glucosamine (N-acetyl)-6-sulfatase (Sanfilippo disease IIID) (GNS) (non-exact 56%) | 1 | Z12173 | | | | | | | | |
| glucose transporter-like protein-III (GLUT3) | 1 | M20681 | | + | + | + | + | + | | |
| glucose transporter-like protein-III (GLUT3) (low match) | 1 | M20681 | | | | | | | | |
| glucosidase, alpha; acid (Pompe disease, glycogen storage disease type II) (GAA) | 1 | Y00839 | + | + | | + | | | + | |
| glucosidase, beta; acid (includes glucosylceramidase) (GBA) | 1 | K02920 | + | + | + | + | | | + | |
| glutamate dehydrogenase 1 (GLUD1) | 1 | M20867 | | + | + | + | + | + | | |

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|---|----|----------|---|---|---|---|---|---|--|
| glutamate-ammonia ligase (glutamine synthase) (GLUL) | 12 | X59834 | + | + | + | + | | + | |
| glutamate-ammonia ligase (glutamine synthase) (GLUL) (low score) | 1 | Y00387 | | | | | | | |
| glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), catalytic (72.8kD) (GLCLC) | 1 | M90656 | | | | + | | | |
| glutamine cyclotransferase | 1 | X71125 | | + | + | | | | |
| glutamine-fructose-6-phosphate transaminase 1 (GFPT1) | 1 | M90516 | | + | | + | | | |
| glutamyl-tRNA synthetase | 1 | X72396 | | | | | | | |
| glutamyl-tRNA synthetase (QARS) | 6 | X76013 | + | + | + | + | | + | |
| glutamyl-prolyl-tRNA synthetase (EPRS) | 1 | X54326 | | | | | | | |
| glutathione peroxidase 1 (GPX1) | 2 | M21304 | + | + | + | + | + | + | |
| glutathione peroxidase 4 (phospholipid hydroperoxidase) (GPX4) | 1 | X71973 | + | + | + | + | | + | |
| glutathione S-transferase pi (GSTP1) | 1 | U30897 | | + | + | + | + | + | |
| glutathione S-transferase subunit 13 homolog | 1 | AF070657 | | | | | | | |
| glyceraldehyde-3-phosphate dehydrogenase (GAPD) | 12 | J02642 | | | | | + | | |
| glycogenin (GYG) | 1 | U31525 | | + | + | + | | + | |
| glycophorin C (Gerbich blood group) (GYPC) | 1 | X12496 | | + | + | + | | + | |
| glycoprotein M6B (GPM6B) | 1 | U45955 | | + | + | | | | |
| glycyl-tRNA synthetase (GARS) | 1 | U09587 | | + | + | + | | + | |

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|--|----|----------|--------|---|---|---|---|---|--|
| glyoxalase I (lactoyl glutathione lyase) (GLYI) | 1 | L07837 | + | + | + | + | | + | |
| golgi autoantigen, golgin subfamily a, 1 (GOLGA1) | 1 | U51587 | | + | | + | | | |
| golgi autoantigen, golgin subfamily a, 2 (GOLGA2) (non-exact, 70%) | 1 | L06147 | | | | | | | |
| golgi autoantigen, golgin subfamily a, 4 (GOLGA4) | 1 | U31906 | | | | | | | |
| golgi autoantigen, golgin subfamily b, macrogolgin (with transmembrane signal), 1 (GOLGB1) | 1 | X75304 | | + | + | + | | + | |
| gp25L2 protein | 4 | X90872 | | | | | | | |
| grancalcin | 8 | M81637 | | + | + | + | | | |
| granulin (GRN) | 16 | X62320 | + | + | + | + | | + | |
| granulin (GRN) (low match) | 1 | X62320 | | | | | | | |
| Granulysin (NKG5) | 5 | M85276 | + | | | | | + | |
| granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated serine esterase 3) (GZMA) | 1 | M18737 | + | + | + | + | | + | |
| GRB2-related adaptor protein (GRAP) | 1 | U52518 | T only | | | | | | |
| Grb2-related adaptor protein 2 (GRAP2) | 1 | AF090456 | T | | | | + | | |
| GRO1 oncogene (melanoma growth stimulating activity, alpha) (GRO1) | 1 | X54489 | | | | + | | + | |
| growth arrest and DNA-damage-inducible gene (GADD153) | 1 | S40706 | | | | | | | |
| growth arrest-specific 7 (GAS7) | 4 | AB007854 | | + | + | | | | |
| growth factor receptor-bound protein 2 (GRB2) | 1 | X62852 | B | + | | | + | + | |
| GS1 (protein of unknown | 1 | M86934 | | + | + | + | | | |

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|---|---|----------|------|---|---|---|---|---|------------------|
| function) | | | | | | | | | |
| GS3955 | 4 | D87119 | | + | + | + | | + | |
| GTP binding protein 1 (GTPBP1) | 1 | U87964 | | + | + | + | | | |
| GTP binding protein similar to <i>S. cerevisiae</i> HBS1 (HBS1) | 1 | U87791 | | + | + | + | | + | |
| GTPase activating protein-like (GAPL) | 1 | AB011110 | | + | + | + | | + | high fetal brain |
| GTP-binding protein (low match) | 1 | Z49068 | | | | | | | |
| GTP-binding protein G(K), alpha subunit (=G(I) ALPHA-3)(=GTP-binding regulatory protein Gi alpha-3 chain) | 1 | P08754 | | | | | | | |
| Gu protein (GURDB) | 2 | U41387 | + | | + | + | | + | |
| guanine nucleotide binding protein | 1 | | | | | | | | |
| guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2 (GNAI2) | 4 | J03004 | + | + | + | + | | + | |
| guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 3 (GNAI3) | 7 | M20597 | + | + | + | + | | + | |
| guanine nucleotide binding protein (G protein), alpha stimulating activity polypeptide 1 (GNAS1) | 2 | X04409 | B, T | + | | | + | + | |
| guanine nucleotide binding protein (G protein), alpha transducing activity polypeptide 2 (GNAT2) | 1 | Z18859 | | | | | | | |
| guanine nucleotide binding protein (G protein), beta 5 (GNB5) | 2 | AF017656 | | + | + | + | | + | |
| guanine nucleotide binding protein (G protein), beta polypeptide 1 (GNB1) | 5 | M36430 | + | + | + | + | + | + | |

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|---|---|----------|---|---|---|---|---|---|-----------------------------|
| guanine nucleotide binding protein (G protein), q polypeptide (GNAQ) | 2 | AF011496 | | + | + | + | | | |
| guanine nucleotide binding protein-like 1 (GNL1) | 1 | L25665 | + | + | + | + | | + | |
| guanine nucleotide exchange factor | 1 | L13857 | + | + | + | + | | | |
| guanine nucleotide regulatory factor (LFP40) | 1 | X15610 | + | + | + | + | | + | |
| guanine nucleotide regulatory factor (LFP40) | 1 | U72206 | + | + | + | + | | + | |
| GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN 12.3 (P205) (RECEPTOR OF ACTIVATED PROTEIN KINASE C 1) (RACK1) | 1 | P25388 | | | | | | | |
| GUANINE-MONOPHOSPHATE SYNTHETASE (GMPS) | 1 | U10860 | | | + | | | | |
| guanosine monophosphate reductase (GMPR) (non-exact, 72%) | 1 | M24470 | | | | | | | |
| guanosine-diphosphatase like protein | 1 | AF016032 | | | | | | | |
| guanylate binding protein 1, interferon-inducible, 67kD (GBP1) | 2 | M55542 | | + | + | + | + | + | |
| guanylate binding protein 2, interferon-inducible (GBP2) | 6 | M55543 | + | + | + | + | | + | |
| H2A histone family, member C (H2AFC) | 1 | Z83742 | | | | | | | |
| H2A histone family, member Y (H2AY) | 2 | AF041483 | + | + | + | + | | + | |
| H2B histone family, member L (H2BFL) | 2 | Z80783 | + | + | + | + | + | + | high in adrenal gland tumor |
| h2-calponin | 1 | D86059 | | | | | | | |
| H-2K binding factor-2 | 1 | L08904 | | + | + | + | | + | |
| H3 histone family, member K (H3FK) | 1 | Z83735 | | | | | | | |

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|---|----|----------|---|---|---|---|---|---|---------------------------|
| H3 histone, family 3A (H3F3A) | 7 | M11353 | + | + | + | + | | + | high in ovary |
| H3 histone, family 3B (H3.3B) (H3F3B) | 15 | Z48950 | + | + | + | + | | + | high in endothelial cells |
| hbc647 | 1 | U68494 | | + | + | + | + | | |
| heat shock 27kD protein 1 (HSPB1) | 1 | U12404 | | + | + | | + | + | |
| heat shock 40kD protein 1 (HSPF1) | 4 | D85429 | + | + | + | + | + | + | high in testis |
| heat shock 60kD protein 1 (chaperonin) (HSPD1) | 3 | M22382 | + | + | + | + | + | + | |
| heat shock 70kD protein 1 (HSPA1A) | 7 | M59828 | + | + | + | + | + | + | high in activated T cells |
| heat shock 70kD protein 5 (glucose-regulated protein, 78kD) (HSPA5) | 13 | X87949 | | + | + | | + | | |
| heat shock 70kD protein 6 (HSP70B') (HSPA6) | 4 | X51757 | + | + | + | | | | |
| heat shock 70kD protein 9B (mortalin-2) (HSPA9B) | 2 | L15189 | | + | + | + | + | + | |
| HEAT SHOCK COGNATE 71 KD PROTEIN | 1 | P11142 | | | | | | | |
| heat shock factor binding protein 1 (HSBP1) | 2 | AF068754 | | | | | | | |
| heat shock protein 90 | 13 | M27024 | + | + | + | + | + | + | high in many libraries |
| heat shock protein, DNAJ-like 2 (HSJ2) | 1 | D13388 | | + | + | | + | + | |
| Hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 1 (HERC1) | 1 | U50078 | | + | + | + | | | |
| hect domain and RLD 2 (HERC2) | 1 | AB002391 | + | + | + | + | | + | |
| helicase-like protein (HLP) | 1 | X98378 | + | + | | + | | + | |
| helix-loop-helix protein HE47 (E2A) | 1 | M65214 | | | | | | + | |

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|---|-----|----------|---|---|---|---|---|---|------------------------|
| hematopoietic cell-specific Lyn substrate 1 (HCLS1) | 18 | X16663 | + | | + | + | | + | |
| heme oxygenase (decycling) 1 (HMOX1) | 1 | X06985 | | + | | + | + | + | |
| HEMOGLOBIN ALPHA CHAIN | 1 | P19015 | | | | | | | |
| hemoglobin beta (beta globin) | 5 | AF117710 | | | | | | | |
| hemoglobin, alpha 1 (HBA1) | 301 | V00491 | | | + | | + | + | |
| hemoglobin, alpha 1 (HBA1) (low match) | 1 | V00491 | | | | | | | |
| hemoglobin, alpha 1 (low match) | 1 | V00493 | | | | | | | |
| hemoglobin, alpha 1 (non- exact, 76%) | 1 | J00153 | | | | | | | |
| hemoglobin, alpha 1 (non- exact, 82%) | 1 | V00493 | | | | | | | |
| hemoglobin, beta (HBB) | 129 | V00497 | + | + | + | + | + | + | high in many libraries |
| hemoglobin, beta (HBB) (low match) | 1 | V00497 | | | | | | | |
| hemoglobin, beta (HBB) (low match) | 1 | L48220 | | | | | | | |
| hemokine (C-X-C motif), receptor 4 (fusin) (CXCR4) | 1 | D10924 | + | + | + | + | | + | |
| hemopoietic cell kinase (HCK) | 5 | M16591 | | | | + | | + | |
| hepatitis C-associated microtubular aggregate protein p44 | 2 | D28908 | | | | | | | |
| hepatoma-derived growth factor | 1 | D16431 | + | + | + | + | | + | |
| Hermansky-Pudlak syndrome (HPS) | 2 | U65676 | | | | | | | |
| HERV-E integrase (non- exact 76%aa) | 1 | AF026246 | | | | | | | |
| heterogeneous nuclear protein similar to rat helix | 2 | S63912 | | + | + | + | | + | |

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|---|----|----------|---|---|---|---|---|---|---------------------------------------|
| destabilizing protein (FBRNP) | | | | | | | | | |
| heterogeneous nuclear ribonucleoprotein (C1/C2) (HNRPC) | 4 | M16342 | | | | | | | |
| heterogeneous nuclear ribonucleoprotein A/B (HNRPAB) | 1 | M65028 | + | + | + | + | + | + | |
| heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) | 20 | X12671 | + | + | + | + | + | + | High in alveolar rhabdomyosarcoma |
| heterogeneous nuclear ribonucleoprotein A2/B1 (HNRPA2B1) | 3 | M29064 | + | + | + | + | + | + | High in activated T cell, fetal brain |
| heterogeneous nuclear ribonucleoprotein D (hnRNP D) | 2 | D55673 | + | + | + | + | + | + | |
| heterogeneous nuclear ribonucleoprotein D-like (HNRPDL) | 5 | D89092 | + | + | + | + | + | + | |
| heterogeneous nuclear ribonucleoprotein F (HNRPF) | 1 | L28010 | + | + | + | + | | + | |
| heterogeneous nuclear ribonucleoprotein F (HNRPF) (83%) | 1 | L28010 | | | | | | | |
| heterogeneous nuclear ribonucleoprotein G (HNRPG) | 2 | Z23064 | | + | + | + | | + | |
| heterogeneous nuclear ribonucleoprotein H (HNRPH) (FTP-3) | 3 | P55795 | | | | | | | |
| heterogeneous nuclear ribonucleoprotein H (HNRPH) (low match) | 1 | P31943 | | | | | | | |
| heterogeneous nuclear ribonucleoprotein H1 (H) (HNRPH1) | 2 | L22009 | + | + | + | + | | + | |
| heterogeneous nuclear ribonucleoprotein K (HNRPK) | 21 | S74678 | + | + | + | + | + | + | |
| heterogeneous nuclear ribonucleoprotein R | 1 | AF000364 | | + | + | + | + | + | |

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|---|---|------------|---|---|---------|---|---|---|--|
| (HNRPR) | | | | | | | | | |
| heterogeneous nuclear ribonucleoprotein U (scaffold, attachment factor A) (HNRPU) | 3 | X65488 | + | + | + | + | + | + | |
| hexokinase 1 (HK1) | 2 | X66957 | | + | + | + | | + | |
| hexokinase 2 (HK2) | 3 | Z46376 | + | + | + | + | | + | |
| hexokinase 3 (HK3) | 2 | U51333 | | | | | | | |
| hexosaminidase A (alpha polypeptide) (HEXA) | 1 | S62047 | | | | | | | |
| HGMP07I gene for olfactory receptor | 2 | U76377 | | | | | | | |
| High density lipoprotein binding protein (HDLBP) | 2 | M64098 | + | + | + | + | + | + | |
| high-mobility group (nonhistone chromosomal) protein 1 (HMG1) | 5 | X12597 | + | + | + | + | + | + | |
| high-mobility group (nonhistone chromosomal) protein 1 (HMG1) (non-exact 60%) | 1 | D63874 | | | | | | | |
| High-mobility group (nonhistone chromosomal) protein 17 (HMG17) | 2 | M12623 | + | + | + | + | | + | |
| high-mobility group (nonhistone chromosomal) protein 2 (HMG2) | 2 | M83665 | + | + | + | + | + | + | |
| high-mobility group (nonhistone chromosomal) protein isoforms I and Y | 2 | L17131 | + | + | + | | + | + | |
| high-risk humanpapilloma viruses E6 oncoproteins targeted protein E6TP1 beta (=AB007900 KIAA0440) | 1 | AF090990.1 | | | | | | | |
| histidine ammonia-lyase (HAL) | 1 | D16626 | | | +, only | | | | |
| histidyl-tRNA synthetase (HARS) | 2 | Z11518 | + | + | + | + | + | + | |
| histocompatibility antigen | 1 | U31372 | | | | | | | |

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|---|-----|----------|---|---|---|---|---|---|------------------------|
| (HLA-Cw3), class I | | | | | | | | | |
| histone deacetylase 1 (HDAC) | 4 | U50079 | + | + | + | + | | + | |
| histone deacetylase 1 (HDAC1) | 2 | D50405 | + | + | + | + | | + | |
| histone deacetylase 5 (NY-CO-9) | 1 | AF039691 | | + | + | | | | |
| HK2 gene for hexokinase II | 1 | Z46362 | | | | | | | |
| HL9 monocyte inhibitory receptor precursor | 2 | U91928 | | | | + | | | |
| HLA class I heavy chain (HLA-Cw*1701) | 1 | | | | | | | | |
| HLA class I locus C heavy chain | 1 | X58536 | | | | | | | |
| HLA class II SB 4-beta chain | 1 | X03022 | | | | | | | |
| HLA class III region containing NOTCH4 gene | 1 | U89335 | + | + | + | + | | + | |
| HLA-A | 1 | Z72423 | | | | | | | |
| HLA-A | 2 | AJ006020 | | | | | | | |
| HLA-A*7402 | 1 | AJ223060 | | | | | | | |
| HLA-A11 | 1 | U02934 | | | | | | | |
| HLA-B | 2 | X75953 | | | | | | | |
| HLA-B | 1 | X83401 | | | | | | | |
| HLA-B | 1 | X78426 | | | | | | | |
| HLA-B associated transcript-1 (D6S81E) | 1 | Z37166 | + | + | + | + | + | + | |
| HLA-B associated transcript-2 (D6S51E) | 2 | M33509 | + | + | + | + | | | |
| HLA-B*1529 | 4 | D44501 | | | | | | | |
| HLA-Bw72 antigen | 119 | L09736 | + | + | + | + | + | + | high in many libraries |
| HLA-C gene (HLA-Cw*0701 allele) | 1 | D83957 | | | | | | | |

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|---|----|------------|---|---|---|---|---|---|----------------|
| HLA-Cw*0701 | 9 | Z46810 | | | | | | | |
| HLA-Cw*0801 | 1 | D64151 | | | | | | | |
| HLA-Cw*1203 | 1 | D64146 | | | | | | | |
| HLA-DC classII histocompatibility antigens alpha-chain (=K01160) | 2 | X00370 | | | | | | | |
| HLA-DR alpha-chain | 17 | M60333 | + | + | + | + | + | + | high in spleen |
| HLA-F (leukocyte antigen F) | 3 | X17093 | | | + | + | | + | |
| HMG box containing protein 1 | 3 | AF019214 | | | | | | | |
| hMLH1 (=U83845) | 1 | AB017806.1 | | | | | | | |
| Hmob33 | 3 | Y14155 | | | | | | | |
| HMT1 (hnRNP methyltransferase, S. cerevisiae)-like.1 (HRMT1L1) | 2 | U80213 | + | + | + | + | | + | |
| hnRNP C1/C2 | 2 | D28382 | | | | | | | |
| homeobox (=X58250 Mouse homeo box protein, put. transcription factor involved in embryogenesis and hematopoiesis) | 1 | M60721 | | | | | | | |
| homeobox protein (HLX1) (=M60721) | 1 | U14326 | | | | | | | |
| homeodomain-interacting protein kinase 3 (HIPK3) | 1 | AF004849 | + | | + | + | | + | |
| homolog of Drosophila past (PAST) | 2 | AF001434 | + | + | + | + | | + | |
| homolog of yeast (S. cerevisiae) ufd2 (UFD2) | 3 | D50916 | | + | + | + | | + | |
| HPV16 E1 protein binding protein | 1 | U96131 | | + | + | | | + | |
| HRIHFB2157 | 1 | AB015344 | | + | + | | | + | |
| HRX-like protein (=AF010403 ALR) | 1 | Y08836 | | | | | | | |

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|---|---|------------|---|---|---|---|---|---|--|
| hsc70 gene for 71 kd heat shock cognate protein | 3 | Y00371 | | | | | | | |
| HSPC012 | 1 | AF077036.1 | | | | | | | |
| HSPC021 | 1 | AF077207.1 | | | | | | | |
| HsPex13p | 1 | U71374 | | | | | | | |
| htra2-beta-2 | 1 | U87836 | + | + | + | + | | + | |
| HU-K4 | 1 | U60644 | | | | | | | |
| hunc18b2 | 1 | U63533 | | + | + | + | | + | |
| HUNKI | 1 | Y12059 | + | + | | + | + | + | |
| huntingtin-interacting protein HYPA/FBP11 (HYPA) | 1 | AF049528 | | | | | | | |
| hVps41p (HVPS41) | 1 | U87309 | | | | | | | |
| hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit (HADHA) | 1 | U04627 | | + | + | | + | | |
| hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) | 1 | D16481 | + | + | + | + | | + | |
| hydroxysteroid (17-beta) dehydrogenase 1 (HSD17B1) | 1 | U34879 | | + | | | + | | |
| hypothetical protein | 1 | | | | | | | | |
| hypothetical protein (AL008729) (dJ257A7.2) | 1 | | | | | | | | |
| hypothetical protein (CIT987SK_2A8_1 chromosome 8) | 1 | U96629 | | | | | | | |
| hypothetical protein (clone 24640) | 1 | AF055004 | | | | | | | |

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|---|---|------------|---|---|---|---|--|---|--|
| hypothetical protein (clone ICRFp507G2490). | 1 | Z70222 | | | | | | | |
| hypothetical protein (dJ1042K10.4) (non-exact 76%) | 1 | AL022238 | | | | | | | |
| hypothetical protein (dJ465N24.1 similar to predicted yeast and worm proteins) | 2 | AL031432 | | | | | | | |
| hypothetical protein (dJ487J7.1.1) | 2 | AL008730 | | | | | | | |
| hypothetical protein (dJ753P9.2) | 2 | AL023653 | | | | | | | |
| hypothetical protein (DKFZp586l111) | 1 | AL050131.1 | | | | | | | |
| hypothetical protein (J257A7.2) | 1 | AL008729 | | | | | | | |
| hypothetical protein (KIAA0440) (=AF026504 R.norvegicus SPA-1 like protein) | 1 | AB007900 | | | | | | | |
| hypothetical protein (L1H 3' region) | 1 | | | | | | | | |
| hypothetical protein (S164) | 1 | P49756 | | | | | | | |
| hypothetical protein (similar to thrombospondin) (non-exact 56%) | 1 | AF109907 | | | | | | | |
| hypothetical protein 3 | 1 | | | | | | | | |
| hypothetical protein B (HSU47926) (non-exact, 56%) | 1 | U47926 | | | | | | | |
| hypothetical protein from BCRA2 region (CG005) | 3 | U50532 | + | + | + | + | | + | |
| hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor) (HIF1A) | 1 | AF050115 | | | | | | | |
| Ia-associated invariant gamma-chain (clones lambda-y (1,2,3)) | 1 | M13555 | | | | | | | |

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|--|---|--------|---|---|---|---|---|---|--|
| iduronate 2-sulfatase (Hunter syndrome) (IDS) | 2 | M58342 | + | + | + | + | | + | |
| Ig heavy chain V region (=D11016) | 1 | L20779 | | | | | | | |
| Ig heavy chain variable region | 2 | M34024 | | | | | | | |
| Ig heavy chain variable region (VH4DJ) (clone T14.4) | 1 | Z75378 | | | | | | | |
| Ig heavy chain variable region (VH4DJ) (clone T22.18) | 1 | Z75392 | | | | | | | |
| Ig J chain | 1 | M12378 | | | | | | | |
| Ig kappa | 1 | S49007 | | | | | | | |
| IG kappa light chain variable region A20 | 1 | X63398 | | | | | | | |
| Ig kappa light chain, V- and J-region (=X59315) | 1 | D90158 | | | | | | | |
| Ig lambda light chain variable region (26-34)ITIIIF120) | 1 | Z85052 | | | | | | | |
| Ig mu-chain VDJ4-region | 1 | M16949 | | | | | | | |
| Ig rearranged anti-myelin kappa-chain (V-J4-region, hybridoma AE6-5) | 1 | M29469 | | | | | / | | |
| Ig rearranged H-chain mRNA V-region | 2 | M97920 | | | | | | | |
| Ig rearranged light-chain V region (=D90158) | 1 | M74020 | | | | | | | |
| IGF-II mRNA-binding protein 3 (KOC1) (non-exact, 75%) | 1 | U97188 | + | + | + | | | | |
| IgG Fc binding protein (FC(GAMMA)BP) | 1 | D84239 | + | + | | + | | + | |
| IgG heavy chain variable region (vH26) | 1 | M83136 | | | | | | | |
| IgM heavy chain (C mu, membrane exons) | 1 | X14939 | | | | | | | |

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|--|---|----------|------|---|---|---|---|---|------------------------|
| IkB kinase-beta (IKK-beta) | 1 | AF029684 | | | | | | | |
| IL-1 receptor type II | 1 | U14177 | | | | | | | |
| IL2-inducible T-cell kinase (ITK) | 2 | S65186 | | | | | | | |
| immediate early protein (ETR101) | 1 | M62831 | + | | + | + | | + | |
| immunoglobulin light chain (lambda) | 1 | D87018 | | | | | | | |
| Immunoglobulin (CD79A) binding protein 1 (IGBP1) | 1 | Y08915 | B, T | + | + | | + | | |
| immunoglobulin C (mu) and C (delta) heavy chain (=K02878) | 2 | X57331 | | | | | | | |
| immunoglobulin G Fc receptor IIIB | 1 | Z46223 | | | | | | | |
| immunoglobulin gamma 3 (Gm marker) (IGHG3) | 3 | Y14737 | + | | | + | | + | high in many libraries |
| immunoglobulin gamma heavy chain variable region (=X61011) | 1 | Z66542 | | | | | | | |
| immunoglobulin heavy chain (VI-3B) | 1 | X62109 | | | | | | | |
| immunoglobulin heavy chain J region | 1 | X86356 | | | | | | | |
| immunoglobulin heavy chain J region, B1 haplotype | 2 | X86355 | | | | | | | |
| immunoglobulin heavy chain variable region (IGH) (clone 21u-48) | 1 | AF062126 | | | | | | | |
| immunoglobulin heavy chain variable region (IGH) (clone 23u-1) | 1 | AF062212 | | | | | | | |
| immunoglobulin heavy chain variable region V1-18 (IGHV@) (=X60503) | 2 | M99641 | | | | | | | |
| immunoglobulin heavy chain variable region V3-43 (IGHV@) | 2 | M99672 | | | | | | | |

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|--|---|--------|---|---|---|---|---|---|--|
| immunoglobulin heavy chain variable region V3-7 (IGHV@) | 3 | M99649 | | | | | | | |
| immunoglobulin IgH heavy chain Fd fragment | 1 | U07986 | | | | | | | |
| immunoglobulin kappa light chain | 1 | X58081 | | | | | | | |
| immunoglobulin kappa light chain V-segment A27 | 1 | X12686 | | | | | | | |
| immunoglobulin light chain | 1 | D86990 | | | | | | | |
| immunoglobulin light chain (low match) | 1 | D86996 | | | | | | | |
| immunoglobulin light chain variable region (lambda IIIb subgroup) from IgM rheumatoid factor | 1 | L29157 | | | | | | | |
| immunoglobulin M heavy chain V region=anti-lipid A antibody | 1 | S50735 | | | | | | | |
| immunoglobulin mu (IGHM) | 9 | X57086 | + | + | | + | | + | |
| immunoglobulin mu binding protein 2 (IGHMBP2) | 1 | L24544 | T | + | | | + | | |
| immunoglobulin superfamily, member 2 (IGSF2) | 1 | Z33642 | | | | | | | |
| Immunoglobulin VH mRNA (487 bp) (=M99652 immunoglobulin heavy chain variable region V3-11 (IGHV@)) | 1 | X61013 | | | | | | | |
| imogen 38 (IMOGEN38) | 1 | Z68747 | | + | + | + | | + | |
| IMP (inosine monophosphate) dehydrogenase 1 (IMPDH1) | 1 | J05272 | + | + | + | + | | | |
| IMP (inosine monophosphate) dehydrogenase 2 (IMPDH2) | 2 | L39210 | + | + | + | + | | + | |
| inc finger protein 151 (pHZ-67) (ZNF151) | 1 | Y09723 | + | + | + | + | | + | |

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|--|---|----------|---|---|---|---|---|---|--|
| inc finger protein, C2H2, rapidly turned over (ZNF20) | 1 | AF011573 | | + | + | | | | |
| inducible poly(A)-binding protein (IPABP) | 1 | U33818 | + | + | + | + | | + | |
| inducible poly(A)-binding protein (IPABP) (low match) | 1 | U33818 | | | | | | | |
| inducible protein (Hs.80313) | 2 | L47738 | + | + | + | + | | + | |
| inhibitor of DNA binding 2, dominant negative helix-loop-helix protein (ID2) | 4 | M97796 | + | + | + | + | + | + | |
| inhibitor of kappa light, polypeptide gene enhancer in B-cells, kinase complex-associated protein (IKBKAP) | 2 | AF044195 | | | | | | | |
| inositol 1,3,4-trisphosphate 5/6-kinase | 1 | U51336 | + | + | + | + | + | + | |
| inositol 1,4,5 trisphosphate receptor type 1 (ITPR1) | 1 | U23850 | | + | + | + | | | |
| inositol 1,4,5-trisphosphate 3-kinase B (ITPKB) | 2 | X57206 | B | + | + | | + | | |
| inositol monophosphatase | 1 | S38980 | | | | | | | |
| inositol polyphosphate-5-phosphatase, 145kD (INPP5D) | 2 | U84400 | + | + | + | + | | + | |
| Ins(1,3,4,5)P4-binding protein | 1 | X89399 | | + | | | | + | |
| insulin-like growth factor 2 receptor (IGF2R) | 5 | Y00285 | + | + | + | + | | + | |
| integral membrane protein 1 (ITM1) | 1 | L38961 | | | + | + | | + | |
| integral membrane protein 2C (ITM2C) | 1 | AF038953 | T | | + | | + | + | |
| integral membrane protein Tmp21-l (p23) | 3 | U61734 | + | + | + | + | + | + | |
| integrin beta 4 binding protein (ITGB4BP) | 2 | AF047433 | | | + | | | + | |

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|--|----|--------|---|---|---|---|---|---|--|
| integrin, alpha 2b (platelet glycoprotein IIb of IIb/IIIa complex, antigen CD41B) (ITGA2B) | 3 | M34480 | | + | | | + | | |
| integrin, alpha 5 (fibronectin receptor, alpha polypeptide) (ITGA5) | 4 | X06256 | + | + | + | | + | + | |
| integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide) (ITGAL) | 6 | Y00796 | | | | | | | |
| integrin, alpha M (complement component receptor 3, alpha; also known as CD11b (p170), macrophage antigen alpha polypeptide) (ITGAM) | 1 | M18044 | | | | | | | |
| integrin, alpha X (antigen CD11C (p150), alpha polypeptide) (ITGAX) | 1 | M81695 | + | + | | | | + | |
| integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2 MSK12) (ITGB1) | 2 | X07979 | | | | | | | |
| integrin, beta 2 (antigen CD18 (p95), lymphocyte function-associated antigen 1; macrophage antigen 1 (mac-1) beta subunit) (ITGB2) | 32 | M15395 | + | + | | + | | + | |
| integrin, beta 7 (ITGB7) | 1 | M68892 | + | | | | | | |
| Integrin-linked kinase (ILK) | 1 | U40282 | + | + | + | + | | + | |
| intercellular adhesion molecule 1 (CD54), human rhinovirus receptor (ICAM1) | 1 | J03132 | + | | | + | + | + | |
| intercellular adhesion molecule 2 (ICAM2) | 1 | X15606 | + | + | + | + | | + | |
| intercellular adhesion molecule 3 (ICAM3) | 6 | X69819 | + | | | | | + | |
| intercellular adhesion molecule 4, Landsteiner-Wiener blood group (ICAM4) | 1 | L27670 | | | | | | + | |

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|---|---|--------|---------------|---|---|---|---|---|----------------------|
| Interferon consensus sequence binding protein 1 (ICSBP1) | 1 | M91196 | W, T lymphoma | | | | | | |
| Interferon consensus sequence binding protein 1 (ICSBP1) (low match) | 1 | M91196 | | | | | | | |
| interferon regulatory factor 2 (IRF2) | 4 | X15949 | + | + | + | + | | | |
| interferon regulatory factor1 (IRF1) | 4 | L05072 | + | + | + | + | | + | |
| interferon regulatory factor5 (IRF5) | 1 | U51127 | + | + | | + | | | |
| interferon, gamma-inducible protein 16 (IFI16) | 2 | M63838 | + | + | + | + | | + | |
| interferon, gamma-inducible protein 30 (IFI30) | 9 | J03909 | + | + | | + | | + | |
| INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1 (GUANINE NUCLEOTIDE-BINDING PROTEIN 1) (non-exact 62%) | 1 | P32455 | | | | | | | |
| interferon-induced protein 17 (IFI17) | 3 | X84958 | | + | + | + | | + | |
| interferon-induced protein 54 (IFI54) | 5 | M14660 | | | | | | | |
| interferon-inducible (1-8D) | 5 | X57351 | T | | + | | + | + | |
| interferon-inducible (1-8U) | 1 | X57352 | | | + | | + | + | |
| interferon-related developmental regulator 1 (IFRD1) | 5 | Y10313 | | + | + | | | + | |
| interferon-stimulated transcription factor 3, gamma (48kD) (ISGF3G) | 2 | M87503 | | + | | + | | + | |
| interleukin 1 receptor, type II (IL1R2) | 1 | U64094 | | | | + | | | |
| Interleukin 10 receptor, beta (I.10RB) | 1 | U08988 | T activated | | + | | | + | |
| interleukin 12 receptor, beta 1 (IL12RB1) | 2 | U03187 | + | | | | | | only found in T cell |

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|--|----|----------|---|---|---|---|---|---|---|
| interleukin 13 receptor, alpha 1 (IL13RA1) | 2 | Y09328 | | + | + | + | + | + | |
| interleukin 16 (lymphocyte chemoattractant factor) (IL16) | 6 | U82972 | | + | | | | | |
| interleukin 18 receptor 1 (IL18R1) | 1 | U43672 | | | | | | | |
| interleukin 2 receptor, beta (IL2RB) | 9 | M26062 | | | | | | | |
| interleukin 2 receptor, gamma (severe combined immunodeficiency) (IL2RG) | 6 | D11086 | + | | + | | | + | |
| interleukin 4 receptor (IL4R) | 3 | X52425 | + | + | | + | | + | |
| interleukin 6 receptor (IL6R) | 5 | X12830 | | + | | | | + | |
| interleukin 6 signal transducer (gp130, oncostatin M receptor) (IL6ST) | 1 | M57230 | | | | | | | |
| interleukin 7 receptor (IL7R) | 14 | M29696 | + | | | | | + | |
| interleukin 7 receptor (IL7R) (low match) | 1 | AF043123 | | | | | | | |
| interleukin 8 (IL8) | 8 | Y00787 | + | | + | | + | | High in activated T cells, bone and pancreatic islets |
| interleukin 8 receptor alpha (IL8RA) | 11 | L19591 | | | | | | | |
| interleukin 8 receptor, beta (IL8RB) | 14 | M94582 | | | | | | | |
| interleukin enhancer binding factor 2, 45kD (ILF2) | 3 | U10323 | + | + | + | + | + | + | high in uterus |
| interleukin enhancer binding factor 3, 90kD (ILF3) | 2 | U10324 | | | | | | | |
| interleukin-1 receptor-associated kinase 1 (IRAK1) | 2 | L76191 | | + | + | + | | + | |

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|--|---|----------|---|---|---|---|---|---|--|
| interleukin-1 receptor-associated kinase 1 (low match) | 1 | U52112 | | | | | | | |
| interleukin-10 receptor, alpha (IL10RA) | 5 | U00672 | + | + | + | + | | | |
| interleukin-11 receptor, alpha (IL11RA) | 7 | Z38102 | | + | + | | | | |
| INTERLEUKIN-14 PRECURSOR (IL-14) (HIGH MOLECULAR WEIGHT B-CELL GROWTH FACTOR) (HMW-BCGF) (non-exact 46%) | 1 | P40222 | | | | | | | |
| intestinal carboxylesterase; liver carboxylesterase-2 (ICE) | 1 | U60553 | | + | | | + | | |
| inversin protein (non-exact 52%) | 1 | AF084367 | | | | | | | |
| IQ motif containing GTPase activating protein 1 (IQGAP1) | 6 | L33075 | | | | | | | |
| IQ motif containing GTPase activating protein 2 (IQGAP2) | 1 | U51903 | | + | | + | | | |
| isocitrate dehydrogenase 1 (NADP+), soluble (IDH1) | 1 | AF020038 | + | + | + | + | + | + | |
| isocitrate dehydrogenase 2 (NADP+), mitochondrial (IDH2) | 2 | X69433 | + | + | + | + | + | + | |
| isocitrate dehydrogenase 3 (NAD+) alpha (IDH3A) | 2 | U07681 | | | + | | | | |
| isocitrate dehydrogenase 3 (NAD+) gamma (IDH3G) | 1 | Z68907 | + | + | + | + | | + | |
| isolate Aus3 cytochrome b (CYTB) | 1 | AF042516 | | | | | | | |
| isolate TzCCR5-179 CCR5 receptor (CCR5) | 1 | AF011524 | | | | | | | |
| isopentenyl-diphosphate delta isomerase (IDI1) | 5 | X17025 | + | + | + | + | | + | |
| Janus kinase 1 (a protein) | 4 | M64174 | + | + | + | + | | + | |

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|---|---|----------|---|---|---|---|---|---|--------------------|
| tyrosine kinase) (JAK1) | | | | | | | | | |
| Janus kinase 2 (a protein tyrosine kinase) (JAK2) | 1 | AF005216 | | | | | | | |
| Jk-recombination signal binding protein (RBPJK) | 2 | L07876 | | | | | | | |
| JM1 protein | 1 | AJ005890 | | + | | + | | | |
| jumonji (mouse) homolog (JMJ) | 1 | U57592 | | + | + | + | | + | |
| jun D proto-oncogene (JUND) | 1 | X51346 | + | + | + | + | | + | |
| jun dimerization protein | 1 | AF111167 | | | | | | | only found in germ |
| junction plakoglobin (JUP) | 1 | M23410 | | + | + | + | | + | |
| kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monoclonal and antibody IA4)) (KAI1) | 1 | U20770 | + | + | + | + | + | + | |
| karyopherin (importin) beta 1 (KPNB1) | 2 | L39793 | + | + | + | + | + | + | |
| karyopherin (importin) beta 2 (KPNB2) | 1 | U72395 | + | + | + | + | | | |
| karyopherin alpha 1 (importin alpha 5) (KPNA1) | 1 | S75295 | + | + | + | | + | | |
| karyopherin alpha 2 (RAG cohort 1, importin alpha 1) (DPNA2) | 1 | U09559 | | | | | | | |
| karyopherin alpha 3 (importin alpha 4) (KPNA3) | 1 | D89618 | | + | | | + | | |
| karyopherin alpha 4 (KPNA4) | 1 | M17887 | | + | + | | | | |
| Katanin (80 kDa) (KAT) | 1 | AF052432 | | + | + | + | | + | |
| KE03 protein | 2 | AF064604 | | | | | | | |
| Kelch-like ECH-associated protein 1 (KIAA0132) (66%aa) | 1 | D50922 | | | | | | | |

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|--|----|--------|---|---|---|---|---|---|--------------------|
| Keratin 8 (KRT8) | 1 | X74929 | | + | + | + | + | + | |
| ketohehexokinase (fructokinase) (KHK) | 1 | X78678 | | + | | + | + | | |
| KIAA0001 (KIAA0001) (72% aa) | 1 | Q15391 | | | | | | | |
| KIAA0001 (KIAA0001) (76% aa) | 1 | Q15391 | | | | | | | |
| KIAA0001 (KIAA0001) (non-exact 72%) | 1 | Q15391 | | | | | | | |
| KIAA0002 (KIAA0002) | 5 | D13627 | | + | + | + | | + | |
| KIAA0005 (KIAA0005) | 4 | D13630 | | + | + | + | | + | |
| KIAA0010 (KIAA0010) | 1 | D13635 | | + | | | | + | |
| KIAA0016 (KIAA0016) | 1 | D13641 | + | + | + | + | | + | |
| KIAA0017 (KIAA0017) | 2 | D87686 | | | | | | | |
| KIAA0022 (KIAA0022) | 2 | D14664 | | + | + | + | | | |
| KIAA0023 (KIAA0023) | 1 | D14689 | | + | | | | | |
| KIAA0024 (KIAA0024) | 1 | D14694 | + | + | + | + | | + | |
| KIAA0025 (KIAA0025) | 1 | D14695 | | + | + | + | + | + | |
| KIAA0026 (KIAA0026) | 2 | D14812 | | + | + | + | | + | |
| KIAA0027 | 1 | D25217 | | + | | | | | |
| KIAA0032 (KIAA0032) | 2 | D25215 | | + | + | + | | | |
| KIAA0040 (KIAA0040) | 1 | D25539 | + | + | + | + | | + | |
| KIAA0050 (KIAA0050) | 4 | D26069 | | | | | | | |
| KIAA0053 (KIAA0053) | 17 | D29642 | + | | + | + | | | |
| KIAA0057 (KIAA0057) | 1 | D31762 | + | + | + | + | + | + | high in fetal lung |
| KIAA0058 (KIAA0058) | 11 | D31767 | + | + | + | + | | + | |
| KIAA0063 (KIAA0063) | 3 | D31884 | + | + | + | + | | + | |
| KIAA0064 (KIAA0064) | 1 | D31764 | + | + | + | + | | + | |
| KIAA0066 | 1 | D31886 | + | + | + | + | | + | |

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|---------------------------|----|----------|---|---|---|---|---|---|--|
| KIAA0068 | 1 | D38549 | | + | + | + | + | + | |
| KIAA0073 | 3 | D38552 | | + | + | + | | + | |
| KIAA0081 | 2 | D42039 | | + | | + | | + | |
| KIAA0084 | 2 | D42043 | + | + | + | + | | + | |
| KIAA0085 | 26 | U30498 | + | + | + | + | + | + | |
| KIAA0088 | 3 | D42041 | + | + | + | + | + | + | |
| KIAA0090 | 2 | D42044 | + | + | + | + | + | + | |
| KIAA0092 (KIAA0092) | 1 | D42054 | | + | + | + | | + | |
| KIAA0094 | 3 | D42084 | | | + | + | | | |
| KIAA0095 (KIAA0095) | 1 | D42085 | | | | | | | |
| KIAA0096 | 1 | D43636 | + | + | + | + | | + | |
| KIAA0097 (KIAA0097) | 1 | X92474 | T | + | + | | + | | |
| KIAA0099 (KIAA0099) | 3 | D43951 | + | + | + | + | + | + | |
| KIAA0102 (KIAA0102) | 2 | D14658 | | + | | + | + | + | |
| KIAA0105 | 1 | D14661 | B | + | | | + | + | |
| KIAA0120 | 2 | P37802 | | | | | | | |
| KIAA0120 (non-exact, 65%) | 1 | M83106 | | | | | | | |
| KIAA0121 (KIAA0121) | 1 | D50911 | + | + | + | + | | + | |
| KIAA0123 | 1 | D21064 | | + | + | + | | + | |
| KIAA0128 | 1 | D50918 | + | + | + | + | | + | |
| KIAA0129 (KIAA0129) | 1 | D50919 | + | + | + | + | | | |
| KIAA0130 (KIAA0130) | 1 | AF055995 | | + | + | + | | | |
| KIAA0136 | 2 | D50926 | | | | | | | |
| KIAA0137 (KIAA0137) | 1 | AB004885 | | + | + | + | | + | |
| KIAA0140 (KIAA0140) | 1 | D50930 | + | + | | + | | + | |
| KIAA0141 (KIAA0141) | 3 | D50931 | | | | | | | |

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|---------------------------------|---|--------|---|---|---|---|---|---|--|
| KIAA0144 (KIAA0144) | 3 | D63478 | + | + | + | + | | + | |
| KIAA0144 (KIAA0144) (low match) | 1 | D63478 | | | | | | | |
| KIAA0144 (non-exact 61%) | 1 | Q14157 | | | | | | | |
| KIAA0144 (non-exact 65%) | 1 | Q14157 | | | | | | | |
| KIAA0146 | 2 | D63480 | | + | + | + | | + | |
| KIAA0148 (KIAA0148) | 1 | D63482 | | + | | | | + | |
| KIAA0154 | 2 | D63876 | + | + | + | + | | + | |
| KIAA0156 | 1 | D63879 | | + | + | + | | + | |
| KIAA0160 | 2 | D63881 | | | | | | | |
| KIAA0161 (KIAA0161) | 1 | D79983 | + | + | | + | | | |
| KIAA0164 (KIAA0164) | 3 | D79986 | | | | | | | |
| KIAA0167 (KIAA0167) | 1 | D79989 | | + | | | | | |
| KIAA0168 (KIAA0168) | 3 | D79990 | | + | + | + | | + | |
| KIAA0169 | 3 | D79991 | | | | | | | |
| KIAA0171 (KIAA0171) | 3 | D79993 | | + | + | + | | + | |
| KIAA0174 (KIAA0174) | 7 | D79996 | + | + | + | + | | + | |
| KIAA0179 | 2 | D80001 | | + | + | + | | + | |
| KIAA0181 | 1 | D80003 | | + | + | + | | + | |
| KIAA0183 | 4 | D80005 | + | + | + | + | + | + | |
| KIAA0184 | 1 | D80006 | + | + | + | + | | + | |
| KIAA0191 (72% aa) | 1 | D83776 | | | | | | | |
| KIAA0191 (non-exact 77%) | 1 | | | | | | | | |
| KIAA0193 (KIAA0193) | 1 | D83777 | + | + | + | + | | + | |
| KIAA0200 (KIAA0200) | 1 | D83785 | | + | + | + | | + | |
| KIAA0210 (KIAA0210) | 3 | D86965 | | | | | | | |
| KIAA0217 | 2 | D86971 | + | + | + | + | | + | |

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|---|----|----------|---|---|---|---|---|---|--|
| KIAA0219 | 2 | U77700 | | + | + | + | | + | |
| KIAA0222 (KIAA0222) | 1 | D86975 | | | | | | | |
| KIAA0223 | 2 | D86976 | | | | | | | |
| KIAA0229 | 1 | D86982 | + | + | | | | | |
| KIAA0232 (KIAA0232) | 1 | D86985 | | + | + | + | | + | |
| KIAA0233 (KIAA0233) | 1 | D87071 | | | | | | | |
| KIAA0235 | 2 | D87078 | + | + | + | + | | | |
| KIAA0239 | 1 | D87076 | + | + | | | | | |
| KIAA0239 (non-exact 80%) | 1 | D87076 | | | | | | | |
| KIAA0240 | 1 | D87077 | | | | | | | |
| KIAA0242 | 4 | D87684 | + | + | + | + | + | + | |
| KIAA0248 | 2 | D87435 | | + | + | + | | + | |
| KIAA0249 (KIAA0249) | 3 | D87436 | + | + | + | + | | + | |
| KIAA0253 | 5 | D87442 | + | + | + | + | + | + | |
| KIAA0254 (KIAA0254) | 1 | D87443 | | + | + | + | | | |
| KIAA0255(KIAA0255) | 4 | D87444 | | + | + | + | | + | |
| KIAA0262 (KIAA0262) | 3 | D87451 | + | + | + | + | | + | |
| KIAA0263 (KIAA0263) | 1 | D87452 | + | + | + | + | | + | |
| KIAA0264 | 3 | D87453 | | + | + | + | | + | |
| KIAA0268 | 1 | D87742 | + | + | | + | | + | |
| KIAA0269 | 1 | Q92558 | | | | | | | |
| KIAA0275 (KIAA0275) | 13 | D87465 | + | + | | + | | + | |
| KIAA0304 (KIAA0304) | 2 | AB002302 | + | + | + | + | + | + | |
| KIAA0308 | 2 | AB002306 | | + | + | | | + | |
| KIAA0310 (KIAA0310) | 1 | AB002308 | | + | + | + | | + | |
| KIAA0314 (=U96635 M.musculus ubiquitin protein ligase Nedd-4) | 3 | AB002312 | | | | | | | |

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|--|---|----------|---|---|---|---|---|---|--|
| KIAA0315 (KIAA0315) | 4 | AB002313 | | + | + | + | + | + | |
| KIAA0325 (=L08505 R.norvegicus cytoplasmic dynein heavy chain (MAP 1C)) | 2 | AB002323 | | | | | | | |
| KIAA0329 (KIAA0329) | 1 | AB002327 | | + | + | + | | + | |
| KIAA0330 | 1 | AB002328 | + | + | + | | | + | |
| KIAA0332 | 1 | AB002330 | | + | + | + | | + | |
| KIAA0333 | 2 | AB002331 | | + | + | + | + | + | |
| KIAA0336 (KIAA0336) | 3 | AB002334 | + | + | + | + | | + | |
| KIAA0336 (KIAA0336) (low match) | 1 | AB002334 | | | | | | | |
| KIAA0342 (KIAA0342) | 1 | AB002340 | | + | + | | | + | |
| KIAA0344 (KIAA0344) | 2 | AB002342 | | | | + | | + | |
| KIAA0354 (KIAA0354) | 1 | AB002352 | + | + | + | + | | + | |
| KIAA0365 (KIAA0365) | 3 | AB002363 | + | + | + | + | + | + | |
| KIAA0370 | 6 | AB002368 | | + | + | + | + | + | |
| KIAA0372 (KIAA0372) | 1 | AB002370 | | | | | | | |
| KIAA0373 (KIAA0373) | 1 | AB002371 | | + | | + | | | |
| KIAA0375 (KIAA0375) | 1 | AB002373 | | + | | + | | | |
| KIAA0377 (KIAA0377) | 1 | AB002375 | | + | | + | + | | |
| KIAA0379 | 1 | AB002377 | | | | + | | | |
| KIAA0379 (non-exact, 65%) | 1 | AB002377 | | | | | | | |
| KIAA0380 (KIAA0380) | 1 | AB002378 | + | + | | + | | + | |
| KIAA0380 (KIAA0380) (60%aa) | 1 | AB002378 | | | | | | | |
| KIAA0382 (KIAA0382) | 2 | AB002380 | | + | + | + | | + | |
| KIAA0383 | 1 | AB002381 | | | | | | | |
| KIAA0386 (KIAA0386) | 5 | AB002384 | | | | | | | |

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|--------------------------|---|----------|---|---|---|---|---|---|---------------|
| KIAA0392 | 1 | AB002390 | | | | | | | |
| KIAA0397 (KIAA0397) | 4 | AB007857 | | + | + | + | + | + | |
| KIAA0403 | 3 | AB007863 | | | | | | | |
| KIAA0404 | 1 | AB007864 | | + | | + | | | |
| KIAA0409 | 1 | AB007869 | | + | | + | | | |
| KIAA0421 | 1 | AB007881 | + | + | + | | | + | |
| KIAA0424 (non-exact 82%) | 1 | AB007884 | | | | | | | |
| KIAA0428 (KIAA0428) | 9 | Y13829 | | | | | | | |
| KIAA0429 (KIAA0429) | 2 | AB007889 | + | + | + | + | | + | |
| KIAA0430 (KIAA0430) | 2 | AB007890 | | | | | | | only in ovary |
| KIAA0432 (KIAA0432) | 2 | U86753 | T | + | + | | | | |
| KIAA0435 (KIAA0435) | 1 | AB007895 | | | | | | | |
| KIAA0438 (KIAA0438) | 1 | AB007898 | | + | + | + | | + | |
| KIAA0447 (KIAA0447) | 3 | AB007916 | + | + | + | + | | + | |
| KIAA0449 | 1 | AB007918 | | + | | | | + | |
| KIAA0456 | 1 | AB007925 | | + | + | + | | + | |
| KIAA0458 (KIAA0458) | 1 | AB007927 | | | | | | | |
| KIAA0462 | 1 | AB007931 | + | + | + | + | | + | |
| KIAA0465 | 1 | AB007934 | | + | + | + | + | + | |
| KIAA0476 (KIAA0476) | 1 | AB007945 | | + | + | + | | | |
| KIAA0489 | 1 | AB007958 | | | | | | | |
| KIAA0494 (KIAA0494) | 1 | AB007963 | + | + | + | + | | + | |
| KIAA0515 | 1 | AB011087 | + | + | + | + | | + | |
| KIAA0521 | 3 | AB011093 | + | + | | | | + | |
| KIAA0525 | 1 | AB011097 | | + | | + | | | |
| KIAA0530 | 1 | AB011102 | | + | + | + | | | |
| KIAA0532 | 1 | AB011104 | + | + | + | + | | + | |

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|---------------------|---|----------|---|---|---|---|--|---|--|
| KIAA0537 (KIAA0537) | 1 | AB011109 | | | | | | | |
| KIAA0540 | 1 | AB011112 | + | + | + | + | | + | |
| KIAA0543 | 1 | AB011115 | | | + | + | | + | |
| KIAA0544 | 1 | AB011116 | | + | + | + | | + | |
| KIAA0549 | 2 | AB011121 | | + | + | + | | + | |
| KIAA0551 | 2 | AB011123 | | + | | | | + | |
| KIAA0554 | 8 | AB011126 | | + | + | + | | + | |
| KIAA0561 | 1 | AB011133 | | + | | + | | | |
| KIAA0562 (KIAA0562) | 1 | AB011134 | | | | | | | |
| KIAA0563 (KIAA0563) | 1 | AB011135 | | | | | | | |
| KIAA0569 (KIAA0569) | 2 | AB011141 | | + | + | + | | + | |
| KIAA0571 (KIAA0571) | 2 | AB011143 | | + | + | + | | | |
| KIAA0573 | 1 | AB011145 | | + | | + | | + | |
| KIAA0576 | 1 | AB011148 | | | | | | | |
| KIAA0580 | 1 | AB011152 | | | | | | | |
| KIAA0584 | 1 | AB011156 | | + | | | | | |
| KIAA0592 | 3 | AB011164 | + | + | + | + | | + | |
| KIAA0596 | 1 | AB011168 | | + | + | | | | |
| KIAA0598 (KIAA0598) | 1 | AB011170 | | + | + | + | | | |
| KIAA0608 | 1 | AB011180 | | | + | + | | | |
| KIAA0614 | 2 | AB014514 | + | + | + | + | | + | |
| KIAA0615 (KIAA0615) | 1 | AB014515 | | | | | | | |
| KIAA0621 | 1 | AB014521 | | + | + | | | + | |
| KIAA0648 | 1 | AB014548 | | + | + | + | | + | |
| KIAA0652 (KIAA0652) | 1 | AB014552 | + | + | + | + | | + | |
| KIAA0668 | 1 | AB014568 | | | | | | | |
| KIAA0669 | 1 | AB014569 | | | | | | | |

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|--------------------------|---|----------|---|---|---|---|---|---|--------------------|
| KIAA0671 (KIAA0671) | 1 | AB014571 | | | + | + | | + | |
| KIAA0675 (KIAA0675) | 1 | AB014575 | | + | | + | + | | |
| KIAA0676 | 1 | AB014576 | | + | + | + | | + | |
| KIAA0677 (KIAA0677) | 2 | AB014577 | | + | + | + | + | + | |
| KIAA0678 | 1 | AB014578 | + | + | + | + | | + | |
| KIAA0679 | 6 | AB014579 | | + | + | + | | + | |
| KIAA0680 (KIAA0680) | 1 | AB014580 | | | | | | | |
| KIAA0692 | 1 | AB014592 | + | + | + | + | | + | |
| KIAA0697 | 1 | AB014597 | | | | | | | |
| KIAA0699 | 1 | AB014599 | + | + | + | + | | + | |
| KIAA0700 | 1 | AB014600 | | + | + | + | | + | |
| KIAA0737 (KIAA0737) | 3 | AF014837 | + | + | + | + | | + | |
| KIAA0748 (KIAA0748) | 2 | AB018291 | | + | | | | | |
| KIAA0763 (KIAA0763) | 2 | AB018306 | + | + | + | + | | + | |
| KIAA0769 (KIAA0769) | 2 | AB018312 | | + | + | + | | + | |
| KIAA0782 | 1 | AB018325 | + | + | | + | | | high in BPH stroma |
| KIAA0796 | 1 | AB018339 | | + | + | + | | + | |
| KIAA0798 (KIAA0798) | 1 | AB018341 | | | | | | | |
| KIAA0823 | 1 | AB020630 | | | | | | | |
| KIAA0854 | 1 | AB020661 | + | + | + | + | | + | |
| KIAA0856 | 1 | AB020663 | | + | + | + | | + | |
| KIAA0860 | 1 | AB020667 | | + | | + | | | |
| KIAA0862 | 1 | AF054828 | | + | + | + | | | |
| KIAA0871 (non-exact 88%) | 1 | AB020678 | | | | | | | |
| KIAA0873 | 1 | AB020680 | | + | + | + | | + | |
| KIAA0892 | 1 | AB020699 | + | + | + | + | | + | |
| KIAA0906 | 1 | AB020713 | + | + | + | + | | + | |

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|--|----|------------|---|---|---|---|---|---|---|-------------------------------|
| KIAA0991 | 1 | AB023208.1 | | | | | | | | |
| killer cell lectin-like receptor subfamily B, member 1 (KLRB1) | 1 | U11276 | | | + | + | | | + | |
| killer cell lectin-like receptor subfamily C, member 4 (KLRC4) | 1 | U96846 | | | | | | | | |
| kinectin 1 (kinesin receptor) (KTN1) | 1 | D13629 | | | | | | | | |
| kinesin family member 5B (KIF5B) | 2 | X65873 | | + | + | + | | | | |
| kinesin-like DNA binding protein | 1 | AB017430 | + | + | + | + | | | + | |
| Krueppel-related DNA-binding protein (TF6) (low match) | 1 | M61869 | | | | | | | | |
| Kruppel related gene (clone pHKR1RS) | 1 | M20675 | | | | | | | | |
| Kruppel-like zinc finger protein Zf9 | 3 | U51869 | + | + | + | + | + | + | | |
| Kruppel-like zinc finger protein Zf9 (non-exact 76%) | 1 | U44975 | | + | + | | | + | + | |
| kruppel-type zinc finger protein, ZK1 | 1 | AB011414.1 | | | | | | | | |
| L apoferritin | 3 | X03742 | | | | | | | | |
| lactate dehydrogenase A (LDHA) | 3 | X02152 | | + | + | + | + | + | | |
| lactate dehydrogenase A (LDHA) (non-exact, 81%) | 1 | X02152 | | | | | | | | |
| lactate dehydrogenase B (LDHB) | 6 | X13794 | + | + | + | + | + | + | | high in fetal lung fibroblast |
| lactotransferrin (LTF) | 1 | U07643 | + | | | + | | | + | high in bone marrow |
| laminin binding protein (low score) | 1 | D28372 | | | | | | | | |
| laminin receptor 1 (67kD); Ribosomal protein SA (LAMR1) | 20 | X15005 | + | + | + | + | + | + | | high in many libraries |

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|--|---|----------|---|---|---|---|---|---|---------------------|
| laminin receptor homolog {3' region} | 1 | S35960 | | | | | | | |
| laminin, gamma 1 (formerly LAMB2) (LAMC1) | 2 | J03202 | + | + | + | | | + | |
| latent transforming growth factor beta binding protein 1 (LTBP1) | 2 | M34057 | | + | + | + | | + | |
| LAZ3/BCL6 (=Z79582;D28522/4) | 1 | Z79581 | | | | | | | |
| LDLC | 2 | Z34975 | + | + | + | + | | + | |
| lecithin-cholesterol acyltransferase (LCAT) (non-exact, 66%) | 1 | M17959 | | | | | | | |
| lectin, galactoside-binding, soluble, 2 (galectin 2) (LGALS2) | 1 | M87842 | | | | + | | | |
| lectin, galactoside-binding, soluble, 3 binding protein (galectin 6 binding protein) (LGALS3BP) | 1 | L13210 | + | + | + | + | | + | |
| leucine rich repeat (in FLII) interacting protein 1 (LRRFIP1) | 5 | AJ223075 | + | + | + | + | + | + | |
| leucocyte immunoglobulin- like receptor-5 (LIR-5) | 2 | AF072099 | | | | + | | | |
| leucocyte immunoglobulin- like receptor-6a (LIR-6) | 7 | AF025530 | | | | | | | |
| leucocyte immunoglobulin- like receptor-7 (LIR-7) | 2 | U82275 | | + | | | | | only found in CNS |
| leukemia virus receptor 1 (GLVR1) | 1 | L20859 | + | + | + | + | | + | |
| leukocyte adhesion protein p150,95 alpha subunit | 1 | M29484 | | | | | | | |
| leukocyte antigen, HLA-A2 | 3 | Y13267 | | | | | | | |
| leukocyte immunoglobulin- like receptor (MIR-10) | 3 | AF025528 | | + | | | | | |
| leukocyte tyrosine kinase (LTK) | 1 | X60702 | + | | | | | | found only in blood |

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|---|---|----------|------|---|---|---|---|---|-----------------------|
| leukocyte-associated Ig-like receptor 1 (LIAR1) | 3 | AF013249 | | | | + | | | |
| leukotriene A4 hydrolase (LTA4H) | 6 | J03459 | + | + | + | + | + | + | |
| leupaxin (LDPL) | 2 | AF062075 | + | | | + | | + | |
| ligase I, DNA, ATP-dependent (LIG1) | 1 | M36067 | B, T | + | + | | + | + | |
| LIM and SH3 protein 1 (LASP1) | 2 | X82456 | + | + | + | + | + | + | |
| LIM domain kinase 2 (LIMK2) | 2 | AC002073 | + | + | + | + | | + | |
| line-1 protein | 1 | | | | | | | | |
| Line-1 repeat mRNA with 2 open reading frames | 1 | U93566 | + | + | + | + | + | + | |
| Line-1 repeat with 2 open reading frames | 1 | M22332 | + | + | + | + | + | + | high in gastric tumor |
| LINE-1 REVERSE TRANSCRIPTASE HOMOLOG | 1 | P08547 | | | | | | | |
| lipase A, lysosomal acid, cholesterol esterase (Wolman disease) (LIPA) | 4 | X76488 | + | + | + | + | | + | |
| lipase, hormone-sensitive (LIPE) | 1 | L11706 | + | + | | | | + | |
| LMP7 | 1 | L11045 | | | | | | | |
| Lon protease-like protein (LONP) | 2 | X74215 | + | + | + | + | | + | |
| low density lipoprotein-related protein 1 (alpha-2-macroglobulin receptor) (LRP1) | 2 | AF058414 | | | | | + | | only in liver |
| low density lipoprotein-related protein-associated protein 1 (alpha-2-macroglobulin receptor-associated protein 1) (LRPAP1) | 1 | M63959 | | + | + | | + | + | |
| low density lipoprotein-related protein-associated protein 1 (alpha-2-macroglobulin receptor- | 1 | M63959 | | | | | | | |

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|---|----|----------|-------------------------|---|---|---|---|---|--|
| associated protein 1) (LRPAP1) (non-exact, 75%) | | | | | | | | | |
| low-affinity Fc-gamma receptor IIA | 1 | L08107 | | | | | | | |
| LPS-induced TNF-alpha factor (PIG7) | 9 | AF010312 | + | + | + | + | + | + | |
| Lst-1 | 1 | U00921 | + | + | + | + | | + | |
| L-type amino acid transporter subunit LAT1 | 1 | AF104032 | | | | | | | |
| lung resistance-related protein (LRP) | 1 | X79882 | + | + | + | + | | + | |
| Lymphocyte antigen 75 (LY75) | 1 | AF011333 | B | | | | | | |
| lymphocyte antigen 9 (LY9) | 2 | L42621 | | | | | | | |
| lymphocyte antigen HLA-B*4402 and HLA-B*5101 | 2 | L42345 | | | | | | | |
| lymphocyte cytosolic protein 1 (L-plastin) (LCP1) | 42 | J02923 | | | | | | | |
| lymphocyte cytosolic protein 2 (SH2 domain-containing leukocyte protein of 76kD) (LCP2) | 4 | U20158 | T lymphoma, T activated | | | | | | |
| lymphocyte glycoprotein T1/Leu-1 | 2 | X04391 | + | | + | | | | |
| lymphocyte-specific protein 1 (LSP1) | 16 | M33552 | + | + | + | + | | + | |
| lymphocyte-specific protein tyrosine kinase (LCK) | 7 | M36881 | | + | | | | + | |
| lymphoid phosphatase LyP1 | 1 | AF001847 | | | | | | | |
| lymphoid-restricted membrane protein (LRMP) | 4 | U10485 | + | | + | + | | | |
| lymphoid-specific SP100 homolog (LYSP100-A) | 1 | U36500 | | | | | | + | |
| lymphoma proprotein convertase (LPC) | 2 | U33849 | + | + | + | + | | + | |

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|--|----|----------|---|---|---|---|---|---|--|
| LYSOSOMAL PROTECTIVE PROTEIN PRECURSOR (CATHEPSIN A) (CARBOXYPEPTIDASE C) | 1 | P10619 | | | | | | | |
| lysosomal-associated membrane protein 1 (LAMP1) | 1 | J04182 | + | + | + | + | + | + | |
| Lysosomal-associated membrane protein 2 (LAMP2) | 1 | J04183 | | + | + | + | + | + | |
| lysozyme (renal amyloidosis) (LYZ) | 39 | M19045 | + | + | + | + | | + | |
| lysyl-tRNA synthetase (KARS) | 2 | D32053 | + | + | + | + | | + | |
| M phase phosphoprotein 10 (U3 small nucleolar ribonucleoprotein) (MPP- 10) | 1 | X98494 | | | | | | | |
| M1-type and M2-type pyruvate kinase | 2 | X56494 | | | | | | | |
| m6A methyltransferase (MT-A70) | 7 | AF014837 | + | + | | + | | | |
| mab-21 (C. elegans)-like 1 (MAB21L1) | 1 | U38810 | | + | + | + | | + | |
| MacMarcks | 1 | X70326 | + | + | + | + | + | + | |
| macrophage-associated antigen (MM130) | 1 | Z22968 | | + | + | + | | + | |
| MADS box transcription enhancer factor 2, polypeptide A (myocyte enhancer factor 2A) (MEF2A) | 1 | U49020 | | + | + | + | | + | |
| MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C) (MEF2C) | 1 | L08895 | | + | + | + | | + | |
| major cytoplasmic tRNA- Val(IAC) (=M33940) | 1 | X17516 | | | | | | | |
| major histocompatibility complex class I beta chain | 1 | M95531 | | | | | | | |

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|--|----|----------|---|---|---|---|---|---|-------------------------|
| (HLA-B) | | | | | | | | | |
| major histocompatibility complex, class I, A (HLA-A) | 41 | Z93949 | + | + | + | + | | + | high in villous adenoma |
| major histocompatibility complex, class I, A (HLA-A) (low match) | 1 | Z72422 | | | | | | | |
| major histocompatibility complex, class I, C (HAL-C) | 82 | M24097 | + | + | + | + | + | + | |
| major histocompatibility complex, class I, E (HLA-E) | 77 | M20022 | + | + | + | + | | + | |
| major histocompatibility complex, class II, DM BETA (HLA-DMB) | 2 | U15085 | + | + | + | + | | + | |
| major histocompatibility complex, class II, DP beta 1 (HLA-DPB1) | 10 | M57466 | + | + | + | + | | + | |
| major histocompatibility complex, class II, DR beta 1 (HLA-DRB1) | 9 | V00522 | + | + | + | + | | + | |
| Major histocompatibility complex, class II, Y box-binding protein I; DNA-binding protein B (YB1) | 2 | M24070 | | + | + | | + | + | |
| malate dehydrogenase 1, NAD (soluble) (mdh1) | 1 | D55654 | + | + | + | + | + | + | |
| malate dehydrogenase 1, NAD (soluble) (MDH1) | 3 | D55654 | | + | + | | + | + | |
| malonyl-CoA decarboxylase precursor | 2 | AF097832 | | | | | | | |
| maltase-glucoamylase (mg) | 1 | AF016833 | | | | + | | | |
| manic fringe (Drosophila) homolog (MFNG) | 1 | U94352 | + | + | + | + | | + | |
| mannose phosphate isomerase (MPI) | 1 | X76057 | | + | + | + | | + | |
| mannose phosphate isomerase (mpi) | 2 | X76057 | | + | + | + | | + | |
| mannose-6-phosphate receptor (cation dependent) (M6PR) | 3 | X56253 | | + | + | | + | + | |

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|---|---|----------|---|---|---|---|---|---|--|
| mannose-P-dolichol utilization defect 1 (MPDU1) | 1 | AF038961 | | + | + | + | | + | |
| mannosidase, alpha B, lysosomal (MANB) | 1 | U60885 | | + | | + | + | + | |
| mannosyl (alpha-1,3-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase (MGAT1) | 1 | M55621 | + | + | + | + | + | + | |
| map 4q35 repeat region | 1 | AF064849 | | | | | | | |
| MAP kinase-interacting serine/threonine kinase 1 (MKNK1) | 2 | AB000409 | | + | + | + | + | + | |
| MAP/ERK kinase kinase 3 (MEKK3) | 5 | U78876 | | + | | | | | |
| MAP/ERK kinase kinase 5 (MEKK5) | 1 | D84476 | | + | + | | + | | |
| MAP/microtubule affinity-regulating kinase 3 (MARK3) | 4 | M80359 | | + | + | | | + | |
| Marenostrin protein | 1 | Y14441 | | | | | | | |
| MASL1 | 1 | AB016816 | | | | | | | |
| MAX dimerization protein (MAD) | 3 | L06895 | | | | | | + | |
| MaxiK potassium channel beta subunit | 1 | AF035046 | | | | | | | |
| MBP-2 for MHC binding protein 2 | 1 | X65644 | | + | + | + | | + | |
| Meis (mouse) homolog 3 (MEIS3) | 1 | U68385 | | + | + | + | | + | |
| melanoma-associated antigen p97 (melanotransferrin) | 1 | M12154 | | | | | | | |
| membrane cofactor protein (CD46, trophoblast-lymphocyte cross-reactive antigen) (MCP) | 4 | X59405 | | + | + | + | | + | |
| membrane component, chromosome 17, surface marker 2 (ovarian carcinoma antigen CA125) | 4 | D14696 | | + | + | + | + | + | |

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|--|---|----------|---|---|---|---|---|---|--|
| (M17S2) | | | | | | | | | |
| membrane metallo- endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10) (MME) | 2 | J03779 | B | | + | + | + | + | |
| membrane protein, palmitoylated 1 (55kD) (MPP1) | 2 | M64925 | | + | + | + | + | + | |
| meningioma expressed antigen (MGEA) | 1 | U94780 | | | | + | | | |
| meningioma-expressed antigen 11 (MEA11) | 1 | U73682 | + | + | | + | + | | |
| Menkes Disease (ATP7A) putative Cu ⁺⁺ -transporting P-type ATPase | 1 | L06133 | | + | | | | | |
| metallothionein 2A (MT2A) | 1 | V00594 | | + | + | + | + | + | |
| metaxin 1 (MTX1) | 1 | U46920 | | + | | + | | + | |
| methionine adenosyltransferase II, alpha (MAT2A) | 2 | X68836 | + | + | + | + | | + | |
| methyl-CpG binding domain protein 1 (MBD1) (non-exact 59%aa) | 1 | Y10746 | | | | | | | |
| methylene tetrahydrofolate dehydrogenase (NAD ⁺ dependent), methenyltetrahydrofolate cyclohydrolase (MTHFD2) | 2 | X16396 | + | + | + | + | | + | |
| methylenetetrahydrofolate dehydrogenase (NADP ⁺ dependent), methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase (MTHFD1) | 1 | J04031 | | + | + | + | + | + | |
| methyltransferase, putative | 2 | AJ224442 | | | | | | | |
| MHC antigen (HLA-B) (=L42024) | 1 | U14943 | | | | | | | |
| MHC class 1 region | 2 | AF055066 | | | | | | | |
| MHC class I antigen (HLA- | 1 | U70863 | | | | | | | |

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|--|---|--------|--|--|--|--|---|--|--|
| MHC class I histocompatibility antigen (HLA-B) (clone C21/14) | 1 | U06697 | | | | | | | |
| MHC class I HLA B71 | 2 | L07950 | | | | | | | |
| MHC class I HLA-A (Aw33.1) | 1 | Flp | | | | | | | |
| MHC class I HLA-B | 1 | U18660 | | | | | | | |
| MHC class I HLA-B (HLA-B-07ZEL allele) (=X86704) | 1 | U18661 | | | | | | | |
| MHC class I HLA-B (HLA-B-08NR allele) | 1 | U28759 | | | | | | | |
| MHC class I HLA-B*3512 | 1 | L76094 | | | | | | | |
| MHC class I HLA-B41 variant (=U17572) | 3 | U17572 | | | | | | | |
| MHC class I HLA-B44.2 chain | 1 | M24038 | | | | | | | |
| MHC class I HLA-B51-cd3.3 | 1 | L41086 | | | | | | | |
| MHC class I HLA-C allele | 2 | Z33459 | | | | | | | |
| MHC class I HLA-Cw*0304 (=M84172; M99389) | 1 | D64150 | | | | | | | |
| MHC class I HLA-Cw*0803 | 3 | Z15144 | | | | | | | |
| MHC class I HLA-Cw6 | 1 | M28206 | | | | | | | |
| MHC class I HLA-J antigen | 1 | L56139 | | | | | | | |
| MHC class I lymphocyte antigen A2 (A2.1) variant DK1 | 1 | M19670 | | | | | | | |
| MHC class I mic-B antigen | 1 | X91625 | | | | | | | |
| MHC class I polypeptide-related sequence A (MICA) | 1 | L14848 | | | | | + | | |
| MHC class I protein HLA-C heavy chain (C*0701new allele) (=AF017331) | 1 | U61274 | | | | | | | |
| MHC class II DNA Sequence (clone A37G7-1C11) | 1 | L18885 | | | | | | | |

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|---|---|----------|---|---|---|---|--|---|--|
| MHC class II DQ-alpha associated with DRw6, DQw1 protein | 1 | M16995 | + | | + | + | | + | |
| MHC class II DQ-beta associated with DR2, DQw1 protein | 2 | M17564 | | + | | + | | + | |
| MHC class II HAL-DQ-LTR5 (DQ,w8) DNA fragment, long terminal repeat region | 1 | M33842 | | | | | | | |
| MHC class II hla-dr alpha-chain (=J00197;M60334;K011171;J00194;M60333;X00274) | 1 | J00195 | | | | | | | |
| MHC class II HLA-DRB1 | 1 | AF007883 | | | | | | | |
| MHC class II HLA-DRw11-beta-I chain (DRw11.3) | 1 | M21966 | | | | | | | |
| MHC class II lymphocyte antigen (DPw4-beta-1) | 1 | M23907 | | | | | | | |
| MHC CLASS II TRANSACTIVATOR CIITA (non-exact 57%) | 1 | P33076 | | | | | | | |
| MHC HLA-E2.1 (=X87679) | 1 | M32507 | | | | | | | |
| MHC HLA-E2.1 (alpha-2 domain) (low match) | 1 | M32507 | | | | | | | |
| Mi-2 autoantigen 240 kDa protein (non-exact 84%) | 1 | U08379 | | | | | | | |
| microsomal stress 70 protein ATPase core (stch) | 1 | U04735 | | | | | | | |
| microtubule-associated protein 4 (MAP4) | 1 | U19727 | + | + | + | + | | + | |
| microtubule-associated protein 7 (MAP7) | 1 | X73882 | | | | | | | |
| mineralocorticoid receptor (aldosterone receptor) (MLR) | 2 | M16801 | | + | | + | | + | |
| minichromosome maintenance deficient (S. cerevisiae) 3 (MCM31) | 1 | X62153 | | + | + | + | | + | |
| minichromosome maintenance deficient (S. | 1 | AB011144 | | + | + | + | | + | |

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|--|----|----------|---|---|---|---|---|---|--|
| cerevisiae) 3-associated protein (MCM3AP) | | | | | | | | | |
| minichromosome maintenance deficient (S. cerevisiae) 5 (cell division cycle 46) (MCM5) | 2 | X74795 | + | + | + | + | + | + | |
| mitochondrial cytochrome b (CYTB) | 1 | AF042517 | | | | | | | |
| mitochondrial 16S rRNA | 11 | Z70759 | | | | | | | |
| mitochondrial ATP synthase (F1-ATPase) alpha subunit | 2 | X59066 | | | | | | | |
| mitochondrial ATP synthase c subunit (P1 form) | 1 | X69907 | | | | | | | |
| mitochondrial cytochrome b (CYTB) | 6 | AF042508 | | | | | | | |
| mitochondrial cytochrome b small subunit of complex II | 1 | AB006202 | | | | | | | |
| mitochondrial CYTOCHROME C OXIDASE POLYPEPTIDE I | 1 | P00395 | | | | | | | |
| mitochondrial CYTOCHROME C OXIDASE POLYPEPTIDE II | 1 | P00403 | | | | | | | |
| mitochondrial cytochrome C oxidase subunit II | 2 | P00403 | | | | | | | |
| mitochondrial cytochrome oxidase subunit II (COII) (=U12692 Hsa4 mitochondrion cytochrome oxidase subunit II) | 5 | U12691 | | | | | | | |
| mitochondrial DNA loop attachment sequences (clone LAS34) | 1 | X89763 | | | | | | | |
| mitochondrial DNA polymerase accessory subunit precursor (MtPolB) nuclear gene encoding mitochondrial protein, | 1 | U94703 | | + | | | | | |
| mitochondrial DNA, | 1 | X93334 | | | | | | | |

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|---|----|----------|---|---|---|---|---|---|--|
| complete genome | | | | | | | | | |
| mitochondrial genes for several tRNAs (Phe, Val, Leu) and 12S and 16S ribosomal RNAs. | 8 | V00710 | | | | | | | |
| mitochondrial genes for tRNA (Phe) and 12S rRNA (fragment) | 3 | V00660 | | | | | | | |
| mitochondrial inner membrane preprotein translocase Tim17a | 1 | AF106622 | | | | | | | |
| mitochondrial isolate Afr7 cytochrome b(CYTB) | 1 | AF042503 | | | | | | | |
| mitochondrial loop attachment sequence (clone LAS88) | 1 | X89843 | | | | | | | |
| mitochondrial NADH dehydrogenase subunit 2 (ND2) | 14 | AF014893 | | | | | | | |
| mitochondrial translational initiation factor 2 (MTIF2) | 1 | L34600 | | + | + | + | | + | |
| mitochondrion cytochrome b | 1 | U09500 | | | | | | | |
| mitogen inducible gene mig-2 | 1 | Z24725 | | + | + | + | | + | |
| mitogen inducible gene mig-2 (non-exact, 71%) | 1 | Z24725 | | | | | | | |
| mitogen-activated protein kinase-activated protein kinase 3 (MAPKAPK3) | 2 | U43784 | | + | + | + | | + | |
| MLN51 | 2 | X80199 | | + | + | + | + | + | |
| MLN64 (=D38255 CAB1) | 1 | X80198 | + | + | + | + | | | |
| moesin (MSN) | 14 | M69066 | + | + | + | + | | + | |
| monocytic leukaemia zinc finger protein (MOZ) | 2 | U47742 | | + | + | + | | + | |
| MOP1 () | 2 | U29165 | | | | | | | |
| motor protein (Hs.78504) | 2 | D21094 | + | + | + | + | | + | |

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|---|----|--------|---|---|---|---|---|---|--|
| mouse double minute 2, human homolog of; p53-binding protein (MDM2) | 1 | U39736 | | | + | + | | | |
| M-phase phosphoprotein 6 (MPP-6) | 1 | X98263 | | + | + | + | | + | |
| M-phase phosphoprotein, mpp11 | 1 | X98260 | | | | | | | |
| MPS1 | 1 | L20314 | | | | | | | |
| Mr 110,000 antigen | 2 | D64154 | | + | | + | + | + | |
| MRC OX-2, V-like region (=M17227) | 1 | X05324 | | | | | | | |
| mu-adaptin-related protein-2; mu subunit of AP-4 (MU-ARP2) | 1 | Y08387 | | | | | | | |
| multifunctional polypeptide similar to SAICAR synthetase and AIR carboxylase (ADE2H1) | 1 | X53793 | + | + | + | + | | + | |
| murine leukemia viral (bmi-1) oncogene homolog (BMI1) | 1 | L13689 | | + | | + | | + | |
| mutant (Daudi) beta2 - microglobulin | 44 | X07621 | | | | | | | |
| mutated in colorectal cancers (MCC) | 1 | M62397 | | + | + | | | + | |
| myeloid cell leukemia sequence 1 (BCL2-related) (MCL1) | 9 | L08246 | + | + | + | + | + | + | |
| myeloid cell nuclear differentiation antigen (MNDA) | 11 | M81750 | + | | | | | + | |
| myeloid differentiation primary response gene (88) (MYD88) | 4 | U70451 | | + | + | + | | + | |
| myeloid leukemia factor 2 (MLF2) | 3 | U57342 | | + | | + | | + | |
| myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 7 (MLLT7) | 8 | U89867 | | + | + | + | | + | |

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|--|----|--------|---|---|---|---|---|---|--|
| MYH9 (cellular myosin heavy chain) | 1 | M81105 | | | | | | | |
| myomesin (M-protein) 2 (165kD) (MYOM2) | 1 | X69089 | | | | | | | |
| myosin IE (MYO1E) | 11 | X98411 | | + | | + | | | |
| myosin light chain kinase (MLCK) | 1 | U48959 | + | | + | + | | + | |
| myosin phosphatase, target subunit 1 (MYPT1) | 2 | D87930 | | + | + | + | | + | |
| myosin regulatory light chain (=U26162) | 2 | D50372 | | | | | | | |
| myosin VIIa (low match 71) | 1 | U55208 | | | | | | | |
| myosin, heavy polypeptide 9, non-muscle (MYH9) | 3 | M81105 | + | + | + | + | | + | |
| myosin, light polypeptide, regulatory, non-sarcomeric (20kD) (MLCB) | 6 | X54304 | + | + | + | + | + | + | |
| myosin-I beta | 1 | X98507 | + | + | + | + | | + | |
| myristoylated alanine-rich protein kinase C substrate (MARCKS, 80K-L) (MACS) | 1 | D10522 | | + | + | | | | |
| myxovirus (influenza) resistance 1, homolog of murine (interferon-inducible protein p78) (MX1) | 1 | M30817 | + | + | + | + | | + | |
| myxovirus (influenza) resistance 2, homolog of murine (MX2) | 3 | M30818 | | | + | | | | |
| N-acetylgalactosaminidase, alpha- (NAGA) | 2 | M62783 | | + | + | | + | + | |
| N-acetylglucosamine receptor 1 (thyroid) (NAGR1) | 1 | L03532 | | + | + | + | | + | |
| NACP/alpha-synuclein | 2 | U46896 | | | | | | | |
| N-acylaminoacyl-peptide hydrolase (APEH) | 1 | D38441 | | + | + | | + | + | |
| N-acylsphingosine amidohydrolase (acid | 11 | U47674 | + | + | + | + | | + | |

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|---|----|----------|---|---|---|---|---|---|------------|
| ceramidase) (ASAH) | | | | | | | | | |
| NAD ⁺ -specific isocitrate dehydrogenase beta subunit precursor (encoding mitochondrial protein) | 1 | U49283 | + | + | + | + | + | + | |
| NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5 (13kD, B13) (NDUFA5) | 1 | U53468.1 | + | + | + | + | + | + | |
| NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5 (16kD, SGDH) (NDUFB5) | 1 | AF047181 | | + | + | + | + | + | |
| NADH dehydrogenase (ubiquinone) Fe-S protein 2 (49kD) (NADH-coenzyme Q eductase) (NDUFS2) | 1 | AF050640 | | + | + | + | + | + | |
| NADH dehydrogenase (ubiquinone) flavoprotein 2 (24kD) (NDUFV2) | 1 | M22538 | | | + | + | + | + | |
| NADH:ubiquinone dehydrogenase 51 kDa subunit (NDUFV1) | 2 | AF053070 | + | + | + | + | + | + | |
| NADH-CYTOCHROME B5 REDUCTASE (B5R) (50%aa) | 1 | P00387 | | | | | | | |
| NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 1 | 1 | P03886 | | | | | | | |
| Nardilysin (N-arginine dibasic convertase) (NRD1) | 2 | U64898 | + | + | + | + | | + | |
| nascent-polypeptide-associated complex alpha polypeptide (NACA) | 5 | X80909 | | + | + | | + | + | |
| natural killer cell group 7 sequence (NKG7) | 8 | S69115 | | | | + | | + | |
| natural killer cell transcript 4 (NK4) | 19 | M32011 | + | | | | | | |
| natural killer-associated transcript 3 (NKAT3) | 1 | U30274 | + | | | | | | blood only |
| natural killer-associated | 1 | AF022045 | + | | | | | | blood only |

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|---|---|----------|---|---|---|---|---|---|----------------|
| transcript 5 (NKAT5) | | | | | | | | | |
| natural killer-tumor recognition sequence (NKTR) | 1 | L04288 | B | | + | | + | + | |
| N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 2 (NDST2) | 2 | AF042084 | + | + | | + | | + | |
| Ndr protein kinase | 3 | Z35102 | | + | | | | | |
| Nedd-4-like ubiquitin-protein ligase WWP1 | 1 | U96113 | | | | | | | |
| nel (chicken)-like 2 (NELL2) | 3 | D83018 | | + | + | | | | |
| N-ethylmaleimide-sensitive factor attachment protein, alpha (NAPA) | 1 | U39412 | | + | | | + | | |
| N-ethylmaleimide-sensitive factor attachment protein, gamma (NAPG) | 1 | U78107 | | + | + | + | | | |
| neural precursor cell expressed, developmentally down-regulated 5 (NEDD5) | 3 | X92544 | + | + | + | + | | + | high in testis |
| neural precursor cell expressed, developmentally down-regulated 8 (NEDD8) | 1 | D23662 | + | + | + | + | + | + | |
| neuregulin 1 (NRG1) | 1 | U02330 | | + | | + | + | | |
| neuroblastoma RAS viral (v-ras) oncogene homolog (NRAS) | 4 | AB020692 | + | + | + | + | | + | |
| Neuroblastoma RAS viral (v-ras) oncogene homolog (NRAS) (low match) | 1 | X68286 | | | | | | | |
| Neurofibromin 2 (bilateral acoustic neuroma) (NF2) | 1 | S73853 | | + | | | | + | |
| neuronal apoptosis inhibitory protein (NAIP) | 2 | U19251 | + | + | + | | | + | |
| neuronal cell adhesion molecule (NRCAM) | 1 | AB002341 | | + | + | + | | + | |
| neuropathy target esterase | 1 | AJ004832 | | + | + | + | | + | |

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|--|----|----------|---|---|---|---|---|---|--|
| (NTE) | | | | | | | | | |
| neuropeptide Y3 receptor, 5'UTR (low score) | 1 | D28433 | | | | | | | |
| neurotrophic tyrosine kinase, receptor, type 1 (NTRK1) | 14 | X03541 | + | + | + | + | + | + | |
| neutrophil cytosolic factor 4 (40kD) | 2 | U50720 | | | | | | | |
| NG31 | 1 | AF129756 | | | | | | | |
| NGAL (=X83006) | 1 | X99133 | | | | | | | |
| nibrin (NBS) | 1 | AF051334 | | | | | | | |
| NIK | 1 | AB014587 | | + | + | + | | + | |
| Ninjurin 1; nerve injury-induced protein-1 | 1 | U72661 | | + | + | + | | + | |
| nitrilase 1 (NIT1) (=AF069984) | 1 | AF069987 | | | | | | | |
| NKG2-D (low match) (non-exact, 58%) | 1 | X54870 | | | | | | | |
| Nmi | 1 | U32849 | | | | | | | |
| N-myristoyltransferase 1 (NMT1) | 1 | AF043324 | | + | + | + | + | + | |
| No arches-like (zebrafish) zinc finger protein (NAR) | 1 | U79569 | | + | + | + | | + | |
| non-histone chromosome protein 2 (S. cerevisiae)-like 1 (NHP2L1) | 1 | D50420 | + | + | + | + | + | + | |
| non-muscle (fibroblast) tropomyosin | 1 | | | | | | | | |
| non-muscle alpha-actinin | 1 | U48734 | | | | | | | |
| non-muscle myosin alkali light chain (Hs.77385) | 3 | M22918 | + | + | + | + | + | + | High in fetal adrenal gland and BPH stroma |
| non-neuronal enolase (EC 4.2.1.11) | 1 | X16289 | | | | | | | |
| non-receptor tyrosine phosphatase 1 | 1 | M33689 | | | | | | | |

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|--|---|--------|---|---|---|---|---|---|------------------------|
| normal keratinocyte subtraction library mRNA, clone H22a | 3 | X53778 | + | + | + | + | + | + | high in many libraries |
| notch group protein (N) | 3 | M99437 | | | | | | | |
| novel protein | 1 | X99961 | | | | | | | |
| novel T-cell activation protein | 1 | X94232 | | + | + | + | | + | |
| N-ras protein NRU | 1 | A60196 | | | | | | | |
| N-sulfoglucosamine sulfohydrolase (sulfamidase) (SGSH) | 1 | U60111 | | + | | | | + | |
| nsulin induced gene 1 (INSIG1) | 1 | U96876 | + | + | + | + | + | + | |
| ntegrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor) (ITGA14) | 3 | L12002 | + | | | + | | | |
| nterferon, gamma-inducible protein 16 (IFI16) | 1 | M63838 | + | + | + | + | | + | |
| nterleukin 1, beta (IL1RB) | 1 | M15330 | | | | | | | |
| nuclear antigen H731-like protein | 2 | U83908 | | + | + | + | | + | |
| nuclear antigen Sp100 (SP100) | 4 | U36501 | + | | | + | + | + | |
| Nuclear antigen Sp100 (SP100) (85%aa) | 1 | P23497 | | | | | | | |
| Nuclear antigen Sp100 (SP100) (89%aa) | 1 | P23497 | | | | | | | |
| nuclear autoantigenic sperm protein (histone-binding) (NASP) | 1 | M97856 | + | | + | | | | |
| nuclear corepressor KAP-1 (KAP-1) (=U95040; X97548 TIF1beta zinc finger protein) | 1 | U78773 | | | | | | | |
| Nuclear domain 10 protein (NDP52) | 4 | U22897 | + | + | + | + | + | + | |
| Nuclear factor (erythroid-derived 2)-like 2 (NFE2L2) | 1 | S74017 | | + | + | + | + | + | |

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|--|----|----------|---|---|---|---|---|---|--|
| Nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105) (NFKB1) | 2 | M58603 | | + | + | | + | + | |
| nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha (NFKBIA) | 3 | M69043 | | + | + | + | | + | |
| nuclear factor related to kappa B binding protein (NFRKB) | 1 | U08191 | | + | + | + | | + | |
| nuclear mitotic apparatus protein 1 (NUMA1) | 3 | Z11583 | + | + | + | + | + | + | |
| nuclear receptor coactivator 2 (GRIP1) | 1 | X97674 | | | | | | | |
| nuclear receptor coactivator 3 (AIB3) | 2 | AF010227 | + | + | + | | | + | |
| nuclear receptor coactivator 4 (ELE1) | 22 | X77548 | | + | + | + | + | + | |
| nuclear receptor interacting protein 1 (NRIP1) | 1 | X84373 | | + | | + | | + | |
| nuclear respiratory factor 1 (NRF1) | 1 | U02683 | B | + | + | | | | |
| nuclear RNA helicase, DECD variant of DEAD box family (DDXL) | 4 | U90426 | + | + | + | + | | + | |
| nuclear transcription factor, Y, alpha (NFYA) | 1 | X59711 | B | | | | | | |
| nuclear transcription factor, X-box binding 1 (NFX1) | 3 | U15306 | | + | + | | + | | |
| nuclear transport factor 2 (placental protein 15) (PP15) | 1 | X07315 | + | + | + | + | | + | |
| nucleobindin (=M96824) | 1 | U31336 | | | | | | | |
| nucleobindin 1 (NUCB1) | 2 | M96824 | + | + | + | + | | + | |
| nucleolar phosphoprotein p130 (P130) | 1 | Z34289 | | + | + | | | | |
| nucleolar protein (KKE/D repeat) (NOP56) | 1 | Y12065 | + | + | + | + | | + | |

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|--|----|----------|---|---|---|---|---|---|--|
| nucleolar protein (MSP58) | 1 | AF015308 | | | | | | | |
| nucleolar protein 1 (120kD) (NOL1) | 1 | M32110 | + | + | | | | | |
| nucleolar protein p40 | 1 | U86602 | + | + | + | + | | + | |
| nucleolin (NCL) | 2 | M60858 | + | + | + | + | | + | |
| nucleophosmin (nucleolar phosphoprotein B23, numatrin) (NPM1) | 14 | M28699 | + | + | + | + | | + | |
| nucleophosmin-retinoic acid receptor alpha fusion protein NPM-RAR long form | 1 | U41742 | | | | | | | |
| nucleoporin (NUP358) (=D42063 RanBP2 (Ran-binding protein 2)). | 2 | L41840 | | | | | | | |
| nucleoporin 153kD (NUP153) | 1 | Z25535 | | | | | | | |
| nucleoporin 98kD (NUP98) | 1 | U41815 | | | | | | | |
| nucleosome assembly protein | 1 | D28430 | | | | | | | |
| nucleosome assembly protein 1-like 1 (NAP1L1) | 1 | M86667 | | + | + | + | | + | |
| nucleosome assembly protein 1-like 4 (NAP1L4) | 2 | U77456 | + | + | + | + | | + | |
| nucleosome assembly protein, 5'UTR | 1 | D28430 | | | | | | | |
| olfactory receptor (OR7-141) | 1 | U86281 | | | | | | | |
| OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (OR17-4) (non-exact 65%) | 1 | P34982 | | | | | | | |
| oligodendrocyte myelin glycoprotein (OMG) | 7 | L05367 | | + | | | | | |
| O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase) (OGT) | 1 | U77413 | + | + | | + | + | + | |

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|--|----|----------|---|---|---|---|---|---|---|
| oncofetal trophoblast glycoprotein 5T4 precursor (non-exact 55%) | 1 | A53531 | | | | | | | |
| Oncogene TIM (TIM) (non-exact 84%) | 1 | U02082 | | | | | | | |
| ORF (Hs.77868) | 1 | M68864 | + | + | + | + | + | + | |
| ORF1; MER37; putative transposase similar to pogo element Length = 454 | 1 | U49973 | | | | | | | |
| origin recognition complex, subunit 2 (yeast homolog)-like (ORC2L) | 2 | U27459 | | | | + | | | |
| origin recognition complex, subunit 4 (yeast homolog)-like (ORC4L) (low match) | 1 | AF022108 | | | | | | | |
| ornithine aminotransferase (gyrate atrophy) (OAT) | 2 | M23204 | | + | + | + | | | |
| ornithine decarboxylase (ODC) | 1 | M20372 | | | | | | | |
| ornithine decarboxylase antizyme, ORF 1 and ORF 2 | 11 | D78361 | + | + | + | + | + | + | High in pancreas, and activated T cells |
| orphan receptor (Hs.100221) | 2 | U07132 | + | + | + | + | | + | |
| OS-9 precursor | 6 | AB002806 | + | + | + | + | + | + | |
| osteonectin (=X82259 BM-40) | 1 | D28381 | | | | | | | |
| ovel centrosomal protein RanBPM (RANBPM) | 1 | AB008515 | | + | + | + | | + | |
| over-expressed breast tumor protein | 1 | L34839 | | | | | | | |
| oviductal glycoprotein 1, 120kD (OVGP1) | 1 | U09550 | | | + | + | + | | |
| oxidase (cytochrome c) assembly 1-like (OXAIL) | 1 | X80695 | | + | + | + | + | + | |
| oxoglutarate dehydrogenase (lipoamide) (OGDH) | 4 | D10523 | T | + | + | | + | + | |

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|--|----|----------|---|---|---|---|---|---|--|
| oxysterol binding protein (OSBP) | 1 | M86917 | + | + | | | + | | |
| OZF | 1 | X70394 | | + | + | + | | + | |
| OZF (non-exact zinc finger) | 1 | X70394 | | | | | | | |
| p21/Cdc42/Rac1-activated kinase 1 (yeast Ste20-related) (PAK1) | 2 | U51120 | + | + | | + | | | |
| P35-related protein (= S80990 ficolin) | 1 | D63392 | | | | | | | |
| p40 | 1 | U93569 | | | | | | | |
| p40phox (=U50720) | 1 | X77094 | | | | | | | |
| P47 LBC oncogene | 4 | U03634 | | | | | | | |
| p53-induced protein (PIG11) | 1 | AF010315 | + | + | + | + | | | |
| p54nrb (low match) | 1 | Y11287 | | | | | | | |
| p62 nucleoporin | 1 | X58521 | | | | | | | |
| p63 mRNA for transmembrane protein | 1 | X69910 | + | + | + | + | | + | |
| PAC clone DJ0701016 from 7q33-q36 (non-exact 54%) | 1 | Q07108 | | | | | | | |
| palmitoyl-protein thioesterase (ceroid-lipofuscinosis, neuronal 1, infantile; Hattia-Santavuori disease) (PPT) | 10 | U44772 | | + | + | + | | + | |
| papillary renal cell carcinoma (translocation-associated) (PRCC) | 1 | X99720 | + | + | + | + | + | + | |
| PAR protein | 1 | AF115850 | | + | | + | | | |
| partial EST (clone c-1gh04) | 1 | Z43627 | | | | | | | |
| PAX3/forkhead transcription factor gene fusion | 1 | U02368 | | | | | | | |
| paxillin (PXN) | 4 | D86862 | | + | + | + | | + | |
| PBK1 protein | 2 | AJ007398 | + | + | + | + | | + | |

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|---|----|----------|------|---|---|---|---|---|------------------------|
| PBS-EST (nz92e01.s1 NCI_CGAP_GCB1 clone IMAGE:1302936) (low score) | 1 | AA732534 | | | | | | | |
| PDZ domain protein (Drosophila inaD-like) (INALD) | 1 | AJ224747 | + | | | + | | + | |
| PEBP2aC Runt domain encoding gene (=Z35728) | 1 | Z38108 | | | | | | | |
| peptidase D (PEPD) | 1 | J04605 | | | | | | | |
| peptidylprolyl isomerase A (cyclophilin A) (PPIA) | 3 | Y00052 | | + | + | + | + | + | high in many libraries |
| peptidylprolyl isomerase D (cyclophilin D) (PPID) | 2 | L11667 | T | + | + | | + | + | |
| peptidylprolyl isomerase E (cyclophilin E) (PPIE) | 1 | AF042386 | | + | + | | + | + | |
| PERB11.1 (=U56942 MHC class I chain-related protein A) | 1 | U69630 | | | | | | | |
| perforin 1 (preforming protein) (PRF1) | 14 | M28393 | | | | | | | |
| peroxisomal acyl-CoA thioesterase (PTE1) | 2 | X86032 | | | | | | | |
| Peroxisomal acyl- coenzyme A oxidase | 1 | X71440 | | + | + | + | + | + | |
| peroxisomal farnesylated protein (PXF) | 1 | X75535 | | + | + | + | + | + | |
| phorbol-12-myristate-13- acetate-induced protein (PMAIP1) | 1 | D90070 | B, W | | | | | | |
| phosphate carrier (mitochondrial gene?) | 1 | X77337 | | | | | | | |
| Phosphate carrier, mitochondrial (PHC) | 3 | X60036 | + | + | + | + | | + | |
| phosphate cytidyltransferase 1, choline, alpha isoform (PCYT1A) | 1 | L28957 | T | | + | | + | | |
| PHOSPHATIDATE CYTIDYLYLTRANSFERAS | 1 | Q92903 | | | | | | | |

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|---|----|----------|---------------|------|---|---|---|---|--|
| E (CDP-DIGLYCERIDE) | | | | | | | | | |
| phosphatidylinositol 3-kinase delta catalytic subunit | 2 | U57843 | | | | | | | |
| phosphatidylinositol 4-kinase, catalytic, beta polypeptide (PIK4CB) | 3 | AB005910 | + | + | + | + | | + | |
| phosphatidylinositol glycan, class H (PIGH) | 1 | L19783 | | + | + | + | + | + | |
| phosphatidylinositol transfer protein (PI-TPbeta) | 2 | D30037 | | | | | | | |
| phosphatidylinositol transfer protein, membrane-associated (PITPNM) | 2 | X98654 | B, T lymphoma | + | | | | | |
| phosphatidylinositol transfer protein, membrane-associated (PITPNM) (non-exact 64%) | 1 | X98654 | | | | | | | |
| phosphatidylinositol-4-phosphate 5-kinase, type II, alpha (PIP5K2A) | 1 | U14957 | | | + | | + | | |
| phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B) | 1 | U85245 | | + | + | + | | + | |
| phosphodiesterase 7A (PDE7A) | 1 | L12052 | B, W | + | + | | + | | |
| phosphodiesterase 1B (PDES1B) | 1 | U56976 | | ONLY | | | | | |
| phosphoglucomutase 1 (PGM1) | 2 | M83088 | | + | + | + | | + | |
| phosphogluconate dehydrogenase (PGD) | 1 | U30255 | | | + | | | | |
| phosphoglycerate kinase 1 (PGK1) | 12 | V00572 | | | | | | | |
| phosphoglycerate mutase 1 (brain) (PGAM1) | 3 | J04173 | + | + | + | + | + | + | |
| phosphoglycerate mutase 2 (muscle) (PGAM2) | 1 | M55673 | | + | + | | | + | |
| phosphoinositide-3-kinase, catalytic, alpha polypeptide | 1 | Z29090 | | + | + | + | | | |

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|---|---|----------|---|---|---|---|---|---|--|
| (PIK3CA) | | | | | | | | | |
| phosphoinositide-3-kinase, catalytic, delta polypeptide (PIK3CD) | 4 | U86453 | | + | + | + | | + | |
| phosphoinositide-3-kinase, catalytic, gamma polypeptide (PIK3CG) | 1 | X83368 | | | | | | | |
| phospholipase C | 1 | X14034 | | | | | | | |
| phospholipase C, delta 1 (PLCD1) | 2 | U09117 | | + | + | + | | + | |
| phospholipase C, gamma 1 (formerly subtype 148) (PLCG1) | 1 | M34667 | + | + | + | + | | + | |
| phospholipid scramblase | 1 | AF008445 | | | | | | | |
| phosphoribosyl pyrophosphate synthetase-associated protein 1 (PRPSAP1) | 1 | D61391 | | + | + | | | + | |
| phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase (GART) | 3 | X54199 | | + | + | + | + | + | |
| phosphorylase kinase, alpha 2 (liver), glycogen storage disease IX (PHKA2) | 3 | D38616 | | + | + | + | + | + | |
| phosphorylase, glycogen; brain (PYGB) | 1 | U47025 | + | + | + | | | + | |
| phosphorylase, glycogen; brain (PYGB) (low match, non-exact, 75%) | 1 | U47025 | | | | | | | |
| phosphorylase, glycogen; liver (Hers disease, glycogen storage disease type VI) (PYGL) | 1 | Y15233 | | + | + | + | | + | |
| phosphorylation regulatory protein HP-10 | 2 | | | | | | | | |
| phosphatidylinositol transfer protein (PITPN) | 1 | D30036 | + | + | + | + | | + | |

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|---|----|--------|-------------------------|---|---|---|---|---|--|
| pigment epithelium-derived factor (PEDF) | 1 | U29953 | + | + | + | + | + | + | |
| pim-1 oncogene (PIM1) | 1 | M24779 | + | + | + | | | + | |
| pinin, desmosome associated protein (PNN) | 1 | U77718 | B, monocyte, T lymphoma | | | | | | |
| placenta (Diff33) | 5 | U49188 | | + | + | + | | + | |
| placenta (Diff33) (non-exact, 69%) | 1 | U49188 | | | | | | | |
| placenta (Diff48) | 18 | U49187 | + | | | | | | |
| placenta (Diff48) (low match) | 1 | U49187 | | | | | | | |
| placenta(Diff48) (low match) | 1 | U49187 | | | | | | | |
| plasminogen activator, urokinase receptor (PLAUR) | 1 | X74039 | | + | | + | | + | |
| platelet factor 4 (PF4) | 1 | M25897 | | | + | | | + | |
| platelet/endothelial cell adhesion molecule (CD31 ntigen) (PECAM1) | 8 | M37780 | | + | + | + | + | + | |
| platelet-activating factor acetylhydrolase 2 (40kD) (PAFAH2) | 4 | U89386 | | + | + | + | | | |
| platelet-activating factor acetylhydrolase, isoform 1b, alpha subunit (45kD) (PAFAH1B1) | 1 | U72342 | + | + | + | + | + | + | |
| platelet-activating factor receptor (PTAFR) | 1 | D10202 | | + | | | | + | |
| pleckstrin (PLEK) | 10 | X07743 | | | + | + | | + | |
| pleckstrin (PLEK) (low match) | 1 | X07743 | | | | | | | |
| pleckstrin homology, Sec7 and coiled/coil domains 1(cytohesin 1) (PSCD1) | 4 | M85169 | + | + | | + | | + | |
| pleckstrin homology, Sec7 and coiled/coil domains, | 4 | L06633 | + | | | + | | | |

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|---|----|--------|---|---|---|---|---|---|--|
| binding protein (PSCDBP) | | | | | | | | | |
| pM5 protein | 1 | X57398 | + | + | + | + | | + | |
| PMP69 | 2 | Y14322 | | | | | | | |
| poly (ADP-ribose) polymerase (NAD (+) ADP- ribosyltransferase) (=X16674) | 1 | X56140 | | | | | | | |
| poly(A) polymerase (PAP) | 1 | X76770 | + | + | + | + | | + | |
| poly(A)-binding protein-like 1 (PABPL1) | 19 | Y00345 | + | + | + | + | + | + | |
| poly(rC)-binding protein 1 (PCBP1) | 3 | X78137 | + | + | + | + | + | + | |
| polyadenylate binding protein | 1 | U75686 | | | | | | | |
| polycystic kidney disease 1 (autosomal dominant) (PKD1) | 5 | U24498 | | | | | | | |
| polymerase (DNA directed), beta (POLB) | 1 | D29013 | | + | | | + | + | |
| polymerase (DNA directed), gamma (POLG) | 6 | D84103 | | | | | | | |
| polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) | 1 | X63564 | + | + | + | + | + | + | |
| polymyositis/scleroderma autoantigen 2 (100kD) (PMSCL2) | 1 | L01457 | + | + | + | + | + | + | |
| polypyrimidine tract binding protein (heterogeneous nuclear ribonucleoprotein I) (PTB) | 1 | X65372 | + | + | + | + | + | + | |
| positive regulator of programmed cell death ICH-1L (Ich-1) | 3 | U13021 | | | + | | | | |
| postmeiotic segregation increased 2-like 12 (PMS2L12) | 1 | M16514 | + | + | + | + | | + | |
| postmeiotic segregation increased 2-like 8 (PMS2L8) | 1 | U38964 | + | + | + | + | | + | |

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|--|---|----------|---|---|---|---|---|---|------------------|
| potassium inwardly-rectifying channel, subfamily J, member 15 (KCNJ15) | 1 | D87291 | | | | + | | + | |
| potassium voltage-gated channel, KQT-like subfamily, member 1 (KCNQ1) | 1 | AF051426 | | + | + | + | | + | |
| POU domain, class 2, associating factor 1 (POU2AF1) | 1 | Z49194 | | | | + | | | |
| POU domain, class 2, transcription factor 1 (POU2F1) | 2 | X13403 | | + | | + | | | |
| PPAR binding protein (PPARBP) | 1 | Y13467 | + | + | + | + | | + | |
| PPAR gamma2 | 1 | D83233 | | | | | | | |
| pre-B-cell colony-enhancing factor (PBEF) | 8 | U02020 | | | | | | | |
| prefoldin 1 (PFDN1) | 1 | Y17392 | + | + | + | + | + | + | |
| prefoldin 5 (PRFLD5) | 3 | D89667 | B | + | + | | + | | |
| prefoldin subunit 3 (=U96759 von Hippel-Lindau binding protein (VBP-1)) | 1 | Y17394 | | | | | | | |
| pregnancy-associated plasma protein A (PAPPA) | 1 | U28727 | | + | | + | | | high in placenta |
| pre-mRNA splicing factor SF3a (60kD), similar to S. cerevisiae PRP9 (spliceosome-associated protein 61) (SF3A60) | 1 | U08815 | + | + | + | + | | + | |
| pre-mRNA splicing factor SF3a (60kD), similar to S. cerevisiae PRP9 (spliceosome-associated protein 61) (SF3A60) (low score) | 1 | U08815 | | | | | | | |
| pre-mRNA splicing factor SRp20, 5'UTR | 2 | D28423 | | | | | | | |
| preprotein translocase (TIM17) | 3 | X97544 | + | + | + | + | | + | |

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|--|---|--------|---|---|---|---|---|---|--|
| prion protein | 1 | X82545 | | | | | | | |
| prion protein (p27-30) (Creutzfeld-Jakob disease, Gerstmann-Strausler- Scheinker syndrome, fatal familial insomnia) (PRNP) | 1 | M13899 | | + | + | + | | + | |
| pristanoyl-CoA oxidase (low match) | 1 | Y11411 | | | | | | | |
| pristanoyl-CoA oxidase (low score) | 1 | Y11411 | | | | | | | |
| procollagen-lysine, 2- oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers- Danlos syndrome type VI) (PLOD) | 1 | M98252 | | + | + | + | | + | |
| procollagen-proline, 2- oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide 1 (P4HA1) | 1 | M24486 | + | + | + | + | + | + | |
| procollagen-proline, 2- oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide (protein disulfide isomerase; thyroid hormone binding protein p55) (P4HB) | 4 | X05130 | + | + | + | + | + | + | |
| profilin 1 (PFN1) | 1 | J03191 | + | + | + | + | + | + | |
| progesterone receptor- associated p48 protein (P48) | 2 | U28918 | | + | | | | | |
| prohibitin (PHB) | 1 | S85655 | | + | + | + | + | + | |
| proliferating cell nuclear antigen (PCNA) | 3 | J04718 | + | + | + | + | | + | |
| proliferation-associated gene A (natural killer- enhancing factor A) (PAGA) | 4 | L19184 | + | + | + | + | + | + | |
| proline-rich protein BstNI subfamily 2 (PRB2) (non- exact, 43%aa) | 1 | S62936 | | | | | | | |
| proline-serine-threonine phosphatase interacting protein 1 (PSTPIP1) | 1 | U94778 | | | | | | | |

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|--|----|--------|---|---|---|---|---|---|--|
| prolyl endopeptidase (PREP) | 2 | X74496 | | + | | + | | + | |
| prolylcarboxypeptidase (angiotensinase C) (PRCP) | 5 | L13977 | | + | + | + | + | + | |
| promyelocytic leukemia (PML) | 1 | M80185 | + | + | + | + | | + | |
| properdin P factor, complement (PFC) | 4 | X57748 | + | | | | | | |
| pro-platelet basic protein (includes platelet basic protein, beta-thromboglobulin, connective tissue-activating peptide III, neutrophil-activating peptide-2) (PPBP) | 1 | M54995 | | | + | + | | + | |
| pro-platelet basic protein (includes platelet basic protein, beta-thromboglobulin, connective tissue-activating peptide III, neutrophil-activating peptide-2) (PPBP) | 7 | M54995 | + | | + | | + | | |
| proprotein convertase subtilisin/kexin type 7 (PCSK7) | 4 | U40623 | | | | | | | |
| prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy) (PSAP) | 89 | D00422 | + | + | + | + | + | + | |
| prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase) (PTGS1) | 1 | U63846 | B | + | | | + | + | |
| prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase) (PTGS2) | 2 | L15326 | | | | | | | |
| prostaglandin-endoperoxide synthase-1 (=L08404; U84208) (all promoters) | 1 | D64068 | | | | | | | |

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|--|----|----------|---|---|---|---|---|---|--|------------------------|
| prostate carcinoma tumor antigen (pcta-1) | 2 | L78132 | | | | | | | | |
| protease inhibitor 1 (anti-elastase), alpha-1-antitrypsin (PI) | 17 | K02212 | | + | + | + | + | + | | high in many libraries |
| protease inhibitor 2 (anti-elastase), monocyte/neutrophil (ELANH2) (low match) | 1 | M93056 | | | | + | | + | | |
| proteasome (prosome, macropain) 26S subunit, ATPase, 1 (PSMC1) | 3 | L02426 | B | + | + | | | + | | |
| proteasome (prosome, macropain) 26S subunit, ATPase, 3 (PSMC3) | 1 | M34079 | + | + | + | + | | + | | |
| proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) | 2 | AF020736 | | | | | | | | |
| proteasome (prosome, macropain) 26S subunit, ATPase, 5 (PSMC5) | 5 | L38810 | + | + | + | + | + | + | | |
| proteasome (prosome, macropain) 26S subunit, ATPase, 6 (PSMC6) | 2 | D78275 | + | + | + | + | | + | | |
| proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 (PSMD11) | 1 | AF001212 | T | + | | | + | | | |
| proteasome (prosome, macropain) 26S subunit, non-ATPase, 2 (PSMD2) | 2 | D78151 | | + | + | | | + | | |
| proteasome (prosome, macropain) 26S subunit, non-ATPase, 5 (PSMD5) | 1 | S79862 | T | + | + | | + | | | |
| proteasome (prosome, macropain) 26S subunit, non-ATPase, 7 (Mov34 homolog) (PSMD7) | 1 | D50063 | | + | + | + | | + | | high in many libraries |
| proteasome (prosome, macropain) 26S subunit, non-ATPase, 12 (PSMD12) | 1 | AB003103 | | + | + | + | | + | | |
| proteasome (prosome, macropain) activator subunit 1 (PA28 alpha) (PSME1) | 3 | L07633 | + | + | + | + | | + | | |

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|--|---|----------|---|---|---|---|---|---|----------------|
| proteasome (prosome, macropain) subunit, alpha type, 3 (PSMA3) | 2 | D00762 | | + | + | + | | + | |
| proteasome (prosome, macropain) subunit, alpha type, 5 (PSMA5) | 3 | X61970 | + | + | + | + | | + | |
| proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7) | 3 | AF054185 | | + | + | + | + | + | |
| proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7) (low match) | 1 | AF022815 | | | | | | | |
| proteasome (prosome, macropain) subunit, beta type, 1 (PSMB1) | 1 | D00761 | + | + | + | + | + | + | |
| proteasome (prosome, macropain) subunit, beta type, 10 (PSMB10) | 1 | X71874 | + | + | | + | + | + | |
| proteasome (prosome, macropain) subunit, beta type, 6 (PSMB6) | 1 | D29012 | | + | + | + | | + | |
| proteasome (prosome, macropain) subunit, beta type, 8 (large multifunctional protease 7) (PSMB8) | 1 | U17497 | + | + | + | + | | + | |
| proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional protease 2) (PSMB9) | 3 | Z14977 | + | | | + | | + | |
| proteasome (prosome, macropain) subunit, beta type, 7 (PSMB7) | 1 | D38048 | + | + | + | + | + | + | |
| protective protein for beta-galactosidase (galactosialidosis) (PPGB) | 3 | M22960 | + | + | + | + | + | + | |
| protein A alternatively spliced form 2 (A-2) | 1 | U47925 | | + | | | | | |
| protein activator of the interferon-induced protein kinase (PACT) | 1 | AF072860 | | + | + | + | | + | high in testis |
| protein disulfide isomerase- | 2 | D49489 | + | + | + | + | + | + | |

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|--|----|----------|---------------|---|---|---|---|---|------------------------|
| related protein (P5) | | | | | | | | | |
| protein geranylgeranyltransferase type I, beta subunit (PGGT1B) | 1 | L25441 | + | + | + | | | | |
| protein homologous to chicken B complex protein, guanine nucleotide binding (H12.3) | 20 | M24194 | + | + | + | + | + | + | high in many libraries |
| protein kinase A anchoring protein | 1 | AF037439 | | + | | | | | |
| protein kinase C substrate 80K-H (PRKCSH) | 2 | U50317 | + | + | + | + | | + | |
| protein kinase C, beta 1 (PRKCB1) | 6 | X06318 | + | + | + | + | | + | |
| protein kinase C, delta (PRKCD) | 1 | D10495 | + | + | + | + | | + | |
| protein kinase C, eta (PRKCH) | 1 | M55284 | | | + | | | + | |
| protein kinase C, mu (PRKCM) (non-exact 78%) | 1 | X75756 | | | | | | | |
| Protein kinase C-like 1 (PRKCL1) | 2 | D26181 | + | + | + | + | | + | |
| protein kinase, AMP-activated, gamma 1 non-catalytic subunit (PRKAG1) | 1 | U42412 | B, T lymphoma | + | + | | | | |
| protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1) (PRKAR1A) | 4 | M18468 | | + | + | + | + | + | |
| protein kinase, DNA-activated, catalytic polypeptide (PRKDC) | 1 | U47077 | | + | + | | + | + | |
| protein kinase, mitogen-activated 1 (MAP kinase 1; p40, p41) (PRKM1) | 1 | Z11695 | B | + | | | + | | |
| protein kinase, mitogen-activated 6 (extracellular signal-regulated kinase, p97) (PRKM6) | 1 | L77964 | | + | | + | + | + | |
| protein kinase, mitogen-activated, kinase 3 (MAP | 1 | U66839 | + | + | + | + | + | | |

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|---|---|----------|---|---|---|---|---|---|--|
| kinase kinase 3) (PRKMK3) | | | | | | | | | |
| protein phosphatase 1, catalytic subunit, alpha isoform (PPP1CA) | 5 | M63960 | + | + | + | + | + | + | |
| protein phosphatase 1, regulatory subunit 10 (PPPR10) | 3 | Y13247 | | + | + | + | | + | |
| protein phosphatase 1, regulatory subunit 7 (PPP1R7) | 2 | Z50749 | + | + | + | + | + | + | |
| protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform (PPP2CB) | 1 | X12656 | + | + | + | + | + | + | |
| protein phosphatase 2 (formerly 2A), regulatory subunit B" (PR 72), alpha isoform and (PR 130), beta isoform (PPP2R3) | 1 | L07590 | | | + | + | | + | |
| protein phosphatase 2, regulatory subunit B (B56), alpha isoform (PPP2R5A) | 2 | L42373 | + | + | + | + | | + | |
| protein phosphatase 2, regulatory subunit B (B56), delta isoform (PPP2R5D) | 3 | D78360 | | + | + | + | | + | |
| protein phosphatase 2, regulatory subunit B (B56), gamma isoform (PPP2R5C) | 1 | D26445 | + | + | + | + | | + | |
| protein phosphatase 2A regulatory subunit alpha-isotype (alpha-PR65) | 5 | J02902 | + | + | + | + | | + | |
| protein phosphatase 4 (formerly X), catalytic subunit (PPP4C) | 2 | AF097996 | + | + | + | + | | + | |
| protein tyrosine kinase 2 beta (PTK2B) | 4 | L49207 | | + | | + | | + | |
| protein tyrosine phosphatase epsilon | 1 | X54134 | | | | | | | |
| protein tyrosine phosphatase type IVA, member 2 (PTP4A2) | 2 | L48723 | + | + | + | + | | + | |

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|--|----|--------|---|---|---|---|---|---|----------------|
| protein tyrosine phosphatase, non-receptor type 1 (PTPN1) | 1 | M31724 | + | + | + | + | | | |
| protein tyrosine phosphatase, non-receptor type 12 (PTPN12) | 1 | M93425 | | + | + | + | | + | high in testis |
| protein tyrosine phosphatase, non-receptor type 12 (PTPN12) (non-exact, 70%) | 1 | M93425 | | | | | | | |
| protein tyrosine phosphatase, non-receptor type 2 (PTPN2) | 2 | M25393 | | + | + | + | | + | |
| protein tyrosine phosphatase, non-receptor type 4 (megakaryocyte) (PTPN4) | 1 | M68941 | | | + | + | | + | |
| protein tyrosine phosphatase, non-receptor type 6 (PTPN6) | 7 | M74903 | + | + | + | + | | + | |
| protein tyrosine phosphatase, non-receptor type 7 (PTPN7) | 1 | D11327 | + | | | + | | + | |
| protein tyrosine phosphatase, receptor type, alpha polypeptide (PTPRA) | 1 | M34668 | + | + | + | + | | + | |
| protein tyrosine phosphatase, receptor type, c polypeptide (PTPRC) | 44 | Y00638 | + | + | | + | | + | |
| protein tyrosine phosphatase, receptor type, M (PTPRM) | 1 | X58288 | | + | + | + | | + | |
| protein tyrosine phosphatase, receptor type, N polypeptide 2 (PTPRN2) | 2 | U81561 | | + | | + | | + | |
| protein with polyglutamine repeat (ERPROT213-21) | 1 | U94836 | + | + | + | + | | + | |
| protein-kinase, interferon-inducible double stranded RNA dependent inhibitor (PRKRI) | 1 | U28424 | | + | + | + | + | + | |

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|--|----|----------|---|---|---|---|---|---|-----------------|
| protein-L-isoaspartate (D-aspartate) O-methyltransferase (PCMT1) | 4 | D13892 | | + | + | | | | |
| proteoglycan 1, secretory granule (PRG1) | 7 | J03223 | | + | | + | | + | |
| prothymosin, alpha (gene sequence 28) (PTMA) | 12 | M14483 | + | + | + | + | + | + | |
| prp28, U5 snRNP 100 kd protein (U5-100K) | 7 | AF026402 | + | + | + | + | | + | |
| PRP4/STKWD splicing factor (HPRP4P) | 1 | AF001687 | | + | + | + | | + | |
| PTK7 protein tyrosine kinase 7 (PTK7) | 1 | U40271 | | + | + | + | | + | |
| purinergic receptor P2X, ligand-gated ion channel, 4 (P2RX4) | 3 | AF000234 | | + | + | + | | + | |
| purinergic receptor P2X, ligand-gated ion channel, 7 (P2RX7) | 1 | Y12851 | + | | | | | | macrophage only |
| puromycin-sensitive aminopeptidase (PSA) | 1 | Y07701 | | + | + | | | + | |
| putative ATP(GTP)-binding protein | 2 | AJ010842 | | + | | | | + | |
| putative brain nuclearly-targeted protein (KIAA0765) | 1 | AB018308 | + | + | + | + | | + | |
| putative chemokine receptor; GTP-binding protein (HM74) | 1 | D10923 | + | | | | | | |
| putative dienoyl-CoA isomerase (ECH1) | 1 | AF030249 | | | | | | | |
| putative G-binding protein | 1 | AF065393 | | | | | | | |
| Putative human HLA class II associated protein I (PHAP1) | 1 | U73477 | B | + | | | + | | |
| Putative L-type neutral amino acid transporter (KIAA0436) | 1 | AB007896 | | | | | | | |
| putative mitochondrial space protein 32.1 | 1 | AF050198 | | | | | | | |

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|---|----|----------|---|---|---|---|---|---|--|
| PUTATIVE MUCIN CORE PROTEIN PRECURSOR 24 (MULTI-GLYCOSYLATED CORE PROTEIN 24) (MGC-24) (MUC-24) | 1 | Q04900 | | | | | | | |
| putative nucleic acid binding protein | 2 | X76302 | + | + | + | + | | + | |
| putative outer mitochondrial membrane 34 kDa translocase Htom34 | 1 | U58970 | | + | + | + | | + | |
| putative p150 (non-exact 88%) | 1 | U93568 | | | | | | | |
| putative translation initiation factor (SUI1) | 1 | L26247 | + | + | + | + | + | + | High in moderately differentiated colon adenocarcinoma |
| putative tumor suppressor protein (123F2) | 1 | AF061836 | | + | + | + | | + | |
| pyrroline 5-carboxylate reductase | 1 | M77836 | + | + | + | + | | + | |
| pyruvate dehydrogenase (lipoamide) alpha 1 (PDHA1) | 1 | D90084 | | + | + | + | + | + | |
| pyruvate dehydrogenase (lipoamide) beta (PDHB) | 2 | J03576 | + | + | + | + | | + | |
| Pyruvate dehydrogenase complex, lipoyl-containing component X; E3-binding protein (PDX1) | 3 | Y13145 | | + | + | | | | |
| pyruvate kinase, muscle (PKM2) | 11 | M23725 | | | | | + | | |
| RAB, member of RAS oncogene family-like (RABL) | 1 | U18420 | | + | + | + | | + | |
| RAB1, member RAS oncogene family (RAB1) | 3 | M28209 | | + | + | + | | + | |
| RAB11A, member RAS oncogene family (RAB11A) | 2 | X56740 | + | + | + | + | | + | high in spleen |
| RAB11B, member RAS oncogene family (Rab11B) | 1 | D45418 | | + | | | | + | |
| RAB27A, member RAS | 3 | U38654 | | | | + | | | |

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|---|----|----------|---|---|---|---|---|---|--|
| oncogene family (RAB27A) | | | | | | | | | |
| RAB5B, member RAS oncogene family (RAB5B) | 1 | X54871 | | + | + | + | | + | |
| RAB6, member RAS oncogene family (RAB6) | 1 | M28212 | | + | | | | + | |
| RAB7, member RAS oncogene family (RAB7) | 1 | X93499 | + | + | + | + | | + | |
| RAB7, member RAS oncogene family-like 1 (RAB7L1) | 2 | D84488 | | + | + | + | | + | |
| RAB9, member RAS oncogene family (RAB9) | 1 | U44103 | | | | | | | |
| RAD50 (S. cerevisiae) homolog (RAD50) | 2 | U63139 | | + | + | + | | | |
| RAD51 (S. cerevisiae) homolog C (RAD51C) | 1 | AF029669 | | + | + | + | | + | |
| Radin blood group (RD) | 2 | L03411 | | + | + | + | | + | |
| RAE1 (RNA export 1, S.pombe) homolog (RAE1) | 3 | U84720 | + | + | + | + | | + | |
| ralA-binding protein (RLIP76) | 2 | L42542 | + | + | + | + | | | |
| RAN binding protein 2-like 1 (RANBP2L1) | 2 | AF012086 | | | | | | | |
| Ran GTPase activating protein 1 (RANGAP1) | 3 | X82260 | + | + | + | + | | + | |
| RAN, member RAS oncogene family (RAN) (low match) | 1 | M31469 | | | | | | | |
| RanBP2 (Ran-binding protein 2) (=U19248; L41840 sapiens nucleoporin (NUP358)) | 1 | D42063 | | | | | | | |
| ransforming growth factor, beta receptor II (70-80kD) (TGFB2) | 4 | D50683 | + | + | + | + | | + | |
| RAP1A, member of RAS oncogene family (RAP1A) | 10 | M22995 | + | + | + | + | + | + | |
| RAR-related orphan | 1 | U16997 | | | | | | + | |

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|--|----|----------|---|---|---|---|---|---|---------------|--|
| receptor C (RORC) | | | | | | | | | | |
| RAS guanyl releasing protein 2 (calcium and DAG-regulated) | 1 | Y12336 | + | + | | | | | | |
| ras homolog gene family, member A (ARHA) | 12 | X05026 | + | + | + | + | + | + | high in ovary | |
| ras homolog gene family, member G (rho G) (ARHG) | 1 | X61587 | + | + | + | + | | | | |
| ras homolog gene family, member H (ARHH) | 2 | Z35227 | + | + | + | | | + | | |
| ras inhibitor (RIN1) | 2 | M37191 | | + | | | | | | |
| Ras-GTPase activating protein SH3 domain-binding, protein 2 (KIAA0660) | 2 | AF053535 | + | + | + | + | | + | | |
| Ras-GTPase-activating protein SH3-domain-binding protein (G3BP) | 3 | U32519 | + | + | + | + | | + | | |
| ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2) (RAC2) | 11 | M29871 | | | + | | | + | | |
| RAS-RELATED PROTEIN RAP-1B (GTP-BINDING PROTEIN SMG P21B) | 1 | P09526 | | | | | | | | |
| RBQ-1 | 1 | X85133 | | + | + | + | | | | |
| rearranged T cell receptor beta variable region (TCRB) (=X58810) | 1 | L06891 | | | | | | | | |
| regulator of Fas-induced apoptosis (TOSO) | 1 | AF057557 | B | | | | | + | | |
| regulator of G protein signalling 6 (RGS6) | 1 | AF073920 | | + | | | | | | |
| regulator of G-protein signalling 14 (RGS14) | 2 | AF037195 | + | + | + | + | | | | |
| regulator of G-protein signalling 2, 24kD (RGS2) | 6 | L13391 | + | + | + | + | | + | | |
| regulator of G-protein signalling 5 (RGS5) (49% aa) | 1 | O15539 | | | | | | | | |

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|---|---|----------|------|---|---|---|---|---|---|--|
| regulatory factor X, 4 (influences HLA class II expression) (RFX4) | 1 | M69297 | | | + | + | | | | |
| regulatory factor X, 5 (influences HLA class II expression) (RFX5) | 2 | X85786 | T | + | + | | | | + | |
| replication protein A1 (RPA1) | 1 | M63488 | + | + | + | + | | | + | |
| replication protein A3 (14kD) (RPA3) (low match) | 1 | L07493 | | | | | | | | |
| reproduction 8 (D8S2298E) | 1 | D83767 | | + | + | + | | | | |
| requiem, apoptosis response zinc finger gene (REQ) | 2 | U94585 | + | + | + | + | | | + | |
| requiem, apoptosis response zinc finger gene (REQ) (=AF001433) (low match) | 1 | U94585 | | | | | | | | |
| restin (Reed-Steinberg cell- expressed intermediate filament-associated protein) (RSN) | 1 | M97501 | B, T | + | + | | | | | |
| retinoblastoma 1 (including osteosarcoma) (RB1) | 3 | L11910 | + | + | + | + | | | | |
| retinoblastoma binding protein 2 homolog 1 (RBBP2H1) | 1 | AF087481 | | | | | | | | |
| retinoblastoma-binding protein 1 (RBBP1) | 1 | S66427 | + | + | | | | | | |
| retinoblastoma-binding protein 2 (RBBP2) | 5 | S66431 | + | + | + | + | | | + | |
| retinoblastoma-binding protein 4 (RBBP4) | 1 | X71810 | | + | + | + | | | + | |
| retinoblastoma-binding protein 4 (RBBP4) | 1 | X74262 | | + | + | + | | | + | |
| retinoblastoma-binding protein 7 (RBBP7) | 1 | U35143 | | | | | | | | |
| retinoblastoma-like 2 (p130) (RBL2) | 1 | X76061 | | + | + | + | | | + | |
| retinoic acid receptor responder (tazarotene) | 1 | AF060228 | | + | | + | + | + | | |

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| nduced) 3 (RARRES3) | | | | | | | | | |
| retinoic acid receptor, alpha (RARA) | 1 | X06538 | + | + | | + | | | |
| retinoic acid responsive (NN8-4AG) | 1 | U50383 | | + | | + | | + | |
| retinoid X receptor beta (RXR-beta) | 2 | X66424 | | + | + | + | | + | |
| REV3 (yeast homolog)-like, catalytic subunit of DNA polymerase zeta (REV3L) | 1 | AF035537 | | | | | | | |
| Rho GDP dissociation inhibitor (GDI) beta (ARHGDIB) | 23 | L07916 | + | + | + | + | + | + | |
| Rho GTPase activating protein 4 (ARHGAP4) | 2 | X78817 | + | + | | | | | |
| Rho GTPase activating protein 4 (ARHGAP4) (low match) | 1 | P98171 | | | | | | | |
| Rho-associated, coiled-coil containing protein kinase 2 (ROCK2) | 1 | AB014519 | | | | | | | |
| ribonuclease 6 precursor (RNASE6PL) | 2 | U85625 | + | + | + | + | + | + | |
| ribonuclease 6 precursor (RNASE6PL) (low match) | 1 | U85625 | | | | | | | |
| ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin) (RNASE2) | 1 | X55988 | | | | | + | | |
| ribonuclease/angiogenin inhibitor (RNH) | 3 | M36717 | + | + | + | + | | + | |
| ribonucleoside diphosphate reductase M1 subunit | 1 | X65708 | | | | | | | |
| ribonucleotide reductase M2 polypeptide (non-exact 91%) | 1 | P31350 | | | | | | | |
| ribophorin I (RPN1) | 1 | Y00281 | + | + | + | + | | + | |
| ribophorin II (RPN2) | 1 | Y00282 | + | + | + | + | + | + | |

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|--|----|--------|---|---|---|---|---|---|---|--------------------------------------|
| ribosomal 18S rRNA | 3 | M10098 | | | | | | | | |
| ribosomal 28S RNA | 1 | M11167 | | | | | | | | |
| ribosomal phosphoprotein P0, 5'UTR (low match) | 1 | D28418 | | | | | | | | |
| Ribosomal protein | 1 | | | | | | | | | |
| ribosomal protein L10 (RPL10) | 30 | L25899 | + | + | + | + | + | + | | high in many libraries |
| RIBOSOMAL PROTEIN L10A (CSA-19) | 2 | P53025 | | | | | | | | |
| ribosomal protein L11 (RPL11) | 4 | X79234 | + | + | + | + | + | + | | Alveolar rhabdomyosarcoma |
| ribosomal protein L12 (RPL19) | 2 | L06505 | + | + | + | + | + | + | | |
| ribosomal protein L13 (PRL13) | 1 | P26373 | + | + | + | + | + | + | | high in many libraries |
| ribosomal protein L14 (RPL14) | 4 | D87735 | + | + | + | + | + | + | | high in many libraries |
| ribosomal protein L17 (RPL17) | 4 | X53777 | + | | | | | | | blood only |
| ribosomal protein L18 (RPL18) | 10 | L11566 | + | + | + | + | | | + | |
| ribosomal protein L18a (RPL18A) | 5 | L05093 | | + | + | + | + | + | | High in fetal adrenal gland and skin |
| ribosomal protein L18a homologue | 2 | X80821 | | | | + | | | | |
| ribosomal protein L19 (RPL19) | 15 | X63527 | + | + | + | + | + | + | | |
| ribosomal protein L21 (RPL21) | 6 | U14967 | + | + | + | + | + | + | | |
| ribosomal protein L22 (RPL22) | 3 | D17652 | + | + | + | + | | | + | |
| ribosomal protein L23 (RPL23) | 2 | X55954 | + | + | + | + | + | + | | high in many libraries |
| ribosomal protein L23a (RPL23A) | 5 | U37230 | + | + | + | + | + | + | | high in many libraries |
| ribosomal protein L26 | 8 | X69392 | + | + | + | + | + | + | | |

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|--|----|----------|---|---|---|---|---|---|--------------------------------------|
| (RPL26) | | | | | | | | | |
| ribosomal protein L27 (RPL27) | 6 | L05094 | + | + | + | + | | + | |
| ribosomal protein L27a (RPL27A) | 10 | U14968 | + | + | + | + | + | + | |
| ribosomal protein L28 (RPL28) | 6 | U14969 | + | + | + | + | | + | |
| ribosomal protein L29 (RPL29) | 6 | U10248 | + | + | + | + | + | + | |
| ribosomal protein L3 (RPL3) | 81 | | + | + | + | + | + | + | high in many libraries |
| ribosomal protein L3 homologue | 81 | X06323 | | | | | | | |
| ribosomal protein L30 (RPL30) | 6 | X79238 | + | + | + | + | + | + | high in lymphoma |
| ribosomal protein L30 (RPL30) (low score) | 1 | X79238 | | | | | | | |
| ribosomal protein L31 (RPL31) | 10 | X15940 | + | + | + | + | + | + | High in alveolar rhabdomyosarcoma |
| ribosomal protein L32 (RPL32) | 3 | X03342 | + | + | + | + | + | + | |
| ribosomal protein L33-like (RPL33L) | 1 | AF047440 | | + | + | + | | + | |
| ribosomal protein L34 (RPL34) | 5 | L38941 | | + | + | + | + | + | |
| ribosomal protein L34 (RPL34) (low match) | 1 | L38941 | | | | | | | |
| ribosomal protein L37 (RPL37) | 5 | D23661 | + | + | + | + | + | + | high in barstead prostate |
| ribosomal protein L37a | 4 | X66699 | + | + | + | + | + | + | high in many libraries |
| ribosomal protein L38 (RPL38) | 1 | Z26876 | + | + | + | + | + | + | high in many libraries |
| ribosomal protein L4 (RPL4) | 27 | D23660 | + | + | + | + | + | + | high in many libraries |
| ribosomal protein L41 (RPL41) | 4 | AF026844 | + | + | + | + | + | + | high in many libraries |

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|---|----|----------|---|---|---|---|---|---|-----------------------------------|
| ribosomal protein L5 (RPL5) | 14 | U14966 | + | + | + | + | + | + | High in alveolar rhabdomyosarcoma |
| ribosomal protein L5 (RPL5) (low match) | 1 | U14966 | | | | | | | |
| ribosomal protein L6 (RPL6) | 7 | X69391 | + | + | + | + | + | + | high in many libraries |
| ribosomal protein L7 (RPL7) | 14 | X52967 | + | + | + | + | + | + | high in conorm |
| ribosomal protein L7a (RPL7A) | 15 | M36072 | + | + | + | + | + | + | High in uterus, and seminoma |
| ribosomal protein L8 (RPL8) | 5 | Z28407 | + | + | + | + | + | + | high in ovary |
| ribosomal protein L9 (RPL9) | 10 | U09953 | | + | + | + | + | + | |
| ribosomal protein S10 (RPS10) | 5 | U14972 | + | + | + | + | + | + | high in many libraries |
| ribosomal protein S11 (RPS11) | 4 | X06617 | + | + | + | + | + | + | high in many libraries |
| ribosomal protein S11 (RPS11) (low match) | 1 | AB007152 | | | | | | | |
| ribosomal protein S12 (RPS12) | 3 | X53505 | + | + | + | + | + | + | high in many libraries |
| ribosomal protein S13 (RPS13) | 2 | L01124 | | + | + | + | + | + | |
| ribosomal protein S14 (RPS14) | 12 | M13934 | + | + | + | + | + | + | |
| ribosomal protein S15 (RPS15) | 2 | M32405 | + | + | + | + | + | + | |
| ribosomal protein S16 (RPS16) | 3 | M60854 | + | + | + | + | + | + | High in prostate invasive tumor |
| ribosomal protein S17 (RPS17) | 2 | M13932 | + | + | + | + | + | + | high in many libraries |
| ribosomal protein S18 | 8 | X69150 | | | | | | | |
| ribosomal protein S19 (RPS19) | 7 | M81757 | + | + | + | + | + | + | high in many libraries |
| ribosomal protein S2 (RPS2) | 4 | X17206 | + | + | + | + | + | + | high in many libraries |

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|---|----|--------|---|---|---|---|---|---|--|
| RIBOSOMAL PROTEIN S2 (RPS4) | 2 | P15880 | | | | | | | |
| ribosomal protein S20 (RPS20) | 7 | L06498 | + | + | + | + | + | + | high in many libraries |
| ribosomal protein S21 (RPS21) | 3 | L04483 | + | + | + | + | + | + | high in CD34+/CD38- hematopoietic cells and skin tumor |
| ribosomal protein S23 (RPS23) | 3 | D14530 | | + | + | + | | + | |
| ribosomal protein S24 (RPS24) | 7 | M31520 | + | + | + | + | + | + | high in uterus |
| ribosomal protein S25 (RPS25) | 3 | M64716 | + | + | + | + | + | + | high in barstead prostate |
| ribosomal protein S26 (RPS26) | 2 | X69654 | | + | + | + | + | + | |
| ribosomal protein S27 ((metalloproteinase 1) (RPS27)) | 5 | U57847 | + | + | + | + | + | + | |
| ribosomal protein S28 (RPS28) | 3 | U58682 | + | + | + | + | | + | |
| ribosomal protein S29 (RPS29) | 2 | U14973 | + | + | + | + | + | + | |
| ribosomal protein S3 (RPS3) | 9 | X55715 | + | + | + | + | + | + | high in many libraries |
| ribosomal protein S3 (RPS3) (low match) | 1 | U14990 | | | | | | | |
| ribosomal protein S3A (RPS3A) | 21 | Z83334 | | + | + | + | + | + | high in many libraries |
| ribosomal protein S3A (RPS3A) (low score) | 1 | M77234 | | | | | | | |
| ribosomal protein S4, X-linked (RPS4X) | 9 | M58458 | + | + | + | + | | + | high in ovary and Synovial sarcoma |
| ribosomal protein S4, Y-linked (RPS4Y) | 2 | M58459 | + | + | + | + | + | + | |
| ribosomal protein S5 (RPS5) | 4 | U14970 | + | + | + | + | + | + | high in lymphoma |
| RIBOSOMAL PROTEIN S6 (PHOSPHOPROTEIN) | 1 | P10660 | | | | | | | |

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|---|----|----------|---|---|---|---|---|---|-------------|
| NP33) | | | | | | | | | |
| ribosomal protein S6 (RPS6) | 22 | M20020 | + | + | + | + | + | + | |
| ribosomal protein S6 (RPS6) (non-exact 86%) | 1 | M77232 | | | | | | | |
| ribosomal protein S6 kinase, 90kD, polypeptide 1 (RPS6KA1) | 3 | L07597 | + | + | + | + | | + | |
| ribosomal protein S6 kinase, 90kD, polypeptide 2 (RPS6KA2) | 1 | X85106 | | | | | | | |
| ribosomal protein S7 (RPS7) | 4 | Z25749 | | + | + | + | + | + | |
| ribosomal protein S8 (RPS8) | 6 | X67247 | | + | + | + | + | + | |
| ribosomal protein S9 (RPS9) | 8 | U14971 | | | | | | | colón tumor |
| ribosomal protein, large, P0 (RPLP0) | 18 | M17885 | T | | + | | | + | |
| ribosomal protein, large, P1 (RPLP1) | 12 | M17886 | T | + | + | | + | | |
| ribosomal RNA 18S (=M10098; K03432) (=polyadenylating sequence) | 11 | X03205 | | | | | | | |
| ribosomal RNA 28S | 2 | M11167 | | | | | | | |
| ribosomal RNA, 16S | 1 | U25123 | | | | | | | |
| ring finger protein (non-exact 58%) | 1 | AJ001019 | | | | | | | |
| ring finger protein 3 (RNF3) | 1 | AJ001019 | | | | | | | |
| ring finger protein 4 (RNF4) | 3 | AB000468 | | + | + | + | | + | |
| ring zinc-finger protein (ZNF127-Xp) | 3 | U41315 | | + | + | + | | + | |
| RNA (guanine-7-) methyltransferase (RNMT) | 1 | AB007858 | | + | + | + | | + | |
| RNA binding motif protein 5 (RBM5) | 4 | U23946 | + | + | + | + | | + | |

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|--|----|----------|---|---|---|---|---|---|---|
| RNA binding motif, single stranded interacting protein 2 (RBMS2) | 1 | D28483 | | + | | + | | + | |
| RNA helicase (putative), (Myc-regulated DEAD box protein) (MRD8) | 1 | X98743 | + | + | + | + | | + | |
| RNA helicase-related protein | 1 | AF083255 | | + | + | + | | + | |
| RNA pol II largest subunit | 2 | X74872 | | | | | | | |
| RNA polymerase I subunit (RPA40) | 1 | AF008442 | | + | + | | | + | |
| RTVP-1 protein | 2 | X91911 | + | + | + | + | | + | |
| S100 calcium-binding protein A10 (annexin II ligand, calpactin I, light polypeptide (p11)) (S100A10) | 2 | M81457 | | | + | | + | + | |
| S100 calcium-binding protein A11 (calgizzarin) (S100A11) | 1 | X80201 | | + | + | + | | + | |
| S100 calcium-binding protein A4 (calcium protein, calvasculin, metastasin, murine placental homolog)(S100A4) | 3 | M80563 | B | | + | | + | | |
| S100 calcium-binding protein A8 (calgranulin A) (S100A8) | 7 | M21005 | | | + | + | | + | high in bone marrow |
| S100 calcium-binding protein A9 (calgranulin B) (S100A9) | 14 | X06233 | | | + | + | | | high in invasive larynx squamous cell carcinoma |
| S164 gene | 1 | AF109907 | | | | | | | |
| S-adenosylmethionine decarboxylase 1 (AMD1) | 3 | M88003 | + | + | + | + | | + | |
| SB classII histocompatibility antigen alpha-chain | 5 | M27487 | + | + | + | + | | + | |
| SC35-interacting protein 1 (SRRP129) | 5 | AF030234 | + | + | + | + | + | + | |
| scaffold attachment factor B (SAFB) | 1 | U72355 | + | + | + | + | | + | |

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|---|----|----------|---|---|---|---|---|---|----------------------------|
| scaffold attachment factor B (SAFB) (non-exact 78%) | 1 | U72355 | | | | | | | |
| scRNA molecule, transcribed from Alu repeat | 1 | L13713 | | | | | | | |
| SEC14 (S. cerevisiae)-like (SEC14L) | 4 | D67029 | | + | + | + | | + | |
| SEC23-like protein B (SEC23B) | 2 | X97065 | + | + | + | + | | + | |
| SEC63 (SEC63) | 1 | AF100141 | | + | + | | | + | |
| secreted protein, acidic, cysteine-rich (osteonectin) (SPARC) | 7 | M25746 | | + | + | + | + | + | high in bone marrow stroma |
| secretory carrier membrane protein 1 (SCAMP1) | 1 | AF038966 | | + | | + | | | |
| secretory carrier membrane protein 2 (SCAMP2) | 1 | AF005038 | + | + | + | + | + | + | |
| secretory carrier membrane protein 3 (SCAMP3) | 1 | AF005039 | | | | | | | |
| secretory granule proteoglycan core (clones lambda-PG[6;7,8]) | 1 | M33649 | | | | | | | |
| selectin L (lymphocyte adhesion molecule 1) (SELL) | 43 | X17519 | + | | | + | | + | |
| selectin P ligand (SELPLG) | 13 | U02297 | + | + | | | | | |
| sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D (SEMA4D) | 2 | U60800 | | + | | + | | + | |
| Ser/Arg-related nuclear matrix protein (plenty of prolines 101-like) (SRM160) | 4 | AF048977 | | + | + | + | + | + | |
| serine palmitoyltransferase subunit I (SPTI) | 1 | Y08685 | | + | + | + | | + | |
| serine palmitoyltransferase, subunit II (LCB2) | 1 | AB011098 | + | + | + | + | | + | |

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|--|---|------------|------|---|---|---|---|---|--|
| serine protease | 1 | J02907 | | | | | | | |
| serine protease inhibitor, Kunitz type, 2 (SPINT2) | 1 | U78095 | + | + | + | + | | + | |
| serine/threonine kinase 10 (STK10) | 1 | AB015718 | + | + | + | + | | + | |
| serine/threonine kinase 19 (STK19) | 1 | L26260 | + | + | + | + | | | |
| serine/threonine kinase 4 (STK4) | 1 | U18297 | | + | | | | + | |
| serine/threonine protein kinase KKIALRE (KKIALRE) | 1 | X66358 | | + | + | + | | + | |
| serine/threonine protein-kinase (NIK) | 1 | Y10256 | | + | + | + | | | |
| SERINE/THREONINE-PROTEIN KINASE RECEPTOR R3 PRECURSOR (SKR3) | 1 | P37023 | | | | | | | |
| serologically defined colon cancer antigen 16 (NY-CO-16) | 2 | AF039694 | | | | | | | |
| serologically defined colon cancer antigen 33 (SDCCAG33) | 1 | AF039698 | B, T | + | + | | + | | |
| serologically defined colon cancer antigen 33 (SDCCAG33) (low score) | 1 | AF039698 | | | | | | | |
| serologically defined colon cancer antigen 33 (SDCCAG33) (low score) | 1 | AF039698 | | | | | | | |
| serum deprivation response (phosphatidylserine-binding protein) (SDPR) (=S67386) | 1 | AF085481.1 | | | | | | | |
| serum/glucocorticoid regulated kinase (SGK) | 2 | Y10032 | + | + | + | + | | + | |
| SET domain, bifurcated 1 (SETDB1) | 2 | D31891 | + | + | + | | | + | |
| SH2 domain protein 1A, Duncan's disease lymphoproliferative | 1 | AF073019 | T | | | | | + | |

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|--|---|----------|---|---|---|---|---|---|--|
| syndrome) (SH2D1A) | | | | | | | | | |
| SH3 binding protein (SAB) | 2 | AB005047 | + | + | + | + | | + | |
| SH3 domain protein 1B (SH3D1B) | 4 | U61167 | + | | | + | | + | |
| SH3BGR PROTEIN (=21-GLUTAMIC ACID-RICH PROTEIN;21-GARP) (non-exact 82%aa) | 1 | P55822 | | | | | | | |
| SH3-binding domain glutamic acid-rich protein like (SH3BGRL) | 1 | AF042081 | + | + | + | + | | + | |
| SH3-domain GRB2-like 1 (SH3GL1) | 1 | U65999 | + | + | + | + | | + | |
| SHC (Src homology 2 domain-containing) transforming protein 1 (SHC1) | 2 | X68148 | | + | + | + | | + | |
| siha binding protein 1 (SiahBP1) | 2 | U51586 | | + | + | + | | + | |
| siha binding protein 1 (SiahBP1) (non-exact, 69%) | 1 | U51586 | | | | | | | |
| Sialomucin CD164 (CD164) | 9 | D14043 | | | | | | | |
| sialophorin (gpL115, leukosialin, CD43) (SNP) | 2 | J04536 | | | | | | | |
| sialyltransferase (STHM) | 1 | U14550 | | | + | + | | + | |
| sialyltransferase 1 (beta-galactoside alpha-2,6-sialyltransferase) (SIAT1) | 2 | X17247 | + | + | + | + | + | + | |
| sialyltransferase 4A (beta-galactosidase alpha-2,3-sialyltransferase) (SIAT4A) | 1 | AF059321 | B | + | + | | + | + | |
| sialyltransferase 8 (alpha-2,8-polysialyltransferase) D (SIAT8D) | 1 | L41680 | | + | | | | | |
| signal peptidase 25kDa subunit | 1 | L38950 | | | | | | | |
| signal recognition particle 14kD (homologous Alu RNA-binding protein) | 1 | X73459 | + | + | + | + | + | + | |

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|--|---|----------|---|---|---|---|---|---|---|--|
| (SRP14) | | | | | | | | | | |
| signal recognition particle 54kD (SRP54) | 1 | U51920 | | | + | + | | | + | |
| signal recognition particle 9kD (SRP9) | 2 | U20998 | | + | + | + | + | + | | |
| signal recognition particle receptor ('docking protein') SRPR | 5 | X06272 | | | | | | | | |
| signal regulatory protein, beta, 1 (SIRP-BETA-1) | 5 | Y10376 | | + | | | | | + | |
| signal sequence receptor, alpha (translocon-associated protein alpha) (SSR1) | 2 | Z12830 | | | | + | | | + | |
| signal sequence receptor, beta (translocon-associated protein beta) (SSR2) | 2 | X74104 | + | + | + | + | | | + | |
| signal transducer and activator of transcription (STAT5A) | 4 | L41142 | + | + | + | + | + | + | | |
| signal transducer and activator of transcription 2, 113KD (STAT2) | 1 | U18671 | | | | | | | + | |
| signal transducer and activator of transcription 3 (acute-phase response factor) (STAT3) | 3 | L29277 | | | | | | | | |
| signal transducer and activator of transcription 5A (STAT5A) | 2 | U48730 | + | + | + | + | + | + | | |
| signal transducing adaptor molecule (SH3 domain and ITAM motif) 1 (STAM) | 1 | U43899 | | | | | | | | |
| silencing mediator of retinoid and thyroid hormone action (SMRT) | 1 | U37146 | | | | | | | | |
| similar to beta-transducin superfamily proteins (SAZD) | 1 | U02609 | + | + | + | | | | + | |
| similar to S. cerevisiae SSM4 (TEB4) | 1 | AB011169 | | + | + | + | | | + | |

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|---|---|------------|---|---|---|---|---|---|------------------------|
| similar to yeast pre-mRNA splicing factors, Prp1/Zer1 and Prp6 | 1 | AF026031 | + | + | + | + | | + | |
| SIT protein | 1 | AJ010059.1 | | | | | | | |
| Sjogren syndrome antigen A1 (52kD, ribonucleoprotein autoantigen SS-A/Ro) (SSA1) | 2 | M62800 | | | | | | + | |
| Sjogren syndrome antigen A1 (52kD, ribonucleoprotein autoantigen SS-A/Ro) (SSA1) (non-exact 63%) (match to zinc finger) | 1 | M62800 | | | | | | | |
| SKAP55 homologue (SKAP-HOM) | 1 | AJ004886 | | + | + | + | | + | |
| skb1 (S. pombe) homolog (SKB1) | 2 | AF015913 | + | + | + | + | | + | |
| skeletal muscle abundant protein | 1 | X87613 | + | + | + | + | | + | |
| SMA3 (SMA3) | 1 | X83300 | + | + | | + | | + | |
| small acidic protein | 3 | U51678 | + | + | + | + | | + | |
| small EDRK-rich factor 2 (SERF2) | 2 | Y10351 | + | + | + | + | + | + | high in fetal lung |
| small inducible cytokine A5 (RANTES) (SCYA5) | 2 | M21121 | + | + | + | + | + | + | high in many libraries |
| small inducible cytokine subfamily C, member 2 (SCYC2) | 1 | D63789 | | | | | | | |
| small nuclear ribonucleoprotein polypeptide B" (SNRPB2) | 2 | M15841 | | + | + | + | | + | |
| small nuclear ribonucleoprotein polypeptide N (SNRPN) | 4 | J04615 | + | + | + | + | + | + | |
| small nuclear ribonucleoprotein polypeptides B and B1 (SNRPB) | 2 | J04564 | + | + | + | + | | + | |
| small nuclear RNA activating complex, | 1 | AF093593 | + | + | + | + | | + | |

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|---|---|----------|-------------|---|---|---|---|---|---|------------------------|
| polypeptide 5, 19kD (SNAPC5) | | | | | | | | | | |
| smallest subunit of ubiquinol-cytochrome c reductase | 1 | D55636 | + | + | + | + | + | + | | high in fetal lung |
| SMC (mouse) homolog, X chromosome (SMCX) | 1 | L25270 | + | + | + | + | | + | | |
| SMT3B protein (2) | 2 | X99585 | + | + | + | + | + | + | | |
| SNARE protein (YKT6) (low match) | 1 | U95735 | | | | | | | | |
| SNC19 | 1 | U20428 | | | | | | | | |
| SNC73 protein (SNC73) | 2 | J00220 | + | + | | + | + | + | | high in many libraries |
| solute carrier family 1 (neutral amino acid transporter), member 5 (SLC1A5) | 2 | U53347 | | + | | + | | + | | |
| Solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1 (SLC11A1) | 7 | D50403 | + | | | | | | | |
| solute carrier family 17 (sodium phosphate), member 3 (SLC17A3) | 1 | U90545 | | | | + | | | | |
| solute carrier family 19 (folate transporter), member 1 (SLC19A1) | 1 | U17566 | B, lymphoma | + | | | | + | | |
| solute carrier family 2 (facilitated glucose transporter), member 1 (SLC2A1) | 1 | K03195 | + | + | + | + | + | + | | |
| solute carrier family 23 (nucleobase transporters), member 2 (SLC23A2) | 3 | D87075 | | + | + | + | | | + | |
| solute carrier family 25 (mitochondrial carrier; oxoglutarate carrier), member 11 (SLC25A11) | 1 | AF070548 | B, T | + | + | | | + | + | |
| solute carrier family 31 (copper transporters), member 2 (SLC31A2) | 3 | U83461 | | + | | + | | | | |
| solute carrier family 4, anion exchanger, member | 1 | X62137 | | + | + | | | | + | |

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|---|---|------------|------|---|---|---|---|---|--|
| 2 (erythrocyte membrane protein band 3-like 1) (SLC4A2) | | | | | | | | | |
| solute carrier family 4, sodium bicarbonate cotransporter, member 8 (SLC4A8) | 1 | AB018282 | | + | | | | | |
| solute carrier family 7 (cationic amino acid transporter, y+ system), member 5 (SLC7A5) | 2 | M80244 | T, W | + | + | | + | | |
| solute carrier family 7 (cationic amino acid transporter, y+ system), member 6 (SLC7A6) | 3 | D87432 | + | + | + | | | + | |
| solute carrier family 7 (cationic amino acid transporter, y+ system), member 6 (SLC7A6) (non-exact 77%) | 1 | D87432 | | | | | | | |
| solute carrier family 9 (sodium/hydrogen exchanger), isoform 6 (SLC9A6) | 1 | AF030409 | | + | + | + | | + | |
| somatic cytochrome c (HCS) | 2 | M22877 | | | | | | | |
| SON DNA binding protein (SON) | 2 | X63753 | | + | + | + | | + | |
| son of sevenless (Drosophila) homolog 1 (SOS1) | 1 | L13858 | + | + | | + | | | |
| sorcin (SRI) | 1 | M32886 | | | | | | | |
| sortilin 1 (SORT1) | 2 | X98248 | | + | | + | | + | |
| sortilin-related receptor, L (DLR class) A repeats-containing (SORL1) | 6 | Y08110 | | | | | | | |
| sorting nexin 1 (SNX1) | 3 | U53225 | + | + | + | + | | + | |
| sorting nexin 2 (SNX2) | 2 | AF043453 | | | | | | | |
| sorting nexin 6 (SNX6) (=U83194.1 TRAF4-associated factor 2) | 1 | AF121856.1 | | | | | | | |

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|---|----|----------|---|---|---|---|---|---|--|
| Sp3 transcription factor (SP3) | 1 | X68560 | + | + | + | + | | + | |
| Sp3 transcription factor, (SP3) | 4 | M97191 | + | + | + | + | | + | |
| special AT-rich sequence binding protein 1 (binds to nuclear matrix/scaffold-associating DNA's) (SATB1) | 1 | M97287 | | | | | | | |
| speckle-type POZ protein (SPOP) | 4 | AJ000644 | | | | | | | |
| speckle-type POZ protein (SPOP) (non-exact) | 1 | AJ000644 | | | | | | | |
| spectrin SH3 domain binding protein 1 (SSH3BP1) | 6 | U87166 | + | + | + | + | | | |
| Spectrin, alpha, non-erythrocytic 1 (alpha-fodrin) (SPTAN1) | 2 | J05243 | | + | + | | | + | |
| spermidine/spermine N1-acetyltransferase (SAT) | 11 | M55580 | | | | | | | |
| spermidine/spermine N1-acetyltransferase (SAT) (non-exact, 84%) | 1 | U40369 | | | | | | | |
| spermine synthase (SMS) | 1 | AD001528 | + | + | + | + | | + | |
| SPF31 (SPF31) | 1 | AF083190 | + | + | + | + | | + | |
| sphingomyelin phosphodiesterase 1, acid lysosomal (acid sphingomyelinase) (SMPD1) | 1 | X52679 | | + | + | | + | | |
| SPINDLIN HOMOLOG (PROTEIN DXF34) | 1 | Q99865 | | | | | | | |
| spinocerebellar ataxia 1 (olivopontocerebellar ataxia 1, autosomal dominant, ataxin 1) (SCA1) | 3 | X79204 | B | + | | | + | | |
| spinocerebellar ataxia 2 (olivopontocerebellar ataxia 2, autosomal dominant, ataxin 2) (SCA2) | 1 | U70323 | B | | | | + | | |

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|---|---|----------|---|---|---|---|---|---|---|--|
| spinocerebellar ataxia 7 (olivopontocerebellar atrophy with retinal degeneration) (SCA7) | 2 | AJ000517 | | + | | | | | | |
| spliceosome associated protein (SAP 145) | 3 | U41371 | | + | + | + | + | + | | |
| splicing factor (CC1.3) (CC1.3) | 2 | L10910 | + | + | + | + | + | + | | |
| splicing factor SRp40-1 (SRp40) | 7 | U30826 | + | + | + | + | + | + | | |
| splicing factor, arginine/serine-rich 11 (SFRS11) | 3 | M74002 | B | + | + | | | + | + | |
| splicing factor, arginine/serine-rich 7 (35kD) (SFRS7) | 4 | L41887 | | + | + | + | | | + | |
| Src-like adapter protein (non-exact, 76%aa) | 1 | U30473 | | | | | | | | |
| Src-like-adapter (SLA) | 6 | D89077 | | + | + | + | | | + | |
| Src-like-adapter (SLA) (low match) | 1 | D89077 | | | | | | | | |
| Src-like-adapter (SLA) (low score) | 1 | U44403 | | | | | | | | |
| stannin (SNN) | 2 | AF030196 | + | + | + | + | | | + | |
| STAT induced STAT inhibitor 3 (SSI-3) | 1 | AB004904 | | | | + | | | | |
| STE20-like kinase 3 (MST- 3) | 2 | AF024636 | + | + | + | + | | | + | |
| step II splicing factor SLU7 (SLU7) | 1 | AF101074 | | + | | + | + | + | | |
| steroid sulfatase | 1 | M17591 | | | | | | | | |
| steroid sulfatase (microsomal), arylsulfatase C, isozyme S (STS) | 1 | J04964 | | + | + | + | | | | |
| sterol carrier protein 2 (SCP2) | 1 | M55421 | | + | + | + | + | + | | |
| sterol O-acyltransferase (acyl-Coenzyme A: cholesterol acyltransferase) | 1 | AF059202 | | | | | | + | | |

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|--|---|----------|---|---|---|---|---|---|--|
| 1 (SOAT1) | | | | | | | | | |
| stimulated trans-acting factor (50 kDa) (STAF50) | 6 | X82200 | + | + | | + | | | |
| Striatin, calmodulin-binding protein (STRN) (low match, 71%aa) | 1 | U17989 | | | | | | | |
| Stromal antigen 2 (STAG2) | 2 | Z75331 | | | + | + | + | + | |
| stromal interaction molecule 1 (STIM1) | 3 | U52426 | + | + | + | + | | + | |
| structure specific recognition protein 1 (SSRP1) | 1 | M86737 | | + | + | + | | + | |
| succinate dehydrogenase complex, subunit A, flavoprotein (Fp) (SDHA) | 5 | L21936 | | | + | | | | |
| succinate dehydrogenase complex, subunit B, iron sulfur (Ip) (SDHB) | 1 | U17248 | + | + | + | + | | + | |
| succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD (SDHC) | 1 | U57877 | + | + | + | + | | + | |
| succinate dehydrogenase complex, subunit D, Integral membrane protein (SDHD) | 3 | AB006202 | | + | + | | + | | |
| succinate-CoA ligase, GDP-forming, beta subunit (SUCLG2) | 1 | AF058954 | | + | + | + | + | + | |
| succinyl CoA synthetase | 1 | Z68204 | | | | | | | |
| sudD (suppressor of bimD6, Aspergillus nidulans) homolog (SUDD) | 2 | AF013591 | | + | | | + | + | |
| sulfotransferase family 1A, phenol-preferring, member 1 (SULT1A1) | 1 | L19999 | | + | | | + | + | |
| sulfotransferase family 1A, phenol-preferring, member 3 (SULT1A3) (non-exact 67%) | 1 | U37686 | | | | | | | |
| superoxide dismutase 1, soluble (amyotrophic lateral | 4 | X02317 | | + | + | | + | + | |

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|--|----|----------|---|---|---|---|---|---|--|
| sclerosis 1 (adult)) (SOD1) | | | | | | | | | |
| superoxide dismutase 2, mitochondrial (SOD2) | 5 | Y00985 | | + | + | + | + | + | |
| supervillin (SVIL) | 2 | AF051851 | | | + | + | | + | |
| suppression of tumorigenicity 5 (ST5) | 2 | U15131 | | + | | + | | + | |
| suppression of tumorigenicity 5 (ST5) (non-exact 82%) | 1 | U15779 | | | | | | | |
| suppressor of K+ transport defect 1 (SKD1) | 1 | AF038960 | | | + | + | | | |
| suppressor of Ty (S.cerevisiae) 3 homolog (SUPT3H) | 1 | AF064804 | + | + | + | + | | + | |
| suppressor of Ty (S.cerevisiae) 4 homolog 1 (SUPT4H1) | 2 | U38817 | + | + | + | + | | + | |
| suppressor of Ty (S.cerevisiae) 5 homolog (SUPT5H) | 2 | U56402 | | + | | | | + | |
| suppressor of Ty (S.cerevisiae) 6 homolog (SUPT6H) | 2 | U46691 | + | + | + | + | + | + | |
| suppressor of variegation 3-9 (Drosophila) homolog-1 (SUV39H1) | 1 | AF019968 | | + | + | + | | | |
| survival of motor neuron 1, telomeric (SMN1) | -1 | U18423 | | | | | | | |
| SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SMARCA1) (non-exact, 75%) | 1 | M88163 | | | + | + | | + | |
| SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2 (SMARCA2) | 2 | D26155 | | + | | | | | |
| SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, | 1 | D26156 | + | + | + | + | + | + | |

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|---|----|------------|------|---|---|---|---|---|--|
| member 4 (SMARCA4) | | | | | | | | | |
| SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 2 (SMARCC2) | 4 | U66616 | + | + | + | + | + | + | |
| SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1 (SMARCE1) | 2 | AF035262 | B, W | + | + | | + | + | |
| synaptobrevin-like 1 (SYBL1) | 1 | X95803 | | + | + | + | | + | |
| synaptosomal-associated protein, 23kD (SNAP23) | 2 | AJ011915 | | + | + | + | | + | |
| syndecan binding protein (syntenin) (SDCBP) | 15 | AF006636 | + | + | + | + | | + | |
| synovial sarcoma, translocated to X chromosome (SSXT) | 2 | X79201 | | + | | | | | |
| syntaxis 16 | 1 | AF038897 | | | | | | | |
| syntaxis 3A (STX3A) | 2 | U32315 | | + | | + | | + | |
| syntaxis 6 (STX6) | 1 | AJ002078.1 | | | | | | | |
| SYNTAXIN BINDING PROTEIN 3 (UNC-18 HOMOLOG 3) (UNC-18C) | 1 | O00186 | | | | | | | |
| syntaxis-16C | 1 | AF008937 | | | | | | | |
| SYT interacting protein (SIP) | 1 | AF080561 | | + | + | + | | + | |
| T cell activation, increased late expression (TACTILE) | 4 | M88282 | | | | + | | | |
| T cell receptor V alpha gene segment V-alpha-7 (clone IGRa11) | 2 | X58744 | | | | | | | |
| T cell receptor V alpha gene segment V-alpha-w27 | 1 | X58740 | | | | | | | |
| T3 receptor-associating cofactor-1 | 5 | S83390 | + | + | + | + | + | + | |

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|--|---|----------|---|---|---|---|---|---|--|
| tafazzin (cardiomyopathy, dilated 3A (X-linked); endocardial fibroelastosis 2; Barth syndrome) (TAZ) | 1 | X92763 | + | + | | + | | + | |
| TAFII100 protein (non-exact 53%) | 1 | U80191 | | | | | | | |
| tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase (TNKS) | 1 | AF082556 | | + | + | + | | + | |
| TAP1, TAP2, LMP2, LMP7 and DOB | 1 | X66401 | | | | | | | |
| TAR DNA-binding protein-43 | 6 | U23731 | + | + | + | + | | + | |
| Tat interactive protein (60kD) (TIP60) | 2 | U40989 | + | + | + | + | | + | |
| TATA box binding protein (TBP)-associated factor, RNA polymerase II, C1, 130kD (TAF2C1) (non-exact, 55%) | 1 | O00268 | | | | | | | |
| TATA box binding protein (TBP)-associated factor, RNA polymerase II, F, 55kD (TAF2F) | 4 | X97999 | | + | + | + | + | + | |
| TATA box binding protein (TBP)-associated factor, RNA polymerase II, G, 32kD (TAF2G) | 2 | U21858 | | + | + | + | + | + | |
| TATA box binding protein (TBP)-associated factor, RNA polymerase II, I, 28kD (TAF2I) | 1 | D63705 | + | + | + | + | | + | |
| Tax1 (human T-cell leukemia virus type I) binding protein 1 (TAX1BP1) | 1 | U33821 | | + | + | + | + | + | |
| T-box 2 (TBX2) (non-exact 77%) | 1 | U28049 | | | + | + | | + | |
| TBP-associated factor 172 (TAF-172) | 1 | AJ001017 | | + | | + | | + | |
| T-cell death-associated gene 8 (TDAG8) | 1 | U95218 | | | | + | | | |

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|--|---|----------|---|---|---|---|---|---|---|---------------------|
| T-cell leukemia/lymphoma 1A (TCL1A) | 1 | X82240 | + | | | | | | | |
| T-cell leukemia/lymphoma 1A (TCL1A) (low match) | 1 | X82240 | | | | | | | | |
| T-cell receptor (delta D2-J1-region) (clone K3B) | 1 | M22197 | | | | | | | | |
| T-cell receptor (V beta 5.1, J beta 1.5, C beta 1) (low match) | 1 | M97705 | | | | | | | | |
| T-cell receptor alpha delta (=M94081) | 2 | AE000662 | | | | | | | | |
| T-cell receptor alpha enhancer-binding protein, short form (=X58636 Mouse LEF1 lymphoid enhancer binding factor 1 (=D16503)) | 1 | B39625 | | | | | | | | |
| T-cell receptor delta gene D2-J1-region, clone K3B | 1 | M22197 | | | | | | | | |
| T-cell receptor germline beta chain gene V-region (V) V-beta-MT1-1 | 1 | M11955 | | | | | | | | |
| T-cell receptor germline beta-chain gene J2.1 exon | 1 | M14159 | + | | | | | | | only in blood |
| T-cell receptor germline delta-chain D-J region | 2 | M22152 | | | | | | | | |
| T-cell receptor interacting molecule (TRIM) protein | 2 | AJ224878 | | | | | | | + | |
| T-cell receptor rearranged delta-chain, V-region (V-delta 3-J) | 1 | M21784 | | | | | | | | |
| T-cell receptor, alpha (V,D,J,C) (TCRA) | 3 | AE000660 | + | + | + | + | | | + | |
| T-cell receptor, beta cluster (TCRB) | 3 | L34740 | + | + | + | + | + | + | + | high in pancreas |
| T-cell receptor, delta (V,D,J,C) (TCRD) | 2 | X73617 | | | + | + | | | + | |
| T-cell, immune regulator 1 (TCIRG1) | 3 | U45285 | | | | | | | | only found in tumor |
| TCF-1 mRNA for T cell | 1 | X59870 | | | | | | | | |

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|--|----|----------|---|---|---|---|---|---|--|
| factor 1 | | | | | | | | | |
| TCF-1 mRNA for T cell factor 1 (splice form B) (low match) | 1 | X59870 | | | | | | | |
| T-COMPLEX PROTEIN 1, ETA SUBUNIT (TCP-1-ETA) (CCT-ETA) (HIV-1 NEF INTERACTING PROTEIN) | 1 | Q99832 | | | | | | | |
| T-COMPLEX PROTEIN 1, THETA SUBUNIT (TCP-1-THETA) (CCT-THETA) (KIAA0002) | 1 | P50990 | | | | | | | |
| TCR eta =T cell receptor(eta-exon) | 1 | S94421 | | | | | | | |
| TCR V Beta 13.2 | 1 | X75419 | | | | | | | |
| TERA | 1 | AC004472 | | | | | | | |
| testis enhanced gene transcript (TEGT) | 33 | X75861 | + | + | + | + | + | + | |
| tetracycline transporter-like protein (TETRAN) | 2 | L11669 | | + | + | + | | + | |
| tetratricopeptide repeat domain 1 (TTC1) | 1 | U46570 | + | + | + | + | | + | |
| tetratricopeptide repeat domain 2 (TTC2) | 1 | U46571 | | + | | + | | + | |
| tetratricopeptide repeat domain 3 (TTC3) | 1 | D84296 | + | + | + | + | | + | |
| TGFB1-induced anti-apoptotic factor 1 (TIAF1) | 1 | D86970 | + | + | + | + | | + | |
| thioredoxin reductase 1 (TXNRD1) | 3 | S79851 | | + | + | + | | + | |
| THIOREDOXIN-DEPENDENT PEROXIDE REDUCTASE PRECURSOR, mitochondrial (ANTI-OXIDANT PROTEIN 1) (AOP-1) | 1 | P30048 | | | | | | | |
| threonyl-tRNA synthetase (TARS) | 1 | M63180 | | + | + | + | | + | |

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|--|----|----------|---|---|---|---|---|---|------------------|
| thrombin inhibitor | 1 | Z22658 | | | | | | | |
| thrombospondin 1 (THBS1) | 2 | X04665 | | + | + | + | + | + | |
| thromboxane A synthase 1 (platelet, cytochrome P450, subfamily V) (TBXAZ1) | 1 | M80647 | | + | | + | + | + | |
| thymidine kinase 2, mitochondrial (TK2) | 2 | X76104 | | + | + | | + | | |
| thymidylate kinase (CDC8) | 1 | L16991 | | + | + | + | | + | |
| thymine-DNA glycosylase (TDG) | 2 | U51166 | + | + | + | + | | + | |
| Thymosin, beta 10 (TMSB10) | 2 | M20259 | + | + | + | + | + | + | |
| thymosin, beta 4, X chromosome (TMSB4X) | 29 | M17733 | | + | + | + | | + | |
| thyroid autoantigen 70kD (Ku antigen) (G22P1) | 7 | J04611 | | | | | | | |
| thyroid hormone receptor coactivating protein (SMAP) | 1 | AF016270 | | + | | + | | + | |
| thyroid hormone receptor interactor 7 (TRIP7) | 2 | L40357 | | + | + | + | | + | |
| thyroid hormone receptor interactor 8r (TRIP8) | 4 | L40411 | | + | | | | | |
| thyroid hormone receptor- associated protein, 230 kDa subunit (TRAP230) | 1 | D83783 | | | | | | | |
| thyroid receptor interacting protein 15 (TRIP15) | 2 | L40388 | + | + | + | + | | | |
| TI-227H | 1 | D50525 | | | | | | | |
| TIA1 cytotoxic granule- associated RNA-binding protein (TIA1) | 1 | M77142 | | + | + | + | | + | |
| tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor) (TIMP1) | 1 | X02598 | + | + | + | + | + | + | |
| tissue inhibitor of metalloproteinase 2 | 1 | M32304 | + | + | + | + | | + | high in placenta |

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|---|---|------------|---|---|---|---|---|---|----------------|
| (TIMP2) | | | | | | | | | |
| tissue specific transplantation antigen P35B (TSTA3) | 1 | U58766 | + | + | + | + | | + | |
| titin (TTN) | 1 | X64697 | + | + | + | + | | + | high in muscle |
| TNF receptor-associated factor 2 (TRAF2) | 1 | U12597 | | + | + | + | | + | |
| TNF receptor-associated factor 3 (TRAF3) | 1 | AF110908.1 | | + | | | | | |
| TNF receptor-associated factor 6 (TRAF6) (low match) | 1 | U78798 | | | | | | | |
| toll-like receptor 1 (TLR1) | 1 | U88540 | | | | + | | | |
| toll-like receptor 2 (TLR2) | 1 | U88878 | + | + | | + | | + | |
| toll-like receptor 4 (TLR4) | 1 | U88880 | | + | | | + | | |
| toll-like receptor 5 (TLR5) | 1 | AF051151 | | + | | + | | | |
| topoisomerase (DNA) I (TOP1) | 1 | J03250 | | + | + | + | | | |
| topoisomerase (DNA) II beta (180kD) (TOP2B) | 2 | X68060 | + | + | + | + | | + | |
| topoisomerase (DNA) III beta (TOP3B) | 3 | D87012 | + | | | | | | |
| TR3beta | 1 | D85245 | | + | | | | | |
| TRAF family member- associated NF-kB activator (TANK) | 3 | U63830 | + | + | + | + | + | + | |
| TRANSALDOLASE | 1 | P37837 | | | | | | | |
| transaldolase 1 (TALDO1) | 4 | L19437 | | + | + | + | + | + | |
| transaldolase-related protein | 1 | AF010398 | | | | | | | |
| transcobalamin II (TCII) | 1 | AF047576 | | | | | | | |
| transcription elongation factor B (SIII), polypeptide 1-like (TCEB1L) | 2 | Z47087 | + | + | + | + | | + | |
| transcription elongation factor B (SIII), polypeptide | 1 | L47345 | + | + | + | + | + | + | |

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|---|---|----------|---|---|---|---|---|---|--|
| 3 (110kD, elongin A) (TCEB3) | | | | | | | | | |
| transcription factor 12 (HTF4, helix-loop-helix transcription factors 4) (TCF12) | 1 | M83233 | + | + | + | + | | + | |
| transcription factor 17 (TCF17) | 2 | D89928 | | + | | + | | | |
| transcription factor 4 (TCF4) | 2 | X52079 | | + | + | + | | + | |
| transcription factor 6-like 1 (mitochondrial transcription factor 1-like) (TCF6L1) | 2 | M62810 | + | + | + | + | | | |
| transcription factor 7-like 2 (T-cell specific, HMG-box) (TCF7L2) | 1 | Y11306 | | + | + | + | | + | |
| transcription factor binding to IGHM enhancer 3 (TFE3) | 1 | X96717 | + | + | + | + | | + | |
| transcription factor IL-4 Stat | 7 | AF067575 | + | + | + | + | + | + | |
| transcription factor IL-4 Stat (low match) | 1 | U16031 | | | | | | | |
| transcription factor ISGF-3 (=M97936) | 4 | M97935 | | | | | | | |
| transcription factor REST | 1 | A56138 | | | | | | | |
| transcription factor TFIIID | 1 | Z22828 | | | | | | | |
| transcriptional adaptor 2 (ADA2, yeast, homolog)- like (TADA2L) | 1 | AF064094 | | | | | | | |
| transcriptional intermediary factor 1 (TIF1) (non-exact 72%) | 1 | AF009353 | | | | | | | |
| transducin (beta)-like 1 (TBL1) | 1 | Y12781 | + | + | + | + | | + | |
| transducin-like enhancer of split 3, homolog of Drosophila E(sp1) (TLE3) | 1 | M99438 | + | + | | | | | |
| Transformation/transcriptio n domain-associated protein (TRRAP) | 1 | AF076974 | + | + | + | + | | + | |

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|---|----|----------|---|---|---|---|---|---|--|
| transformation-sensitive, similar to <i>Saccharomyces cerevisiae</i> STI1 (STI1L) | 2 | M86752 | | + | + | + | | + | |
| transforming growth factor beta-activated kinase 1 (TAK1) (non-exact 78%) | 1 | AB009356 | | | | | | | |
| transforming growth factor beta-stimulated protein TSC-22 (TSC22) | 3 | AJ222700 | + | + | + | + | | + | |
| transforming growth factor, beta receptor III (betaglycan, 300kD) (TGFB3) | 1 | L07594 | | + | + | + | | + | |
| transforming growth factor, beta-induced, 68kD (TGFB1) | 2 | 4507466 | + | + | + | + | + | + | |
| TRANSFORMING GROWTH FACTOR-BETA INDUCED PROTEIN IG-H3 PRECURSOR (BETA IG-H3) | 2 | Q15582 | | | | | | | |
| transforming, acidic coiled-coil containing protein 1 (TACC1) (non-exact 70%) | 1 | AF049910 | | | | | | | |
| transgelin 2 (TAGLN2) | 14 | D21261 | + | + | + | + | + | + | |
| transgelin 2 (TAGLN2) (non-exact) | 1 | D21261 | | | | | | | |
| trans-Golgi network protein (46, 48, 51kD isoforms) (TGN51) | 2 | AF029316 | | + | | + | | | |
| transient receptor potential channel 1 (TRPC1) | 1 | X89066 | | + | + | + | | + | |
| transketolase (Wernicke-Korsakoff syndrome) (TKT) | 7 | L12711 | | + | + | + | | + | |
| translation factor sui1 homolog (GC20) | 1 | AF064607 | | + | + | + | + | + | |
| translin (TSN) | 3 | X78627 | + | + | + | + | | + | |
| translin-associated factor X (TSNAX) | 1 | X95073 | | + | + | + | | + | |
| transmembrane glycoprotein (A33) | 1 | U79725 | | | | | | | |

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|--|---|----------|---|---|---|---|---|---|------------------------|
| transmembrane protein (63kD), endoplasmic reticulum/Golgi intermediate compartment (P63) | 1 | X69910 | + | + | + | + | | + | |
| transmembrane protein 1 (TMEM2) | 1 | AB001523 | | + | | + | | + | |
| TRANSMEMBRANE PROTEIN SEX PRECURSOR (non-exact 65%) | 1 | P51805 | | | | | | | |
| transmembrane trafficking protein (TMP21) | 2 | X97442 | + | + | + | + | + | + | |
| transporter 1, ABC (ATP binding cassette) (TAP1) | 3 | L21208 | + | + | + | + | | + | |
| Treacher Collins-Franceschetti syndrome 1 (TCOF1) | 2 | U40847 | + | + | + | + | | + | high in many libraries |
| triosephosphate isomerase 1 (TPI1) | 2 | X69723 | + | + | + | + | + | + | |
| tropomyosin | 2 | X04201 | | + | + | + | | + | |
| tropomyosin 4 (TPM4) | 2 | X05276 | + | + | + | + | | + | |
| TRPM-2 protein | 2 | M63376 | | | | | | | |
| tryptase I precursor (non-exact 64%)(=P20231) | 1 | A35863 | | | | | | | |
| tryptophan rich basic protein (WRB) | 1 | Y12478 | | | | | | | |
| tryptophanyl-tRNA synthetase (WARS) | 1 | X59892 | + | + | + | + | + | + | |
| Ts translation elongation factor, mitochondrial (TSFM) | 1 | L37936 | + | + | | + | | + | |
| ttopoisomerase (DNA) II beta (180kD) | 1 | Z15115 | | + | + | | | + | |
| Tu translation elongation factor, mitochondrial (TUFM) | 4 | L38995 | | | | | | | |
| tuberous sclerosis 1 (TSC1) | 1 | AF013168 | | + | + | + | | + | |

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|---|----|----------|--------|---|---|---|---|---|--|
| tuberous sclerosis 2 (TSC2) | 1 | X75621 | | + | + | + | | + | |
| tubulin, alpha 1 (testis specific) (TUBA1) | 1 | X06956 | | + | | | + | | |
| tubulin, alpha, ubiquitous (K-ALPHA-1) | 11 | K00558 | + | + | + | + | + | + | high in many libraries |
| tubulin, alpha, ubiquitous (K-ALPHA-1) (low match) | 1 | K00558 | | | | | | | |
| tubulin-specific chaperone c (TBCC) | 1 | U61234 | | + | + | + | | + | |
| tumor necrosis factor (ligand) superfamily, member 10 (TNFSF10) | 7 | U37518 | | + | + | + | | + | |
| tumor necrosis factor (ligand) superfamily, member 13 (TNFSF13) | 1 | AF046888 | + | + | | + | | + | |
| tumor necrosis factor (ligand) superfamily, member 14 (TNFSF14) | 1 | AF036581 | | | | | | | |
| tumor necrosis factor (ligand) superfamily, member 6 (TNFSF6) | 1 | D38122 | + | | | | | | Found only in library 386: T-cell lymphoma |
| tumor necrosis factor (ligand) superfamily, member 8 (TNFSF8) | 1 | L09753 | B only | | | | | | |
| tumor necrosis factor alpha-inducible cellular protein containing leucine zipper domains (FIP2) | 1 | AF061034 | | + | + | + | | + | |
| Tumor necrosis factor receptor superfamily member 7 (TNFRSF7) | 2 | M63928 | | + | | | | + | |
| tumor necrosis factor receptor superfamily, member 10b (TNFRSF10B) | 1 | AF016266 | | + | + | + | + | + | |
| tumor necrosis factor receptor superfamily, member 10c, decoy without an intracellular domain (TNFRSF10C) | 3 | AF012629 | | | | | | + | |
| tumor necrosis factor receptor superfamily, member 10d, decoy with | 1 | AF023849 | | | | | | | found only in prostate |

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|---|----|----------|------|---|---|---|---|---|--|
| truncated death domain (TNFRSF10D) (non-exact 84%) | | | | | | | | | |
| tumor necrosis factor receptor superfamily, member 12 (translocating chain-association membrane protein) (TNFRSF12) | 1 | U94508 | + | + | + | + | | + | |
| tumor necrosis factor receptor superfamily, member 14 (herpesvirus entry mediator) (TNFRSF14) | 1 | U70321 | + | + | + | + | | + | |
| tumor necrosis factor receptor superfamily, member 1B (TNFRSF1B) | 5 | U52165 | + | + | + | + | | + | |
| tumor necrosis factor receptor superfamily, member 6 (TNFRSF6) | 1 | X63717 | B, W | | | | | + | |
| tumor necrosis factor receptor superfamily, member 7 (TNFRSF7) | 1 | M63928 | + | + | | | | | |
| tumor necrosis factor, alpha-induced protein 2 (TNFAIP2) | 8 | M92357 | | + | + | | + | | |
| tumor necrosis factor, alpha-induced protein 3 (TNFAIP3) | 2 | M59465 | | | | | | | |
| tumor protein 53-binding protein, 1 (TP53BP1) | 1 | AF078776 | | + | + | + | | + | |
| tumor protein p53 (Li-Fraumeni syndrome) (TP53) | 1 | M14695 | + | + | | | | + | |
| Tumor protein p53-binding protein (TP53BPL) | 1 | U82939 | + | | | + | | + | |
| tumor protein, translationally-controlled 1 (TPT1) | 35 | X16064 | | | | | | | |
| tumor protein, translationally-controlled 1 (TPT1) (low score) | 1 | X16064 | | | | | | | |

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|--|---|----------|---|---|---|---|---|---|----------------------------------|
| tumor rejection antigen (gp96) 1 (TRA1) | 9 | X15187 | + | + | + | + | + | + | |
| tumorous imaginal discs (Drosophila) homolog (TID1) | 2 | AF061749 | | + | | | | | |
| TXK tyrosine kinase (TXK) | 2 | L27071 | | | | | | | |
| type II integral membrane protein (NKG2-E) | 1 | AJ001685 | | | | | + | | found only in fetal liver/spleen |
| TYRO protein tyrosine kinase binding protein (TYROBP) | 3 | AF019562 | | | + | | | | |
| tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide (YWHAB) | 1 | X57346 | + | + | + | + | | + | high in ecnorm |
| tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide (YWHAZ) | 1 | M86400 | | | | | | | |
| tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide (YWHAZ) | 1 | M86400 | | | | | | | |
| Tyrosine kinase 2 (TYK2) | 3 | X54637 | | + | + | + | | + | |
| TYROSINE-PROTEIN KINASE ZAP-70 (70 KD ZETA-ASSOCIATED PROTEIN) (SYK-RELATED TYROSINE KINASE) | 2 | P43403 | | | | | | | |
| tyrosyl-tRNA synthetase (YARS) | 1 | U89436 | + | + | + | + | | + | |
| U1 small nuclear RNA | 1 | M14387 | | | | | | | |
| U19H snoRNA (=M63485 R.norvegicus matrin 3) | 1 | AJ224166 | | | | | | | |
| U2(RNU2) small nuclear RNA auxiliary factor 1 (non-standard symbol) (U2AF1) | 1 | M96982 | | + | + | + | | + | |

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|--|---|----------|---|---|---|---|---|---|---|--------------------|
| U22 snoRNA host gene (UHG) | 2 | U40580 | | | | | | | | |
| U4/U6-associated RNA splicing factor (HPRP3P) | 4 | AF016370 | | + | + | + | | | + | |
| U49 small nuclear RNA | 1 | X96649 | | | | | | | | |
| U5 snRNP-specific protein (220 kD), ortholog of <i>S. cerevisiae</i> Prp8p (PRP8) | 1 | AB007510 | + | + | + | + | | | + | |
| U5 snRNP-specific protein, 116 kD (U5-116KD) | 4 | D21163 | + | + | + | + | | | + | |
| U5 snRNP-specific protein, 200 kDa (DEXH RNA helicase family) (U5-200-KD) | 3 | Z70200 | | | | | | | | |
| Uba80 mRNA for ubiquitin | 4 | S79522 | + | + | + | + | + | + | | high in ovary |
| ubiquinol-cytochrome c reductase (6.4kD) subunit (UQCR) | 1 | D55636 | + | + | + | + | + | + | | high in fetal lung |
| UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT PRECURSOR (RIESKE IRON-SULFUR PROTEIN) (RISP) (low match) | 1 | P47985 | | | | | | | | |
| ubiquitin A-52 residue ribosomal protein fusion product 1 (UBA52) | 2 | X56999 | | | | | | | | |
| ubiquitin activating enzyme E1-like protein (GSA7) | 1 | AF094516 | | + | + | | | | + | |
| ubiquitin C (UBC) | 5 | AB009010 | | + | + | + | + | + | | high in ovary |
| ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase) (UCHL3) | 1 | M30496 | + | + | + | + | | | + | |
| ubiquitin fusion degradation 1-like (UFD1L) | 1 | U64444 | + | + | + | + | | | + | |
| ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) | 1 | U84404 | B | + | + | | | | + | |

| | | | | | | | | | |
|--|---|----------|---|---|---|---|---|---|--|
| ubiquitin specific protease 10 (USP10) | 4 | D80012 | + | + | + | + | | + | |
| ubiquitin specific protease 11 (USP11) | 1 | U44839 | + | + | + | + | + | + | |
| ubiquitin specific protease 15 (USP15) | 3 | AB011101 | + | + | + | + | | + | |
| ubiquitin specific protease 19 (USP19) | 1 | AB020698 | | + | | | | | |
| ubiquitin specific protease 4 (proto-oncogene) (USP4) | 1 | AF017305 | B | + | + | | + | + | |
| ubiquitin specific protease 4 (proto-oncogene) (USP4) (non-exact, 66%) | 1 | AF017306 | | | | | | | |
| ubiquitin specific protease 7 (herpes virus-associated) (USP7) | 1 | Z72499 | | + | + | + | | + | |
| ubiquitin specific protease 8 (USP8) | 5 | D29956 | | + | + | + | | + | |
| UBIQUITIN-ACTIVATING ENZYME E1 (A1S9 PROTEIN) (56%) | 1 | P22314 | | | | | | | |
| ubiquitin-activating enzyme E1 (A1S9T and BN75 temperature sensitivity complementing) (UBE1) | 1 | M58028 | + | + | + | + | | + | |
| ubiquitin-activating enzyme E1, like (UBE1L) | 1 | L34170 | + | + | | + | | + | |
| UBIQUITIN-BINDING PROTEIN P62; phosphotyrosine independent ligand for the Lck SH2 domain p62 (P62) | 1 | U41806 | | | + | | + | | |
| ubiquitin-conjugating enzyme E2 variant 1 (UBE2V1) | 2 | U49278 | + | + | + | + | + | + | |
| ubiquitin-conjugating enzyme E2 variant 2 (UBE2V2) | 1 | X98091 | | | | | | | |
| UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) | 1 | Q16781 | | | | | | | |

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|---|---|----------|---|---|---|---|---|---|--|
| ubiquitin-conjugating enzyme E2B (RAD6 homolog) (UBE2B) | 1 | M74525 | + | + | + | + | | + | |
| ubiquitin-conjugating enzyme E2G 2 (homologous to yeast UBC7) (UBE2G2) | 1 | AF032456 | + | + | + | + | | + | |
| ubiquitin-conjugating enzyme E2H (homologous to yeast UBC8) (UBE2H) | 1 | Z29328 | + | + | + | + | | + | |
| ubiquitin-conjugating enzyme E2L 1 (UBE2L1) | 1 | X92962 | | + | + | | | + | |
| ubiquitin-conjugating enzyme E2L 3 (UBE2L3) | 3 | AJ000519 | | + | + | + | | + | |
| ubiquitin-conjugating enzyme E2L 6 (UBE2L6) | 4 | AF031141 | | + | + | + | + | + | |
| ubiquitin-like 1 (sentrin) (UBL1) | 2 | U61397 | + | + | + | + | | + | |
| UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylglucosaminyltransferase 2 (GalNAc-T2) (GALNT2) | 2 | X85019 | | | | | | | |
| UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylglucosaminyltransferase 3 (GalNAc-T3) (GALNT3) (non-exact 65%) | 1 | X92689 | | | | | | | |
| inactive progesterone receptor, 23 Kd (P23) | 2 | L24804 | | + | + | + | | + | |
| unconventional myosin-ID (MYO1F) | 3 | U57053 | | | | | | | |
| uncoupling protein homolog (UCPH) | 1 | U94592 | | | | | | | |
| uncoupling protein homolog (UCPH) (low match 67%) | 1 | U94592 | | | | | | | |
| Unknown gene product | 1 | AC002310 | | | | | | | |
| unknown mRNA (clone 24514) | 1 | AF070542 | | | | | | | |

| | | | | | | | | | |
|---|----|----------|---|---|---|---|---|---|---------------|
| unknown protein (clone ICRFp507L0677) | 2 | Z70223 | | | | | | | |
| unknown protein (Hs.93832) | 1 | AF070626 | + | + | + | + | + | + | |
| unknown protein IT14 | 1 | AF040966 | | | | | | | |
| uppressor of Ty (S.cerevisiae) 6 homolog | 1 | D79984 | + | + | + | + | + | + | |
| upregulated by 1,25-dihydroxyvitamin D-3 (VDUP1) | 74 | S73591 | + | + | + | + | | + | high in heart |
| upregulated by 1,25-dihydroxyvitamin D-3 (VDUP1) (low match) | 1 | S73591 | | | | | | | |
| upregulated by 1,25-dihydroxyvitamin D-3 (VDUP1) (low match) | 1 | S73591 | | | | | | | |
| upregulated by 1,25-dihydroxyvitamin D-3 (VDUP1) (low score) | 1 | S73591 | | | | | | | |
| upstream binding factor (hUBF) | 1 | X53461 | + | + | | + | | + | |
| UV radiation resistance associated gene (UVRAG) | 2 | X99050 | | + | + | + | | + | |
| vacuolar proton-ATPase, subunit D; V-ATPase, subunit D (ATP6DV) | 4 | X71490 | | + | + | + | + | + | |
| v-akt murine thymoma viral oncogene homolog 1 (AKT1) | 1 | M63167 | + | + | + | + | | + | |
| Vanin 2 (VNN2) | 3 | AJ132100 | | | | | | | |
| vasodilator-stimulated phosphoprotein (VASP) | 3 | Z46389 | + | | + | + | | + | |
| vav.1 oncogene (VAV1) | 1 | M59834 | | | | | | + | |
| vav 2 oncogene (VAV2) | 1 | S76992 | + | + | | | | | |
| v-crk avian sarcoma virus CT10 oncogene homolog (CRK) | 1 | D10656 | W | + | + | | + | | |
| v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 3 | 1 | M29366 | | | | | | + | |

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|---|----|----------|---|---|---|---|---|---|--|------------------------|
| (ERBB3) | | | | | | | | | | |
| VERSICAN CORE PROTEIN PRECURSOR | 1 | P13611 | | | | | | | | |
| Vesicle-associated membrane protein 1 (synaptobrevin 1) (VAMP1) | 1 | M36196 | | + | + | + | | + | | |
| vesicle-associated membrane protein 3 (cellubrevin) (VAMP3) | 1 | U64520 | | | | | | | | |
| v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS) | 26 | K00650 | | + | + | + | + | + | | high in aorta |
| v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS) (low match) | 1 | K00650 | | | | | | | | |
| villin 2 (ezrin) (VIL2) | 1 | X51521 | + | + | + | + | | + | | |
| villin-like protein | 1 | D88154 | | | | | | | | |
| vimentin (VIM) | 12 | X56134 | | + | + | + | + | + | | high in many libraries |
| vinculin (VCL) | 4 | M33308 | | + | + | + | | + | | |
| vitamin A responsive; cytoskeleton related (JWA) | 6 | AF070523 | | + | + | + | | + | | |
| v-jun avian sarcoma virus 17 oncogene homolog (JUN) | 2 | U65928 | + | + | + | + | | + | | |
| v-myb avian myeloblastosis viral oncogene homolog (MYB) | 1 | M15024 | | | + | | | + | | |
| voltage-dependent anion channel 1 (VDAC1) | 1 | L06132 | + | + | + | + | | + | | |
| voltage-dependent anion channel 3 (VDAC3) | 4 | U90943 | | + | + | + | | + | | |
| von Hippel-Lindau syndrome (VHL) | 1 | L15409 | | + | + | + | | + | | |
| von Willebrand factor (vWF) (low matched) | 1 | X06828 | | | | | | | | |
| v-raf murine sarcoma 3611 viral oncogene homolog 1 | 2 | L24038 | + | + | + | + | | | | |

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|--|----|----------|---|---|---|---|---|---|----------------|
| (ARAF1) | | | | | | | | | |
| v-raf-1 murine leukemia viral oncogene homolog 1 (RAF1) | 1 | X03484 | + | + | + | + | | + | |
| v-ral simian leukemia viral oncogene homolog B (ras related; GTP binding protein) (RALB) | 3 | M35416 | | | | | | | |
| V-rel avian reticuloendotheliosis viral oncogene homolog A (nuclear factor of kappa light polypeptide gene enhancer in B-cells 3 (p65)) (RELA) | 1 | L19067 | | + | + | + | | + | |
| v-yes-1 Yamaguchi sarcoma viral related oncogene homolog (LYN) | 2 | M16038 | + | + | | + | | + | |
| WD repeat domain 1 (WDR1) | 1 | AB010427 | + | + | + | + | + | + | |
| WDR1 (=AF020260) | 1 | AF020056 | | | | | | | |
| WD-repeat protein (HAN11) | 2 | U94747 | | + | + | | | + | |
| Williams-Beuren syndrome chromosome region 1 (WBSCR1) | 12 | AF045555 | + | + | + | + | + | + | |
| Wiskott-Aldrich syndrome protein interacting protein (WASPIP) | 4 | X86019 | + | + | + | | | + | |
| X (inactive)-specific transcript (XIST) | 2 | M97168 | | | | | | | |
| xeroderma pigmentosum, complementation group C (XPC) | 3 | D21089 | + | + | + | + | | | |
| XIAP associated factor-1 | 2 | X99699 | | | | + | | | |
| XIB | 1 | X90392 | | + | + | | + | + | |
| X-linked anhidrotic ectodermal dysplasia | 1 | AF003528 | | | | | | | |
| X-ray repair complementing defective repair in Chinese hamster cells 5 (double- | 1 | M30938 | + | + | + | + | | + | high in spleen |

| | | | | | | | | | |
|--|---|----------|---|---|---|---|--|---|------|
| strand-break rejoining; Ku autoantigen, 80kD) (XRCC5) | | | | | | | | | |
| XRP2 protein | 1 | AJ007590 | | | | | | | |
| yeloid differentiation primary response gene (88) (MYD88) | 1 | U84408 | | + | + | + | | + | |
| zeta-chain (TCR) associated protein kinase (70kD) (ZAP70) | 1 | L05148 | + | | | + | | | |
| zeta-chain (TCR) associated protein kinase (70kD) (ZAP70) (low match) | 1 | L05148 | | | | | | | |
| zinc finger protein (Hs.47371) | 2 | U69274 | + | + | + | + | | + | |
| zinc finger protein (Hs.78765) | 1 | U69645 | + | + | + | + | | + | |
| zinc finger protein 10 (KOX 1) (ZNF10) | 1 | X78933 | | | | | | + | only |
| ZINC FINGER PROTEIN 124 (HZF-16) (non-exact 51%) | 1 | Q15973 | | | | | | | |
| zinc finger protein 124 (HZF-16) (ZNF124) (non- exact, 78%) | 1 | S54641 | | | | | | | |
| ZINC FINGER PROTEIN 133 | 1 | P52736 | | | | | | | |
| zinc finger protein 136 (clone pHZ-20) (ZNF136) | 1 | U09367 | | | + | + | | | |
| zinc finger protein 140 (clone pHZ-39) (ZNF140) | 1 | U09368 | | + | | + | | + | |
| zinc finger protein 140 (clone pHZ-39) (ZNF140) (non-exact 59%) | 1 | AF060865 | | | | | | | |
| zinc finger protein 140 (clone pHZ-39) (ZNF140) (non-exact 73%) | 1 | U09368 | | | | | | | |
| zinc finger protein 140 (clone pHZ-39) (ZNF140) | 1 | S66508 | | | | | | | |

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|--|---|----------|-------------|---|---|---|---|---|--|------------------|
| (non-exact 73%aa) | | | | | | | | | | |
| zinc finger protein 140 (clone pHZ-39) (ZNF140) (non-exact, 80%) | 1 | U09368 | | | | | | | | |
| zinc finger protein 143 (clone pHZ-1) (ZNF143) | 2 | U09850 | + | + | + | + | + | + | | |
| zinc finger protein 143 (clone pHZ-1) (ZNF143) (low match) | 1 | U09850 | | | | | | | | |
| zinc finger protein 148 (pHZ-52) (ZNF148) | 1 | AF039019 | + | | | | | | | |
| ZINC FINGER PROTEIN 151 (MIZ-1 PROTEIN) (low match) | 1 | Q13105 | | | | | | | | |
| zinc finger protein 173 (ZNF173) | 1 | U09825 | B, T | + | + | | + | | | |
| zinc finger protein 192 (ZNF192) (non-exact, 66%) | 1 | U57796 | | | | | | | | |
| zinc finger protein 198 (ZNF198) | 1 | AJ224901 | | + | + | + | | | | |
| zinc finger protein 2 (ZNF2) (low match) | 1 | X60152 | | | | | | | | |
| zinc finger protein 200 (ZNF200) | 1 | AF060866 | | + | | + | | | | |
| zinc finger protein 207 (ZNF207) | 6 | AF046001 | + | + | + | + | + | + | | high in prostate |
| zinc finger protein 216 (ZNF216) | 2 | AF062072 | + | + | + | + | | + | | |
| zinc finger protein 217 (ZNF217) | 1 | AF041259 | T activated | | | | | + | | |
| ZINC FINGER PROTEIN 22 (ZINC FINGER PROTEIN KOX15) (non- exact 58%) | 1 | P17026 | | | | | | | | |
| zinc finger protein 230 (ZNF230) | 1 | U95044 | | + | | | | | | |
| Zinc finger protein 239 (ANF239) | 1 | L26914 | | + | | + | | | | |

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|---|---|----------|---|---|---|---|--|---|----------------------|
| zinc finger protein 261 (ZNF261) | 1 | AB002383 | | + | + | + | | + | |
| zinc finger protein 262 (ANF262) | 1 | AB007885 | | + | + | + | | + | |
| zinc finger protein 263 (ZNF263) | 1 | D88827 | | | | | | | |
| zinc finger protein 264 (ZNF264) | 1 | AB007872 | | + | + | + | | | |
| ZINC FINGER PROTEIN 33A (ZINC FINGER PROTEIN KOX31) (KIAA0065) (HA0946) | 1 | Q06730 | | | | | | | |
| zinc finger protein 42 (myeloid-specific retinoic acid- responsive) (ZNF42) | 1 | M58297 | + | + | + | + | | + | |
| zinc finger protein 43 (HTF6) (ZNF43) (low match) | 1 | X59244 | | | | | | | |
| zinc finger protein 43 (HTF6) (ZNF43) (non-exact, 54%) | 1 | X59244 | | | | | | | |
| zinc finger protein 43 (HTF6) (ZNF43) (non-exact, 71%) | 1 | X59244 | | | | | | | |
| ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6) (non-exact 67%) | 1 | P28160 | | | | | | | |
| zinc finger protein 45 (a Kruppel-associated box (KRAB) domain polypeptide) (ZNF45) | 1 | L75847 | | | | | | | only found in testis |
| ZINC FINGER PROTEIN 46 (ZINC FINGER PROTEIN KUP) (non-exact 62%) | 1 | P24278 | | | | | | | |
| zinc finger protein 6 (CMPX1) (ZNF6) | 1 | X56465 | | + | + | + | | + | |
| zinc finger protein 74 (Cos52) (ZNF74) (non-exact, 67%) | 1 | X71623 | | | | | | | |
| zinc finger protein 76 (expressed in testis) | 1 | M91592 | | + | + | + | | + | |

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|---|---|----------|-------------|---|---|---|---|---|------------|
| (ZNF76) | | | | | | | | | |
| ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1) (non-exact 65%) | 1 | P51522 | | | | | | | |
| zinc finger protein 84 (HPF2) (ZNF84) | 1 | M27878 | T activated | + | + | | | + | |
| zinc finger protein 85 (ZNF85)) | 2 | U35376 | | + | + | + | | | |
| zinc finger protein 9 (ZNF9) | 5 | M28372 | | + | + | + | + | + | |
| ZINC FINGER PROTEIN 93 (=ZINC FINGER PROTEIN HTF34) (non-exact 70%) | 1 | P35789 | | | | | | | |
| zinc finger protein C2H2-25 (ZNF25) | 3 | U38904 | | + | + | + | | | |
| zinc finger protein clone L3-4 | 1 | AF024706 | | | | | | | |
| zinc finger protein homologous to Zfp-36 in mouse (ZFP36) | 4 | M92843 | + | | | | | | blood only |
| ZINC FINGER PROTEIN HRX (ALL-1) (71%a.a.) | 1 | Q03164 | | | | | | | |
| zinc finger protein HZF4 | 1 | X78927 | | | | | | | |
| zinc finger protein RIZ | 1 | D45132 | + | + | + | + | | + | |
| zinc finger protein, subfamily 1A, 1 (Ikaros) (LYF1) | 1 | U40462 | + | | | | | | |
| zinc finger protein, subfamily 1A, 1 (Ikaros) (LYF1) (low match) | 1 | U40462 | | | | | | | |
| zinc finger transcriptional regulator (GOS24) | 1 | M92844 | | | | | | | |
| zinc-finger helicase (hZFH) | 2 | U91543 | + | + | + | + | | + | |
| Zn-15 related zinc finger protein (rlf) | 1 | U22377 | | + | + | + | | | |
| Zn-15 related zinc finger protein (rlf) (non-exact | 1 | U22377 | | | | | | | |

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|--|---|--------|--|---|--|--|--|--|--|--|
| 56%) | | | | | | | | | | |
| ZNF80-linked ERV9 long terminal repeat | 1 | X83497 | | | | | | | | |
| ZW10 (Drosophila) homolog, centromere/kinetochore protein (ZW10) | 2 | U54996 | | + | | | | | | |
| zyxin (ZYG) | 4 | X95735 | | | | | | | | |

| TABLE 3A | | | | | |
|--|----------|---|--------------------|----------------------|-----------------------|
| Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension | | | | | |
| Spot | p-value | Description | Gene Accession No. | Unig n Accession No. | Protein Accession No. |
| 195 | 0.020318 | X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-break rejoining; Ku autoantigen; 80kDa) (XRCC5), mRNA /cds=(34,2232) /gb=NM_021141 /gi=12408650 /ug=Hs.84981 /len=3310. | NM_021141 | Hs.84981 | NP_066964 |
| 248 | 0.004993 | hemoglobin, beta (HBB), mRNA /cds=(51,494) /gb=NM_000518 /gi=28302128 /ug=Hs.155376 /len=626 | NM_000518 | Hs.155376 | NP_000509 |
| 288 | 0.039781 | phosphodiesterase 8B (PDE8B), mRNA /cds=(46,2703) /gb=NM_003719 /gi=26006850 /ug=Hs.78106 /len=3567 | NM_003719 | Hs.78106 | NP_003710 |
| 310 | 0.037168 | kinesin family member 13B (KIF13B), mRNA /cds=(38,5518) /gb=NM_015254 /gi=13194196 /ug=Hs.15711 /len=8743 | NM_015254 | Hs.15711 | NP_056069 |
| 323 | 0.01661 | associated molecule with the SH3 domain of STAM (AMSH), mRNA /cds=(188,1462) /gb=NM_006463 /gi=17738303 /ug=Hs.12479 /len=2107 | NM_006463 | Hs.12479 | NP_006454 |
| 338 | 0.042541 | chromosome 11 hypothetical protein ORF3 (LOC56851), mRNA /cds=(14,742) /gb=NM_020154 /gi=9910345 /ug=Hs.4245 /len=1072 | NM_020154 | Hs.4245 | NP_064539 |
| 357 | 0.02428 | deleted in pancreatic carcinoma (DPC4) gene, exon 3 | AF045440 | | |
| 362 | 0.039781 | reversion-inducing-cysteine-rich protein with kazal motifs (RECK), mRNA /cds=(93,3008) /gb=NM_021111 /gi=11863155 /ug=Hs.29640 /len=4414 | NM_021111 | Hs.29640 | NP_066934 |
| 367 | 0.037046 | RNA (guanine-7-) methyltransferase (RNMT), mRNA /cds=(197,1627) /gb=NM_003799 /gi=4506566 /ug=Hs.8086 /len=6203 | NM_003799 | Hs.8086 | NP_003790 |
| 394 | 0.006608 | FLJ11874 fis, clone HEMBA1007073 /cds=UNKNOWN /gb=AK021936 /gi=10433239 /ug=Hs.367819 /len=2737 | AK021936 | Hs.367819 | |
| 434 | 0.032363 | phosphoglycerate kinase 1 (PGK1), mRNA /cds=(70,1323) /gb=NM_000291 /gi=22095338 /ug=Hs.78771 /len=2338 | NM_000291 | Hs.78771 | NP_000282 |
| 448 | 0.028082 | laminin receptor 1 (ribosomal protein SA, 67kDa) (LAMR1), mRNA /cds=(86,973) /gb=NM_002295 /gi=9845501 /ug=Hs.181357 /len=1039 | NM_002295 | Hs.181357 | NP_002286 |
| 460 | 0.03016 | sorting nexin 3 (SNX3), transcript variant 3, mRNA /cds=(326,667) /gb=NM_152828 /gi=23111042 /ug=Hs.12102 /len=1559 | NM_152828 | Hs.12102 | NP_690041 |
| 462 | 0.048903 | erg protein (ets-related gene) | M21535 | | NP_004440 |

| Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension | | | | | |
|--|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 475 | 0.039781 | clone IMAGE:5303725, mRNA /gb=BC041987 /gi=27469480 /ug=Hs.434826 /len=2021 | BC041987 | Hs.434826 | |
| 589 | 0.039763 | AGENCOURT_6640990 NIH_MGC_68 cDNA clone IMAGE:5735856 5', mRNA sequence /clone=IMAGE:5735856 /clone_end=5' /gb=BM907553 /gi=19357932 /ug=Hs.424427 /len=645 | BM907553 | Hs.424427 | |
| 599 | 0.022196 | hypothetical protein similar to RNA-binding protein lark (MGC10871), mRNA /cds=(54,1133) /gb=NM_031492 /gi=13899353 /ug=Hs.49994 /len=1821 | NM_031492 | Hs.49994 | NP_113680 |
| 600 | 0.024315 | fascin 1, actin-bundling protein (Strongylocentrotus purpuratus) (FSCN1), mRNA /cds=(112,1593) /gb=NM_003088 /gi=4507114 /ug=Hs.118400 /len=2767 | NM_003088 | Hs.118400 | NP_003079 |
| 626 | 0.020362 | RTC domain containing 1 (RTCD1), mRNA /cds=(171,1271) /gb=NM_003729 /gi=4506588 /ug=Hs.27076 /len=1539 | NM_003729 | Hs.27076 | NP_003720 |
| 627 | 0.047109 | methionine-tRNA synthetase (MARS), mRNA /cds=(24,2726) /gb=NM_004990 /gi=14043021 /ug=Hs.279946 /len=2795 | NM_004990 | Hs.279946 | NP_004981 |
| 633 | 0.014533 | A kinase (PRKA) anchor protein 13 (AKAP13), transcript variant 2, mRNA /cds=(214,8655) /gb=NM_007200 /gi=21493028 /ug=Hs.301946 /len=10156 | NM_007200 | Hs.301946 | NP_658913 |
| 652 | 0.042641 | cDNA FLJ38331 fis, clone FCBBF3025285, moderately similar to Mus musculus peripheral benzodiazepine receptor associated protein (Pap7) mRNA. /gb=AK095650 /gi=21754954 /ug=Hs.9052 /len=3547 | AK095650 | Hs.9052 | |
| 657 | 0.015956 | FLJ30577 fis, clone BRAWH2006760 /cds=UNKNOWN /gb=AK055139 /gi=16549803 /ug=Hs.324815 /len=2353 | AK055139 | Hs.324815 | |
| 658 | 0.01469 | KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3 (KDEL3), transcript variant 1, mRNA /cds=(157,801) /gb=NM_006855 /gi=8051612 /ug=Hs.250696 /len=1705 | NM_006855 | Hs.250696 | NP_057839 |
| 662 | 0.007887 | insulin-like growth factor binding protein 5 (IGFBP5), mRNA /cds=(752,1570) /gb=NM_000599 /gi=10834981 /ug=Hs.380833 /len=1722 | NM_000599 | Hs.380833 | NP_000590 |
| 669 | 0.005341 | putative zinc finger protein NY-REN-34 antigen (NY-REN-34), mRNA /cds=(129,704) /gb=NM_016119 /gi=7705832 /ug=Hs.279799 /len=1323 | NM_016119 | Hs.279799 | NP_057203 |

| Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension | | | | | |
|--|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 691 | 0.034482 | U5 snRNP-specific protein, 200-KD (U5-200KD), mRNA /cds=(189,5624) /gb=NM_014014 /gi=24307974 /ug=Hs.246112 /len=5898 | NM_014014 | Hs.246112 | NP_054733 |
| 692 | 0.042541 | chitinase 3-like 1 (cartilage glycoprotein-39) (CHI3L1), mRNA /cds=(127,1278) /gb=NM_001276 /gi=4557017 /ug=Hs.75184 /len=1925 | NM_001276 | Hs.75184 | NP_001267 |
| 697 | 0.048529 | interferon, alpha-inducible protein (clone IFI-6-16) (G1P3), transcript variant 3, mRNA /cds=(108,524) /gb=NM_022873 /gi=13259549 /ug=Hs.265827 /len=841 | NM_022873 | Hs.265827 | NP_075011 |
| 721 | 0.019388 | mitochondrion, complete genome | NC_001807 | | |
| 722 | 0.032363 | glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase 1) (GOT1), mRNA /cds=(25,1266) /gb=NM_002079 /gi=4504066 /ug=Hs.597 /len=1941 | NM_002079 | Hs.597 | NP_002070 |
| 726 | 0.005026 | tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide (YWHAG), mRNA /cds=(192,935) /gb=NM_012479 /gi=21464100 /ug=Hs.25001 /len=3747 | NM_012479 | Hs.25001 | NP_036611 |
| 771 | 0.042541 | zinc finger protein (ZFD25) (62% aa) | AB027251 | | NP_057304 |
| 772 | 0.007887 | acid sphingomyelinase (ASM) gene, exons a, and alternative a (3' end), b and c (5' end) | M59917 | | |
| 774 | 0.045456 | BAF53 (BAF53A), mRNA /cds=(137,1426) /gb=NM_004301 /gi=4757717 /ug=Hs.274350 /len=1842 | NM_004301 | Hs.274350 | NP_829888 |
| 807 | 0.037168 | KIAA0102 gene product (KIAA0102), mRNA /cds=(308,679) /gb=NM_014752 /gi=7661907 /ug=Hs.77665 /len=1370 | NM_014752 | Hs.77665 | NP_055567 |
| 808 | 0.017954 | PIX1 mRNA (ORF) | AF037219 | | NP_570854 |
| 809 | 0.002077 | methylcrotonoyl-Coenzyme A carboxylase 1 (alpha) (MCCC1), mRNA /cds=(133,2310) /gb=NM_020166 /gi=13518227 /ug=Hs.47649 /len=2528 | NM_020166 | Hs.47649 | NP_064551 |
| 810 | 0.028082 | KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3 (KDEL3), transcript variant 1, mRNA /cds=(157,801) /gb=NM_006855 /gi=8051612 /ug=Hs.250696 /len=1705 | NM_006855 | Hs.250696 | NP_057839 |
| 847 | 0.037168 | peroxisomal biogenesis factor 3 (PEX3), mRNA /cds=(64,1185) /gb=NM_003630 /gi=4505726 /ug=Hs.7277 /len=1979 | NM_003630 | Hs.7277 | NP_003621 |

| Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension | | | | | |
|--|----------|---|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Prot in Accession No. |
| 851 | 0.007223 | of89c05.s1 NCI_CGAP_Li5 cDNA clone IMAGE:1437512 3' similar to contains Alu repetitive element,, mRNA sequence /clone=IMAGE:1437512 /clone_end=3' /gb=AA894384 /gi=3030785 /ug=Hs.432123 /len=296 | AA894384 | Hs.432123 | |
| 865 | 0.028082 | mitochondrion, complete genome | NC_001807 | | |
| 870 | 0.020917 | KIAA0062 mRNA, partial cds /cds=(1,1598) /gb=D31887 /gi=505101 /ug=Hs.89868 /len=4573 | D31887 | Hs.89868 | |
| 877 | 0.013076 | ring finger protein 11 (RNF11), mRNA /cds=(128,592) /gb=NM_014372 /gi=7657519 /ug=Hs.96334 /len=2529 | NM_014372 | Hs.96334 | NP_055187 |
| 886 | 0.005026 | hemoglobin, beta (HBB), mRNA /cds=(51,494) /gb=NM_000518 /gi=28302128 /ug=Hs.155376 /len=626 | NM_000518 | Hs.155376 | NP_000509 |
| 887 | 0.01661 | polyadenylate binding protein-interacting protein 1 (PAIP1), mRNA /cds=(188,1627) /gb=NM_006451 /gi=17511254 /ug=Hs.109643 /len=2764 | NM_006451 | Hs.109643 | NP_006442 |
| 888 | 0.017954 | protein tyrosine phosphatase, non-receptor type 13 (APO-1/CD95 (Fas)-associated phosphatase) (PTPN13), transcript variant 4, mRNA /cds=(64,7536) /gb=NM_080685 /gi=18375649 /ug=Hs.211595 /len=8133 | NM_080685 | Hs.211595 | NP_542416 |
| 918 | 0.015351 | AGENCOURT_6456859 NIH_MGC_92 cDNA clone IMAGE:5576908 5', mRNA sequence /clone=IMAGE:5576908 /clone_end=5' /gb=BM466169 /gi=18515211 /ug=Hs.439148 /len=1150 | BM466169 | Hs.439148 | |
| 921 | 0.013076 | mitochondrion, complete genome | NC_001807 | | |
| 923 | 0.008602 | eukaryotic translation initiation factor 3, subunit 3 gamma, 40kDa (EIF3S3), mRNA /cds=(6,1064) /gb=NM_003756 /gi=4503514 /ug=Hs.58189 /len=1280 | NM_003756 | Hs.58189 | NP_003747 |
| 928 | 0.032363 | apoptosis inhibitor 5 (API5), mRNA /cds=(133,1647) /gb=NM_006595 /gi=5729729 /ug=Hs.227913 /len=3739 | NM_006595 | Hs.227913 | NP_006586 |
| 930 | 0.026124 | FK506 binding protein 9, 63 kDa (FKBP9), mRNA /cds=(457,885) /gb=NM_007270 /gi=24307926 /ug=Hs.302749 /len=2517 | NM_007270 | Hs.302749 | NP_009201 |
| 943 | 0.005512 | XIST, coding sequence "a" mRNA (locus DXS399E): /gb=X56199 /gi=37987 /ug=Hs.352403 /len=1614 | X56199 | Hs.352403 | |
| 968 | 0.027649 | translin (TSN), mRNA /cds=(236,922) /gb=NM_004622 /gi=20302160 /ug=Hs.75066 /len=3408 | NM_004622 | Hs.75066 | NP_004613 |

| Genes Corrsponding To Differentially Expressed Genes in Figure 8 - Hypertension | | | | | |
|---|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 991 | 0.03649 | P311 protein (P311), mRNA /cds=(203,409) /gb=NM_004772 /gi=4758865 /ug=Hs.413760 /len=2036 | NM_004772 | Hs.413760 | NP_004763 |
| 998 | 0.001683 | down-regulator of transcription 1, TBP-binding (negative cofactor 2) (DR1), mRNA /cds=(548,1078) /gb=NM_001938 /gi=4503380 /ug=Hs.16697 /len=1375 | NM_001938 | Hs.16697 | NP_001929 |
| 1008 | 0.005026 | Alg5, <i>S. cerevisiae</i> , of (ALG5), mRNA /cds=(28,1002) /gb=NM_013338 /gi=9665250 /ug=Hs.227933 /len=1125 | NM_013338 | Hs.227933 | NP_037470 |
| 1026 | 0.032363 | methionine adenosyltransferase II, beta (MAT2B), mRNA /cds=(73,1077) /gb=NM_013283 /gi=20127525 /ug=Hs.54642 /len=2054 | NM_013283 | Hs.54642 | NP_037415 |
| 1028 | 0.032363 | ATP synthase, H transporting, mitochondrial F1 complex, epsilon subunit (ATP5E), nuclear gene encoding mitochondrial protein, mRNA /cds=(95,250) /gb=NM_006886 /gi=21327678 /ug=Hs.177530 /len=417 | NM_006886 | Hs.177530 | NP_008817 |
| 1031 | 0.01661 | decorin (DCN), transcript variant A1, mRNA /cds=(200,1279) /gb=NM_001920 /gi=19743844 /ug=Hs.433989 /len=1751 | NM_001920 | Hs.433989 | NP_598014 |
| 1051 | 0.008602 | HSPC133 protein (HSPC133), mRNA /cds=(83,481) /gb=NM_014168 /gi=7661791 /ug=Hs.273063 /len=963 | NM_014168 | Hs.273063 | NP_054887 |
| 1099 | 0.03649 | DKFZP586O0120 protein (DKFZP586O0120), mRNA /cds=(21,359) /gb=NM_014077 /gi=7661695 /ug=Hs.4766 /len=1465 | NM_014077 | Hs.4766 | NP_054796 |
| 1104 | 0.028082 | eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA /cds=(63,1451) /gb=NM_001402 /gi=25453469 /ug=Hs.422118 /len=1837 | NM_001402 | Hs.422118 | NP_001393 |
| 1121 | 0.045685 | cDNA FLJ31399 fis, clone NT2NE1000181. /gb=AK055961 /gi=16550820 /ug=Hs.179833 /len=2159 | AK055961 | Hs.179833 | |
| 1163 | 0.022547 | reticulon 4 (RTN4), mRNA /cds=(245,3823) /gb=NM_020532 /gi=24638438 /ug=Hs.65450 /len=4166 | NM_020532 | Hs.65450 | NP_722550 |
| 1168 | 0.013076 | thymosin, beta 4, X chromosome (TMSB4X), mRNA /cds=(78,212) /gb=NM_021109 /gi=11056060 /ug=Hs.75968 /len=556 | NM_021109 | Hs.75968 | NP_066932 |
| 1170 | 0.020917 | myosin, light polypeptide 6, alkali, smooth muscle and non-muscle (MYL6), transcript variant 3, mRNA /cds=(41,514) /gb=NM_079425 /gi=17986263 /ug=Hs.77385 /len=717 | NM_079425 | Hs.77385 | NP_524149 |

| Genes Corresponding To Differentially Expressed Genes in Figure-8 - Hypertension | | | | | |
|--|----------|---|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 1189 | 0.013587 | mRNA; cDNA DKFZp451A142 (from clone DKFZp451A142) /cds=(39,1898) /gb=AL834245 /gi=21739785 /ug=Hs.124918 /len=4902 | AL834245 | Hs.124918 | |
| 1198 | 0.026124 | hypothetical protein FLJ20729 (FLJ20729); mRNA /cds=(135,1547) /gb=NM_017953 /gi=20149642 /ug=Hs.5111 /len=2821 | NM_017953 | Hs.5111 | NP_060423 |
| 1274 | 0.01205 | HSJ1a (HSJ1) mRNA, complete cds; alternatively spliced. /cds=(26,859) /gb=S37375 /gi=250081 /ug=Hs.433237 /len=1760 | S37375 | Hs.433237 | |
| 1301 | 0.006608 | actin, beta (ACTB), mRNA /cds=(74,1201) /gb=NM_001101 /gi=5016088 /ug=Hs.426930 /len=1793 | NM_001101 | Hs.426930 | NP_001092 |
| 1304 | 0.037168 | eukaryotic translation elongation factor 1 beta 2 (EEF1B2), transcript variant 1, mRNA /cds=(236,913) /gb=NM_001959 /gi=16519564 /ug=Hs.421608 /len=961 | NM_001959 | Hs.421608 | NP_066944 |
| 1305 | 0.001683 | cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA /cds=(90,281) /gb=NM_001867 /gi=18105039 /ug=Hs.430075 /len=448 | NM_001867 | Hs.430075 | NP_001858 |
| 1306 | 0.019388 | poly(A) binding protein, cytoplasmic 1 (PABPC1), mRNA /cds=(503,2404) /gb=NM_002568 /gi=4505574 /ug=Hs.172182 /len=2848 | NM_002568 | Hs.172182 | NP_002559 |
| 1370 | 0.024342 | solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6 (SLC25A6), nuclear gene encoding mitochondrial protein, mRNA /cds=(93,989) /gb=NM_001636 /gi=27764862 /ug=Hs.407372 /len=1455 | NM_001636 | Hs.407372 | NP_001627 |
| 1386 | 0.039164 | AGENCOURT_6424254 NIH_MGC_67 cDNA clone IMAGE:5491531 5', mRNA sequence /clone=IMAGE:5491531 /clone_end=5' /gb=BM479954 /gi=18528996 /ug=Hs.381243 /len=1112 | BM479954 | Hs.381243 | |
| 1389 | 0.032363 | heparan sulfate proteoglycan (HSPG2) mRNA, complete cds | M85289 | | NP_005520 |
| 1427 | 0.048529 | small nuclear RNA activating complex, polypeptide 1, 43kDa (SNAPC1), mRNA /cds=(13,1119) /gb=NM_003082 /gi=19923159 /ug=Hs.179312 /len=2594 | NM_003082 | Hs.179312 | NP_003073 |
| 1430 | 0.020917 | synovial sarcoma, X breakpoint 2 interacting protein (SSX2IP), mRNA /cds=(265,2109) /gb=NM_014021 /gi=7662381 /ug=Hs.22587 /len=5835 | NM_014021 | Hs.22587 | NP_054740 |

| Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension | | | | | |
|--|----------|---|-------------------------|-----------------------------|-----------------------------|
| Spot | p-value | Description | Gen Accession No. | Unigene Accession No. | Protein Accession No. |
| 1431 | 0.02428 | inhibitor of growth family, member 1 (ING1), mRNA /cds=(433,1701) /gb=NM_005537 /gi=19923770 /ug=Hs.46700 /len=2886 | NM_005537 | Hs.46700 | NP_005528 |
| 1455 | 0.045456 | CDC5 cell division cycle 5-like (S. pombe) (CDC5L), mRNA /cds=(260,2668) /gb=NM_001253 /gi=16357499 /ug=Hs.155174 /len=3012 | NM_001253 | Hs.155174 | NP_001244 |
| 1456 | 0.026124 | CGI-74 protein (CGI-59), mRNA /cds=(1,1209) /gb=NM_016019 /gi=7706309 /ug=Hs.7194 /len=2296 | NM_016019 | Hs.7194 | NP_057103 |
| 1476 | 0.015351 | tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide (YWHAB), transcript variant 1, mRNA /cds=(277,1017) /gb=NM_003404 /gi=21328444 /ug=Hs.279920 /len=1117 | NM_003404 | Hs.279920 | NP_647539 |
| 1482 | 0.048529 | ATP synthase, H ⁺ transporting, mitochondrial F1 complex, epsilon subunit (ATP5E), nuclear gene encoding mitochondrial protein, mRNA /cds=(95,250) /gb=NM_006886 /gi=21327678 /ug=Hs.177530 /len=417 | NM_006886 | Hs.177530 | NP_008817 |
| 1497 | 0.01661 | hypothetical protein MGC45474 (MGC45474), mRNA /cds=(218,2035) /gb=NM_152369 /gi=22748794 /ug=Hs.234101 /len=2384 | NM_152369 | Hs.234101 | |
| 1506 | 0.017954 | septin 2 (SEP2) mRNA, partial cds /cds=(1,1528) /gb=AF179995 /gi=9957543 /ug=Hs.80712 /len=4344 | AF179995 | Hs.80712 | |
| 1535 | 0.03016 | mRNA for KIAA0752 protein, partial cds. /cds=(1,1006) /gb=AB018295 /gi=3882224 /ug=Hs.126779 /len=4332 | AB018295 | Hs.126779 | NP_775934 |
| 1577 | 0.02428 | POM121 membrane glycoprotein (rat) (POM121), mRNA /cds=(978,3932) /gb=NM_172020 /gi=26051277 /ug=Hs.295112 /len=6014 | NM_172020 | Hs.295112 | NP_742017 |
| 1648 | 0.002819 | mRNA; cDNA DKFZp564E193 (from clone DKFZp564E193) /gb=AL049259 /gi=4500005 /ug=Hs.333141 /len=1691 | AL049259 | Hs.333141 | |
| 1665 | 7.89E-04 | eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA /cds=(63,1451) /gb=NM_001402 /gi=25453469 /ug=Hs.422118 /len=1837 | NM_001402 | Hs.422118 | NP_001393 |
| 1683 | 0.037168 | mitochondrion, complete genome | NC_001807 | | |
| 1720 | 0.013076 | KIAA0971 protein (KIAA0971), mRNA /cds=(59,2005) /gb=NM_014929 /gi=7662421 /ug=Hs.84429 /len=4999 | NM_014929 | Hs.84429 | NP_055744 |

| Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension | | | | | |
|--|----------|---|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 1723 | 0.02428 | CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5, EJ16, EJ30, EL32 and G344) (CD59), mRNA /cds=(50,436) /gb=NM_000611 /gi=20127410 /ug=Hs.278573 /len=1946 | NM_000611 | Hs.278573 | NP_000602 |
| 1724 | 0.034698 | zinc finger RNA binding protein (ZFR), mRNA /cds=(44,1300) /gb=NM_016107 /gi=7706372 /ug=Hs.173518 /len=2734 | NM_016107 | Hs.173518 | NP_057191 |
| 1749 | 0.004165 | hypothetical protein MGC20781 (MGC20781), mRNA /cds=(366,1139) /gb=NM_052935 /gi=16418414 /ug=Hs.237536 /len=1476 | NM_052935 | Hs.237536 | NP_443167 |
| 1751 | 0.007887 | insulin induced protein 2 (LOC51141), mRNA /cds=(141,857) /gb=NM_016133 /gi=23821030 /ug=Hs.7089 /len=1358 | NM_016133 | Hs.7089 | NP_057217 |
| 1756 | 0.039781 | uronyl-2-sulfotransferase (UST), mRNA /cds=(104,1324) /gb=NM_005715 /gi=5032218 /ug=Hs.134015 /len=4196 | NM_005715 | Hs.134015 | NP_005706 |
| 1790 | 0.034698 | hypothetical protein FLJ21749 (FLJ21749), mRNA /cds=(102,689) /gb=NM_025124 /gi=13376700 /ug=Hs.288761 /len=961 | NM_025124 | Hs.288761 | NP_079400 |
| 1799 | 0.019388 | hypothetical protein MGC10911 (MGC10911), mRNA /cds=(234,602) /gb=NM_032302 /gi=14150059 /ug=Hs.85573 /len=985 | NM_032302 | Hs.85573 | NP_115678 |
| 1830 | 6.88E-04 | calmodulin-I (CALM1) mRNA, 3'UTR, partial sequence. /gb=U16850 /gi=576644 /ug=Hs.374441 /len=2383 | U16850 | Hs.374441 | |
| 1855 | 0.011093 | protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting 1 (PIN1), mRNA /cds=(25,516) /gb=NM_006221 /gi=5453897 /ug=Hs.161362 /len=994 | NM_006221 | Hs.161362 | NP_006212 |
| 1919 | 0.01661 | cellular fibronectin (non-exact, 62%) | M10905 | | NP_473375 |
| 1946 | 0.02428 | sphingolipid activator protein 1 | J03015 | | NP_002769 |
| 1963 | 0.045456 | Fanconi anemia, complementation group G (FANCG), mRNA /cds=(493,2361) /gb=NM_004629 /gi=4759335 /ug=Hs.8047 /len=2649 | NM_004629 | Hs.8047 | NP_004620 |
| 1974 | 0.026124 | CDC20 cell division cycle 20 (S. cerevisiae) (CDC20), mRNA /cds=(111,1610) /gb=NM_001255 /gi=4557436 /ug=Hs.82906 /len=1686 | NM_001255 | Hs.82906 | NP_001246 |
| 1999 | 0.045456 | chromosome 20 open reading frame 40 (C20orf40), mRNA /cds=(208,396) /gb=NM_014054 /gi=7661709 /ug=Hs.105379 /len=417 | NM_014054 | Hs.105379 | NP_054773 |

| Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension | | | | | |
|--|----------|---|--------------------|----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigen Accession No. | Protein Accession No. |
| 2033 | 0.002819 | calmodulin 1 (phosphorylase kinase, delta) (CALM1), mRNA /cds=(200,649) /gb=NM_006888 /gi=5901911 /ug=Hs.282410 /len=1526 | NM_006888 | Hs.282410 | NP_008819 |
| 2041 | 0.039781 | ribosomal protein L32 (RPL32), mRNA /cds=(51,458) /gb=NM_000994 /gi=15812220 /ug=Hs.169793 /len=521 | NM_000994 | Hs.169793 | NP_000985 |
| 2070 | 0.020917 | myotubular myopathy 1 (MTM1), mRNA /cds=(55,1866) /gb=NM_000252 /gi=4557895 /ug=Hs.75302 /len=3411 | NM_000252 | Hs.75302 | NP_000243 |
| 2073 | 0.02428 | transcription factor B1, mitochondrial (TFB1M), mRNA /cds=(73,1113) /gb=NM_016020 /gi=7705784 /ug=Hs.279908 /len=1290 | NM_016020 | Hs.279908 | NP_057104 |
| 2075 | 0.01661 | TRAF family member-associated NFKB activator (TANK), transcript variant 1, mRNA /cds=(159,1436) /gb=NM_004180 /gi=19743568 /ug=Hs.146847 /len=2089 | NM_004180 | Hs.146847 | NP_597841 |
| 2105 | 0.042541 | potassium channel, subfamily K, member 1 (KCNK1), mRNA /cds=(183,1193) /gb=NM_002245 /gi=15451900 /ug=Hs.79351 /len=1901 | NM_002245 | Hs.79351 | NP_002236 |
| 2164 | 0.03016 | KIAA1074 protein (KIAA1074), mRNA /cds=(151,5280) /gb=NM_014915 /gi=7662473 /ug=Hs.129218 /len=5360 | NM_014915 | Hs.129218 | NP_055730 |
| 2181 | 0.019388 | nucleobindin 2 (NUCB2), mRNA /cds=(220,1482) /gb=NM_005013 /gi=4826869 /ug=Hs.3164 /len=1586 | NM_005013 | Hs.3164 | NP_005004 |
| 2194 | 0.039781 | monocytic leukemia zinc finger protein-related factor (MORF), mRNA /cds=(316,6537) /gb=NM_012330 /gi=6912511 /ug=Hs.27590 /len=6537 | NM_012330 | Hs.27590 | NP_036462 |
| 2234 | 0.048529 | early endosome antigen 1, 162kD (EEA1), mRNA /cds=(137,4369) /gb=NM_003566 /gi=4503468 /ug=Hs.2864 /len=5028 | NM_003566 | Hs.2864 | NP_003557 |
| 2241 | 0.022547 | bone morphogenetic protein 6 (BMP6), mRNA /cds=(180,1721) /gb=NM_001718 /gi=4809281 /ug=Hs.285671 /len=2943 | NM_001718 | Hs.285671 | NP_001709 |
| 2245 | 0.028082 | ribosomal protein L15 (RPL15), mRNA /cds=(37,651) /gb=NM_002948 /gi=15431292 /ug=Hs.74267 /len=2018 | NM_002948 | Hs.74267 | NP_002939 |
| 2252 | 0.028082 | UI-CF-DU1-aag-k-05-0-UI.s1 UI-CF-DU1 cDNA clone UI-CF-DU1-aag-k-05-0-UI 3', mRNA sequence /clone=UI-CF-DU1-aag-k-05-0-UI /clone_end=3' /gb=BU676081 /gi=23520708 /ug=Hs.389894 /len=731 | BU676081 | Hs.389894 | |
| 2309 | 0.013076 | GTPase-activating protein GAPIII | U20238 | | NP_033051 |

| Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension | | | | | |
|--|----------|---|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 2317 | 0.006039 | mRNA for KIAA0570 protein, partial cds. /cds=(480,10718) /gb=AB011142 /gi=20521084 /ug=Hs.180948 /len=11269 | AB011142 | Hs.180948 | |
| 2318 | 0.006608 | mRNA for KIAA0611 protein, partial cds. /cds=(1,2740) /gb=AB014511 /gi=3327035 /ug=Hs.406434 /len=7176 | AB014511 | Hs.406434 | |
| 2412 | 0.01205 | guanine nucleotide binding protein (G protein), beta polypeptide 2 (GNB2), mRNA /cds=(259,1281) /gb=NM_005273 /gi=20357528 /ug=Hs.91299 /len=1666 | NM_005273 | Hs.91299 | NP_005264 |
| 2480 | 0.032363 | topoisomerase (DNA) I (TOP1), mRNA /cds=(247,2544) /gb=NM_003286 /gi=19913404 /ug=Hs.317 /len=3734 | NM_003286 | Hs.317 | NP_003277 |
| 2520 | 0.037168 | KIAA0164 gene product (KIAA0164), mRNA /cds=(254,3016) /gb=NM_014739 /gi=7661957 /ug=Hs.80338 /len=5538 | NM_014739 | Hs.80338 | NP_055554 |
| 2527 | 0.045456 | hypothetical protein FLJ12476 (FLJ12476), mRNA /cds=(564,2429) /gb=NM_022784 /gi=12232474 /ug=Hs.88144 /len=3623 | NM_022784 | Hs.88144 | NP_073621 |
| 2557 | 0.009373 | leucine-rich PPR-motif containing (LRPPRC), mRNA /cds=(46,3867) /gb=NM_133259 /gi=18959201 /ug=Hs.182490 /len=4782 | NM_133259 | Hs.182490 | NP_573566 |
| 2678 | 0.032363 | protein-L-isoaspartate (D-aspartate) O-methyltransferase (PCMT1), mRNA /cds=(74,757) /gb=NM_005389 /gi=4885538 /ug=Hs.79137 /len=1599 | NM_005389 | Hs.79137 | NP_005380 |
| 2681 | 0.008602 | HBS1-like (S. cerevisiae) (HBS1L), mRNA /cds=(194,2248) /gb=NM_006620 /gi=24431963 /ug=Hs.221040 /len=7163 | NM_006620 | Hs.221040 | NP_006611 |
| 2786 | 0.039781 | pogo transposable element with ZNF domain (POGZ), transcript variant 1, mRNA /cds=(6,4079) /gb=NM_015100 /gi=22027468 /ug=Hs.107088 /len=6157 | NM_015100 | Hs.107088 | NP_665739 |
| 2797 | 0.026124 | zinc finger homeobox 1b (ZFHX1B), mRNA /cds=(445,4089) /gb=NM_014795 /gi=7662183 /ug=Hs.34871 /len=5523 | NM_014795 | Hs.34871 | NP_055610 |
| 2799 | 0.022547 | glia maturation factor, beta (GMFB), mRNA /cds=(98,526) /gb=NM_004124 /gi=4758441 /ug=Hs.151413 /len=4131 | NM_004124 | Hs.151413 | NP_004115 |
| 2801 | 0.048529 | Rattus norvegicus mitochondrial genome | NC_001665 | | |
| 2802 | 0.037168 | HT001 protein (HT001), mRNA /cds=(242,1204) /gb=NM_014065 /gi=7661837 /ug=Hs.279040 /len=1402 | NM_014065 | Hs.279040 | NP_054784 |

| Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension | | | | | |
|--|----------|---|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 2810 | 0.042541 | ATP synthase, H transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3 (ATP5G3), mRNA /cds=(255,683) /gb=NM_001689 /gi=4502300 /ug=Hs.429 /len=826 | NM_001689 | Hs.429 | NP_001680 |
| 2813 | 0.003435 | ribosomal protein L37a (RPL37A), mRNA /cds=(36,314) /gb=NM_000998 /gi=16306561 /ug=Hs.296290 /len=392 | NM_000998 | Hs.296290 | NP_000989 |
| 2815 | 0.004165 | proteasome (prosome, macropain) subunit, alpha type, 6 (PSMA6), mRNA /cds=(110,850) /gb=NM_002791 /gi=23110943 /ug=Hs.410276 /len=1035 | NM_002791 | Hs.410276 | NP_002782 |
| 2821 | 0.037168 | transcription factor forkhead-like 7 (FKHL7) gene, complete cds | AF048693 | | |
| 2848 | 0.008602 | BJ-HCC-24 tumor antigen mRNA, complete cds /cds=(2,1240) /gb=AY121805 /gi=22002585 /ug=Hs.433489 /len=1488 | AY121805 | Hs.433489 | |
| 2849 | 0.007223 | chromosome 14 open reading frame 2 (C14orf2), mRNA /cds=(61,237) /gb=NM_004894 /gi=4758939 /ug=Hs.109052 /len=627 | NM_004894 | Hs.109052 | NP_004885 |
| 2850 | 0.03016 | helicase II (RAD54L) mRNA, complete cds. /cds=(54,4979) /gb=U09820 /gi=606832 /ug=Hs.96264 /len=6115 | U09820 | Hs.96264 | NP_612115 |
| 2884 | 0.020917 | mitochondrial ribosomal protein S30 (MRPS30), mRNA /cds=(39,1358) /gb=NM_016640 /gi=16950598 /ug=Hs.28555 /len=1482 | NM_016640 | Hs.28555 | NP_057724 |
| 2885 | 0.048529 | chromosome 1 specific transcript KIAA0491 | AB007960 | | NP_057093 |
| 2910 | 0.045456 | Sm protein F (LSM6), mRNA /cds=(82,324) /gb=NM_007080 /gi=5901997 /ug=Hs.42438 /len=596 | NM_007080 | Hs.42438 | NP_009011 |
| 2913 | 0.005512 | mortality factor 4 like 1 (MORF4L1), mRNA /cds=(132,1103) /gb=NM_006791 /gi=5803101 /ug=Hs.6353 /len=1766 | NM_006791 | Hs.6353 | NP_006782 |
| 2928 | 0.042541 | ligase IV, DNA, ATP-dependent (LIG4), mRNA /cds=(274,3009) /gb=NM_002312 /gi=23199992 /ug=Hs.166091 /len=3325 | NM_002312 | Hs.166091 | NP_002303 |
| 2930 | 0.022547 | vascular Rab-GAP/TBC-containing (VRP), mRNA /cds=(1118,3811) /gb=NM_007063 /gi=5902153 /ug=Hs.164170 /len=4404 | NM_007063 | Hs.164170 | NP_008994 |
| 2931 | 0.048529 | peptidylprolyl isomerase A (cyclophilin A) (PPIA), mRNA /cds=(45,542) /gb=NM_021130 /gi=10863926 /ug=Hs.401787 /len=753 | NM_021130 | Hs.401787 | NP_066953 |

| Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension | | | | | |
|--|----------|--|-------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gen Accession No. | Unigene Accession No. | Protein Accession No. |
| 2966 | 0.009373 | RAB14, member RAS oncogene family (RAB14), mRNA /cds=(184,831) /gb=NM_016322 /gi=19923482 /ug=Hs.5807 /len=4106 | NM_016322 | Hs.5807 | NP_057406 |
| 2967 | 0.020917 | matrix metalloproteinase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase) (MMP2), mRNA /cds=(290,2272) /gb=NM_004530 /gi=11342665 /ug=Hs.111301 /len=3069 | NM_004530 | Hs.111301 | NP_004521 |
| 2989 | 0.013076 | hypothetical protein DKFZp434B195 (DKFZP434B195), mRNA /cds=(514,1290) /gb=NM_031284 /gi=21361960 /ug=Hs.10748 /len=2262 | NM_031284 | Hs.10748 | NP_112574 |
| 2990 | 0.019388 | cDNA FLJ31057 fis, clone HSYRA2000787. /gb=AK055619 /gi=16550395 /ug=Hs.296261 /len=2168 | AK055619 | Hs.296261 | |
| 2996 | 0.009373 | ribosomal protein L12 (RPL12), mRNA /cds=(89,586) /gb=NM_000976 /gi=15431291 /ug=Hs.405042 /len=632 | NM_000976 | Hs.405042 | NP_000967 |
| 3025 | 0.013076 | FLJ30708 fis, clone FCBBF2001238 /cds=UNKNOWN /gb=AK055270 /gi=16549967 /ug=Hs.94812 /len=1965 | AK055270 | Hs.94812 | |
| 3029 | 2.91E-04 | Yip1p-interacting factor (YIF1P), mRNA /cds=(116,997) /gb=NM_020470 /gi=9994168 /ug=Hs.406422 /len=1078 | NM_020470 | Hs.406422 | NP_065203 |
| 3032 | 0.019388 | golgi-specific brefeldin A resistance factor 1 (GBF1), mRNA /cds=(241,5820) /gb=NM_004193 /gi=4758415 /ug=Hs.155499 /len=6376 | NM_004193 | Hs.155499 | NP_004184 |
| 3034 | 0.015351 | serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 6 (SERPINB6), mRNA /cds=(75,1205) /gb=NM_004568 /gi=28077084 /ug=Hs.41072 /len=1361 | NM_004568 | Hs.41072 | NP_004559 |
| 3065 | 8.68E-04 | KIAA0433 protein (KIAA0433), mRNA /cds=(510,4241) /gb=NM_015216 /gi=7662117 /ug=Hs.26179 /len=5814 | NM_015216 | Hs.26179 | NP_056031 |
| 3070 | 0.006039 | signal sequence receptor, beta (translocon-associated protein beta) (SSR2), mRNA /cds=(51,602) /gb=NM_003145 /gi=6552341 /ug=Hs.74564 /len=1093 | NM_003145 | Hs.74564 | NP_003136 |
| 3108 | 0.01661 | glycogen synthase 1 (muscle) (GYS1), mRNA /cds=(161,2374) /gb=NM_002103 /gi=4504232 /ug=Hs.772 /len=3531 | NM_002103 | Hs.772 | NP_002094 |
| 3113 | 0.013076 | phosphodiesterase 4D interacting protein (myomegalin) (PDE4DIP), mRNA /cds=(658,4056) /gb=NM_014644 /gi=11036643 /ug=Hs.265848 /len=5676 | NM_014644 | Hs.265848 | NP_055459 |

| Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension | | | | | |
|--|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 3137 | 0.03016 | yp24c06.s1 Soares breast 3NbHBst cDNA clone IMAGE:188362 3' similar to gb:M10942_cds1 metallothionein-le gene mRNA sequence /clone=IMAGE:188362 /clone_end=3' /gb=H43642 /gi=919694 /ug=Hs.418241 /len=452 | H43642 | Hs.418241 | |
| 3138 | 0.032363 | NCAG1 (NCAG1), mRNA /cds=(1477,5145) /gb=NM_032160 /gi=23943786 /ug=Hs.124673 /len=9528 | NM_032160 | Hs.124673 | NP_115536 |
| 3139 | 0.037168 | mRNA for KIAA0530 protein, partial cds. /cds=(1,4693) /gb=AB011102 /gi=3043583 /ug=Hs.173081 /len=6578 | AB011102 | Hs.173081 | |
| 3141 | 0.034698 | 3-oxoacid CoA transferase (OXCT), nuclear gene encoding mitochondrial protein, mRNA /cds=(99,1661) /gb=NM_000436 /gi=4557816 /ug=Hs.177584 /len=3337 | NM_000436 | Hs.177584 | NP_000427 |
| 3144 | 0.007887 | solute carrier family 20 (phosphate transporter), member 1 (SLC20A1), mRNA /cds=(371,2410) /gb=NM_005415 /gi=7382462 /ug=Hs.78452 /len=3220 | NM_005415 | Hs.78452 | NP_005406 |
| 3149 | 0.015351 | thioredoxin domain-containing (TXNDC), mRNA /cds=(118,960) /gb=NM_030755 /gi=13559515 /ug=Hs.24766 /len=1112 | NM_030755 | Hs.24766 | NP_110382 |
| 3165 | 0.026124 | SOCS box-containing WD protein SWIP-1 (WSB1), transcript variant 3, mRNA /cds=(317,1051) /gb=NM_134264 /gi=20143909 /ug=Hs.187991 /len=4243 | NM_134264 | Hs.187991 | NP_599027 |
| 3173 | 0.032363 | hypothetical protein FLJ11730 (FLJ11730), mRNA /cds=(33,608) /gb=NM_022756 /gi=20149668 /ug=Hs.17118 /len=1558 | NM_022756 | Hs.17118 | NP_073593 |
| 3174 | 1.72E-04 | lectin, galactoside-binding, soluble, 1 (galectin 1) (LGALS1), mRNA /cds=(69,476) /gb=NM_002305 /gi=6006015 /ug=Hs.382367 /len=526 | NM_002305 | Hs.382367 | NP_002296 |
| 3219 | 0.010202 | actin, alpha, cardiac muscle (ACTC), mRNA /cds=(1,1134) /gb=NM_005159 /gi=10938011 /ug=Hs.118127 /len=1294 | NM_005159 | Hs.118127 | NP_005150 |
| 3233 | 0.013076 | uncharacterized hematopoietic stem/progenitor cells protein MDS027 (MDS027), mRNA /cds=(21,248) /gb=NM_018462 /gi=27544938 /ug=Hs.421654 /len=888 | NM_018462 | Hs.421654 | NP_060932 |

| Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension | | | | | |
|--|----------|---|--------------------------|-----------------------------|-----------------------------|
| Spot | p-value | D scription | G ne Accession No. | Unigene Accession No. | Protein Accession No. |
| 3245 | 0.007289 | procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide (protein disulfide isomerase; thyroid hormone binding protein p55) (P4HB), mRNA /cds=(45,1571) /gb=NM_000918 /gi=20070124 /ug=Hs.410578 /len=2438 | NM_000918 | Hs.410578 | NP_000909 |
| 3254 | 0.039781 | splicing factor, arginine/serine-rich 2 (SFRS2), mRNA /cds=(156,821) /gb=NM_003016 /gi=4506898 /ug=Hs.73965 /len=1879 | NM_003016 | Hs.73965 | NP_003007 |
| 3266 | 0.03016 | DKFZP564C186 protein (DKFZP564C186), mRNA /cds=(16,2265) /gb=NM_015658 /gi=7661605 /ug=Hs.134200 /len=2762 | NM_015658 | Hs.134200 | NP_056473 |
| 3288 | 0.005026 | cyclin G2 (CCNG2), mRNA /cds=(136,1170) /gb=NM_004354 /gi=4757935 /ug=Hs.79069 /len=2044 | NM_004354 | Hs.79069 | NP_004345 |
| 3300 | 0.032363 | 3-hydroxy-3-methylglutaryl-Coenzyme A reductase (HMGCR), mRNA /cds=(51,2717) /gb=NM_000859 /gi=4557642 /ug=Hs.11899 /len=4471 | NM_000859 | Hs.11899 | NP_000850 |
| 3302 | 0.048529 | immature colon carcinoma transcript 1 (ICT1), mRNA /cds=(3,623) /gb=NM_001545 /gi=4557656 /ug=Hs.9078 /len=888 | NM_001545 | Hs.9078 | NP_001536 |
| 3316 | 0.017954 | glutathione S-transferase M3 (brain) (GSTM3), mRNA /cds=(311,988) /gb=NM_000849 /gi=23065551 /ug=Hs.2006 /len=1572 | NM_000849 | Hs.2006 | NP_000840 |
| 3318 | 0.002302 | endothelial protein C receptor | AB026584 | | |
| 3322 | 0.045456 | ribonuclease P (30kD) (RPP30), mRNA /cds=(295,1101) /gb=NM_006413 /gi=19923360 /ug=Hs.139120 /len=2643 | NM_006413 | Hs.139120 | NP_006404 |
| 3354 | 0.001871 | ribosomal protein L23 (RPL23), mRNA /cds=(27,449) /gb=NM_000978 /gi=14591907 /ug=Hs.234518 /len=493 | NM_000978 | Hs.234518 | NP_000969 |
| 3355 | 0.020917 | ets variant gene 5 (ets-related molecule) (ETV5), mRNA /cds=(224,1756) /gb=NM_004454 /gi=4758315 /ug=Hs.43697 /len=4071 | NM_004454 | Hs.43697 | NP_004445 |
| 3390 | 0.011093 | phosphoribosyl pyrophosphate synthetase-associated protein 2 (PRPSAP2), mRNA /cds=(212,1321) /gb=NM_002767 /gi=22538484 /ug=Hs.13339 /len=1890 | NM_002767 | Hs.13339 | NP_002758 |

| Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension | | | | | |
|--|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 3405 | 0.020917 | lectin, galactoside-binding, soluble, 1 (galectin 1) (LGALS1), mRNA /cds=(69,476) /gb=NM_002305 /gi=6006015 /ug=Hs.382367 /len=526 | NM_002305 | Hs.382367 | NP_002296 |
| 3433 | 0.048529 | interferon induced transmembrane protein 3 (1-8U) (IFITM3), mRNA /cds=(238,639) /gb=NM_021034 /gi=11995467 /ug=Hs.381234 /len=808 | NM_021034 | Hs.381234 | NP_066362 |
| 3440 | 0.010202 | TERF1 (TRF1)-interacting nuclear factor 2 (TINF2), mRNA /cds=(263,1327) /gb=NM_012461 /gi=6912715 /ug=Hs.7797 /len=2095 | NM_012461 | Hs.7797 | NP_036593 |
| 3444 | 0.037168 | laminin receptor 1 (ribosomal protein SA, 67kDa) (LAMR1), mRNA /cds=(86,973) /gb=NM_002295 /gi=9845501 /ug=Hs.181357 /len=1039 | NM_002295 | Hs.181357 | NP_002286 |
| 3507 | 0.011093 | UI-H-DT0-atx-I-07-0-UI.s1 NCI_CGAP_DT0 cDNA clone IMAGE:5865750 3', mRNA sequence /clone=IMAGE:5865750 /clone_end=3' /gb=BM994183 /gi=19719084 /ug=Hs.412022 /len=1284 | BM994183 | Hs.412022 | |
| 3512 | 0.011093 | eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA /cds=(63,1451) /gb=NM_001402 /gi=25453469 /ug=Hs.422118 /len=1837 | NM_001402 | Hs.422118 | NP_001393 |
| 3548 | 0.005026 | eukaryotic translation initiation factor 3, subunit 6 48kDa (EIF3S6), mRNA /cds=(23,1360) /gb=NM_001568 /gi=4503520 /ug=Hs.106673 /len=1510 | NM_001568 | Hs.106673 | NP_001559 |
| 3607 | 0.004578 | mitochondrion, complete genome | NC_001807 | | |
| 3609 | 0.039781 | mortality factor 4 like 1 (MORF4L1), mRNA /cds=(132,1103) /gb=NM_006791 /gi=5803101 /ug=Hs.6353 /len=1766 | NM_006791 | Hs.6353 | NP_006782 |
| 3619 | 0.01205 | cytochrome c oxidase subunit IV isoform 1 (COX4I1), nuclear gene encoding mitochondrial protein, mRNA /cds=(165,674) /gb=NM_001861 /gi=17017985 /ug=Hs.433419 /len=802 | NM_001861 | Hs.433419 | NP_001852 |
| 3641 | 0.004578 | hypothetical protein CL25084 (CL25084), mRNA /cds=(132,1583) /gb=NM_015701 /gi=20070263 /ug=Hs.7100 /len=2412 | NM_015701 | Hs.7100 | NP_056516 |
| 3642 | 0.004578 | chromosome 1 open reading frame 22 (C1orf22), mRNA /cds=(54,2723) /gb=NM_025191 /gi=19923618 /ug=Hs.279951 /len=6298 | NM_025191 | Hs.279951 | NP_079467 |

| Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension | | | | | |
|--|----------|---|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 3688 | 0.045456 | isoleucine-tRNA synthetase (IARS), transcript variant long, mRNA /cds=(256,4044) /gb=NM_013417 /gi=7770071 /ug=Hs.172801 /len=4508 | NM_013417 | Hs.172801 | NP_038203 |
| 3733 | 0.037168 | MAGEF1 protein (MAGEF1), mRNA /cds=(177,1103) /gb=NM_022149 /gi=11545891 /ug=Hs.306123 /len=1615 | NM_022149 | Hs.306123 | NP_071432 |
| 3755 | 0.009373 | zinc finger protein 84 (HPF2) (ZNF84), mRNA /cds=(352,2568) /gb=NM_003428 /gi=4508036 /ug=Hs.9450 /len=3257 | NM_003428 | Hs.9450 | NP_003419 |
| 3791 | 0.045456 | TNF receptor-associated factor 4 (TRAF4), transcript variant 1, mRNA /cds=(86,1498) /gb=NM_004295 /gi=22027621 /ug=Hs.8375 /len=1999 | NM_004295 | Hs.8375 | NP_665694 |
| 3800 | 0.011093 | ribosomal protein, large, P0 (RPLP0), transcript variant 2, mRNA /cds=(111,1064) /gb=NM_053275 /gi=16933545 /ug=Hs.406511 /len=1148 | NM_053275 | Hs.406511 | NP_444505 |
| 3801 | 0.048529 | ribosomal protein S7 (RPS7), mRNA /cds=(91,675) /gb=NM_001011 /gi=15431308 /ug=Hs.301547 /len=729 | NM_001011 | Hs.301547 | NP_001002 |
| 3830 | 0.015351 | eukaryotic translation elongation factor 1 beta 2 (EEF1B2), transcript variant 1, mRNA /cds=(236,913) /gb=NM_001959 /gi=16519564 /ug=Hs.421608 /len=961 | NM_001959 | Hs.421608 | NP_066944 |
| 3844 | 0.02428 | CGI-101 protein (F-LAN-1), mRNA /cds=(7,636) /gb=NM_016041 /gi=7705603 /ug=Hs.286131 /len=1123 | NM_016041 | Hs.286131 | NP_057125 |
| 3861 | 0.03016 | basigin (BSG), mRNA /cds=(58,867) /gb=NM_001728 /gi=4502458 /ug=Hs.74631 /len=1638 | NM_001728 | Hs.74631 | NP_001719 |
| 3872 | 0.039781 | 6-phosphogluconolactonase (PGLS), mRNA /cds=(18,794) /gb=NM_012088 /gi=6912585 /ug=Hs.100071 /len=1010 | NM_012088 | Hs.100071 | NP_036220 |
| 3888 | 0.01661 | SAC2 suppressor of actin mutations 2-like (yeast) (SACM2L), transcript variant 1, mRNA /cds=(245,2416) /gb=NM_080564 /gi=18379336 /ug=Hs.169407 /len=2985 | NM_080564 | Hs.169407 | NP_542131 |
| 3901 | 0.01205 | estrogen receptor 1 (ESR1), mRNA /cds=(361,2148) /gb=NM_000125 /gi=4503602 /ug=Hs.1657 /len=6450 | NM_000125 | Hs.1657 | NP_000116 |
| 3936 | 0.02428 | hypothetical protein AF311304 (AF311304), mRNA /cds=(21,185) /gb=NM_031214 /gi=13654285 /ug=Hs.300624 /len=1138 | NM_031214 | Hs.300624 | NP_112491 |

| Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension | | | | | |
|--|----------|---|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 3942 | 0.032363 | spectrin, alpha, non-erythrocytic 1 (alpha-fodrin) (SPTAN1), mRNA /cds=(103,7521) /gb=NM_003127 /gi=4507190 /ug=Hs.77196 /len=7787 | NM_003127 | Hs.77196 | NP_003118 |
| 3954 | 0.03016 | esophageal cancer related gene 4 protein (ECRG4), mRNA /cds=(109,555) /gb=NM_032411 /gi=14165275 /ug=Hs.43125 /len=772 | NM_032411 | Hs.43125 | NP_115787 |
| 3960 | 0.045456 | RaIGDS-like gene (RGL), mRNA /cds=(450,2861) /gb=NM_015149 /gi=20127535 /ug=Hs.79219 /len=5111 | NM_015149 | Hs.79219 | NP_055964 |
| 3968 | 0.019388 | protein tyrosine phosphatase type IVA, member 2 (PTP4A2), transcript variant 1, mRNA /cds=(1011,1514) /gb=NM_003479 /gi=18104974 /ug=Hs.82911 /len=3925 | NM_003479 | Hs.82911 | NP_536317 |
| 4007 | 0.037168 | chondroitin sulfate proteoglycan 6 (bamacan) (CSPG6), mRNA /cds=(92,3745) /gb=NM_005445 /gi=24475891 /ug=Hs.24485 /len=4096 | NM_005445 | Hs.24485 | NP_005436 |
| 4037 | 0.007223 | coagulation factor VIII | AF062515 | | |
| 4038 | 0.006608 | multiple PDZ domain protein (MPDZ), mRNA /cds=(47,6175) /gb=NM_003829 /gi=4505230 /ug=Hs.169378 /len=6582 | NM_003829 | Hs.169378 | NP_003820 |
| 4070 | 0.005026 | ribosomal protein L26 (RPL26), mRNA /cds=(41,478) /gb=NM_000987 /gi=17017970 /ug=Hs.406682 /len=525 | NM_000987 | Hs.406682 | NP_000978 |
| 4092 | 0.02428 | NADH dehydrogenase (ubiquinone) Fe-S protein 3, 30kDa (NADH-coenzyme Q reductase) (NDUFS3), mRNA /cds=(13,807) /gb=NM_004551 /gi=4758787 /ug=Hs.429506 /len=899 | NM_004551 | Hs.429506 | NP_004542 |
| 4118 | 0.001513 | HSPC154 protein (HSPC154), mRNA /cds=(200,946) /gb=NM_014177 /gi=7661809 /ug=Hs.7922 /len=1343 | NM_014177 | Hs.7922 | NP_054896 |
| 4133 | 0.004578 | vimentin (VIM), mRNA /cds=(123,1523) /gb=NM_003380 /gi=4507894 /ug=Hs.297753 /len=1851 | NM_003380 | Hs.297753 | NP_000995 |
| 4146 | 0.048529 | serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 6 (SERPINB6), mRNA /cds=(75,1205) /gb=NM_004568 /gi=28077084 /ug=Hs.41072 /len=1361 | NM_004568 | Hs.41072 | NP_004559 |
| 4152 | 0.048529 | CG9469 gene product | AAF57414 | | |
| 4159 | 0.02428 | suppressor of Ty 3 (S. cerevisiae) (SUPT3H), mRNA /cds=(72,1025) /gb=NM_003599 /gi=4507308 /ug=Hs.304173 /len=1165 | NM_003599 | Hs.304173 | NP_003590 |

| Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension | | | | | |
|--|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 4176 | 0.03016 | mitotic control protein dis3 (DIS3), mRNA /cds=(37,2913) /gb=NM_014953 /gi=19923415 /ug=Hs.323346 /len=7320 | NM_014953 | Hs.323346 | NP_055768 |
| 4189 | 3.75E-04 | fatty-acid-Coenzyme A ligase, long-chain 4 (FACL4), transcript variant 2, mRNA /cds=(507,2642) /gb=NM_022977 /gi=12669908 /ug=Hs.81452 /len=5356 | NM_022977 | Hs.81452 | NP_075266 |
| 4194 | 0.032363 | peptidase D (PEPD), mRNA /cds=(17,1498) /gb=NM_000285 /gi=4557834 /ug=Hs.73947 /len=1888 | NM_000285 | Hs.73947 | NP_000276 |
| 4197 | 0.048529 | putative translation initiation factor (SUI1), mRNA /cds=(148,489) /gb=NM_005801 /gi=20070210 /ug=Hs.150580 /len=1324 | NM_005801 | Hs.150580 | NP_005792 |
| 4200 | 0.037168 | PTD013 protein (PTD013), mRNA /cds=(87,812) /gb=NM_015952 /gi=7706269 /ug=Hs.22679 /len=982 | NM_015952 | Hs.22679 | NP_057036 |
| 4206 | 0.02428 | ring finger protein 4 (RNF4), mRNA /cds=(271,843) /gb=NM_002938 /gi=4506560 /ug=Hs.66394 /len=2918 | NM_002938 | Hs.66394 | NP_002929 |
| 4216 | 0.014175 | KIAA0076 gene product (KIAA0076), mRNA /cds=(87,5183) /gb=NM_014780 /gi=7661893 /ug=Hs.51039 /len=5253 | NM_014780 | Hs.51039 | NP_055595 |
| 4220 | 0.008602 | ribosomal protein S2 (RPS2), mRNA /cds=(12,893) /gb=NM_002952 /gi=15055538 /ug=Hs.356360 /len=978 | NM_002952 | Hs.356360 | NP_002943 |
| 4221 | 0.03016 | ras inhibitor | M37190 | | NP_061866 |
| 4223 | 0.002819 | solute carrier family 25 (carnitine/acylcarnitine translocase), member 20 (SLC25A20), mitochondrial protein encoded by nuclear gene, mRNA /cds=(37,942) /gb=NM_000387 /gi=6006040 /ug=Hs.13845 /len=1219 | NM_000387 | Hs.13845 | NP_000378 |
| 4234 | 0.015351 | ribosomal protein S4, Y-linked (RPS4Y), mRNA /cds=(13,804) /gb=NM_001008 /gi=17981706 /ug=Hs.180911 /len=931 | NM_001008 | Hs.180911 | NP_000999 |
| 4274 | 0.020917 | laminin receptor 1 (ribosomal protein SA, 67kDa) (LAMR1), mRNA /cds=(86,973) /gb=NM_002295 /gi=9845501 /ug=Hs.181357 /len=1039 | NM_002295 | Hs.181357 | NP_002286 |
| 4294 | 0.004578 | hypothetical protein FLJ20729 (FLJ20729), mRNA /cds=(135,1547) /gb=NM_017953 /gi=20149642 /ug=Hs.5111 /len=2821 | NM_017953 | Hs.5111 | NP_060423 |
| 4301 | 0.013076 | mRNA for KIAA1404 protein, partial cds. /cds=(65,5842) /gb=AB037825 /gi=7243188 /ug=Hs.200317 /len=7204 | AB037825 | Hs.200317 | NP_066363 |
| 4307 | 1.31E-04 | HT015 protein (HT015) | AF223466 | | NP_061049 |

| Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension | | | | | |
|--|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 4313 | 0.007223 | chromosome 20 open reading frame 167 (C20orf167), mRNA /cds=(64,1053) /gb=NM_052951 /gi=16418440 /ug=Hs.26213 /len=1296 | NM_052951 | Hs.26213 | NP_443183 |
| 4369 | 0.037168 | ribosomal protein L36 (RPL36), transcript variant 2, mRNA /cds=(153,470) /gb=NM_015414 /gi=16117793 /ug=Hs.433411 /len=545 | NM_015414 | Hs.433411 | NP_378669 |
| 4425 | 0.032363 | gene amplified in squamous cell carcinoma 1 (GASC1), mRNA /cds=(151,3321) /gb=NM_015061 /gi=24307986 /ug=Hs.149918 /len=4239 | NM_015061 | Hs.149918 | NP_055876 |
| 4435 | 0.045456 | clone IMAGE:3633225, mRNA /gb=BC012758 /gi=15706478 /ug=Hs.356377 /len=1914 | BC012758 | Hs.356377 | |
| 4509 | 0.042541 | likely ortholog of mouse deleted in polyposis 1 (DP1), mRNA /cds=(38,595) /gb=NM_005669 /gi=24307896 /ug=Hs.178112 /len=3000 | NM_005669 | Hs.178112 | NP_005660 |
| 4530 | 0.009373 | I factor (complement) (IF), mRNA /cds=(15,1766) /gb=NM_000204 /gi=4504578 /ug=Hs.36602 /len=1963 | NM_000204 | Hs.36602 | NP_000195 |
| 4584 | 0.042541 | Rho-associated, coiled-coil containing protein kinase 1 (ROCK1), mRNA /cds=(1,4065) /gb=NM_005406 /gi=4885582 /ug=Hs.17820 /len=4065 | NM_005406 | Hs.17820 | NP_005397 |
| 4657 | 0.032363 | PR domain containing 4 (PRDM4), mRNA /cds=(123,2528) /gb=NM_012406 /gi=9055315 /ug=Hs.21807 /len=3901 | NM_012406 | Hs.21807 | NP_036538 |
| 4672 | 0.01205 | coronin, actin binding protein, 1C (CORO1C), mRNA /cds=(97,1521) /gb=NM_014325 /gi=27477119 /ug=Hs.17377 /len=3828 | NM_014325 | Hs.17377 | NP_055140 |
| 4678 | 0.009373 | hydroxysteroid (17-beta) dehydrogenase 4 (HSD17B4), mRNA /cds=(49,2259) /gb=NM_000414 /gi=4504504 /ug=Hs.75441 /len=2593 | NM_000414 | Hs.75441 | NP_000405 |
| 4687 | 0.039781 | CREBBP/EP300 inhibitory protein 1 (CRI1), mRNA /cds=(63,626) /gb=NM_014335 /gi=7656937 /ug=Hs.381137 /len=1719 | NM_014335 | Hs.381137 | NP_055150 |
| 4703 | 0.03016 | leukotriene A4 hydrolase (LTA4H), mRNA /cds=(69,1904) /gb=NM_000895 /gi=4505028 /ug=Hs.81118 /len=2060 | NM_000895 | Hs.81118 | NP_000886 |
| 4720 | 0.010202 | heterogeneous nuclear ribonucleoprotein R (HNRPR), mRNA /cds=(91,1992) /gb=NM_005826 /gi=14141188 /ug=Hs.15265 /len=2663 | NM_005826 | Hs.15265 | NP_005817 |

| Genes Corrsponding To Differentially Expressed Genes in Figure 8 - Hypertension | | | | | |
|---|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 4724 | 0.020917 | Niemann-Pick disease, type C1 (NPC1), mRNA /cds=(124,3960) /gb=NM_000271 /gi=4557802 /ug=Hs.76918 /len=4673 | NM_000271 | Hs.76918 | NP_000262 |
| 4741 | 0.048529 | hypothetical protein MGC21981 (MGC21981), mRNA /cds=(66,764) /gb=NM_153267 /gi=23397567 /ug=Hs.131987 /len=1727 | NM_153267 | Hs.131987 | NP_694999 |
| 4758 | 0.015351 | inhibin, beta A (activin A, activin AB alpha polypeptide) (INHBA), mRNA /cds=(86,1366) /gb=NM_002192 /gi=4504698 /ug=Hs.727 /len=1840 | NM_002192 | Hs.727 | NP_002183 |
| 4774 | 0.003113 | ribosomal protein S19 (RPS19), mRNA /cds=(70,507) /gb=NM_001022 /gi=14591914 /ug=Hs.298262 /len=569 | NM_001022 | Hs.298262 | NP_001013 |
| 4778 | 0.015351 | ribosomal protein, large, P1 (RPLP1), mRNA /cds=(130,474) /gb=NM_001003 /gi=16905511 /ug=Hs.424299 /len=512 | NM_001003 | Hs.424299 | NP_000994 |
| 4782 | 0.022547 | CDC-like kinase1 (CLK1), mRNA /cds=(156,1610) /gb=NM_004071 /gi=4758007 /ug=Hs.2083 /len=1834 | NM_004071 | Hs.2083 | NP_004062 |
| 4794 | 0.008602 | mitochondrion, complete genome | NC_001807 | | |
| 4805 | 0.010202 | high-mobility group box 1 (HMGB1), mRNA /cds=(77,724) /gb=NM_002128 /gi=20149538 /ug=Hs.6727 /len=1207 | NM_002128 | Hs.6727 | NP_002119 |
| 4810 | 0.028082 | mRNA; cDNA DKFZp7271051 (from clone DKFZp7271051); partial cds /cds=(1,2099) /gb=AL117478 /gi=5911952 /ug=Hs.239370 /len=2480 | AL117478 | Hs.239370 | NP_056412 |
| 4814 | 0.045456 | ribosomal protein L10a (RPL10A), mRNA /cds=(16,669) /gb=NM_007104 /gi=15431287 /ug=Hs.425293 /len=700 | NM_007104 | Hs.425293 | NP_009035 |
| 4819 | 0.005026 | ribosomal protein L28 (RPL28), mRNA /cds=(43,456) /gb=NM_000991 /gi=13904865 /ug=Hs.356371 /len=500 | NM_000991 | Hs.356371 | NP_000982 |
| 4821 | 0.034698 | eukaryotic translation termination factor 1 (ETF1), mRNA /cds=(136,1449) /gb=NM_004730 /gi=4759033 /ug=Hs.77324 /len=3653 | NM_004730 | Hs.77324 | NP_004721 |
| 4833 | 0.022547 | ATP synthase, H transporting, mitochondrial F0 complex, subunit b, isoform 1 (ATP5F1), mRNA /cds=(98,868) /gb=NM_001688 /gi=21361564 /ug=Hs.81634 /len=1230 | NM_001688 | Hs.81634 | NP_001679 |
| 4837 | 0.039781 | UI-H-BW1-amj-g-07-0-UI.s1 NCI_CGAP_Sub7 cDNA clone IMAGE:3070261 3', mRNA sequence /clone=IMAGE:3070261 /clone_end=3' /gb=BF513214 /gi=11598393 /ug=Hs.445888 /len=620 | BF513214 | Hs.445888 | |

| Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension | | | | | |
|--|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | UniGene Accession No. | Protein Accession No. |
| 4848 | 0.045456 | aggrecan 1 (chondroitin sulfate proteoglycan 1, large aggregating proteoglycan, antigen identified by monoclonal antibody A0122) (AGC1), transcript variant 2, mRNA /cds=(61,7308) /gb=NM_013227 /gi=6995993 /ug=Hs.2159 /len=7434 | NM_013227 | Hs.2159 | NP_037359 |
| 4861 | 0.013076 | protein serine kinase H1 (PSKH1), mRNA /cds=(131,1405) /gb=NM_006742 /gi=27901802 /ug=Hs.150601 /len=3460 | NM_006742 | Hs.150601 | NP_006733 |
| 4862 | 0.005512 | mRNA for FLJ00005 protein, partial cds. /cds=(1,338) /gb=AK000005 /gi=7209310 /ug=Hs.367690 /len=4706 | AK000005 | Hs.367690 | |
| 4863 | 0.026124 | FLJ14819 fis, clone OVARC1000241, moderately similar to HYPOXIA-INDUCIBLE FACTOR 1 ALPHA | AK027725 | | NP_690009 |
| 4874 | 0.048529 | ankyrin repeat domain 10 (ANKRD10), mRNA /cds=(136,1398) /gb=NM_017664 /gi=8923103 /ug=Hs.172572 /len=2509 | NM_017664 | Hs.172572 | NP_060134 |
| 4877 | 0.007223 | chromosome 20 open reading frame 31 (C20orf31), mRNA /cds=(83,1819) /gb=NM_018217 /gi=8922666 /ug=Hs.93871 /len=1885 | NM_018217 | Hs.93871 | NP_060687 |
| 4878 | 0.042541 | ribosomal protein L35a (RPL35A), mRNA /cds=(74,406) /gb=NM_000996 /gi=16117790 /ug=Hs.288544 /len=511 | NM_000996 | Hs.288544 | NP_000987 |
| 4898 | 0.022547 | cDNA FLJ12024 fis, clone. HEMBB1001797. /gb=AK022086 /gi=10433407 /ug=Hs.8958 /len=1672 | AK022086 | Hs.8958 | |
| 4900 | 0.020917 | hypothetical protein FLJ10702 (FLJ10702), mRNA /cds=(175,735) /gb=NM_018184 /gi=8922600 /ug=Hs.104222 /len=2944 | NM_018184 | Hs.104222 | NP_060654 |
| 4916 | 0.01205 | collagen, type X, alpha 1 (Schmid metaphyseal chondrodysplasia) (COL10A1), mRNA /cds=(97,2139) /gb=NM_000493 /gi=18105031 /ug=Hs.179729 /len=3285 | NM_000493 | Hs.179729 | NP_000484 |
| 4939 | 0.03016 | UI-H-DH0-aui-p-19-0-UI.s1 NCI_CGAP_DH0 cDNA clone IMAGE:5871234 3', mRNA sequence /clone=IMAGE:5871234 /clone_end=3' /gb=BM994422 /gi=19719323 /ug=Hs.289721 /len=2081 | BM994422 | Hs.289721 | |
| 4942 | 0.005512 | AF034176 mRNA (Tripodis and Ragoussis) cDNA clone ntcon5 contig /gb=AF034176 /gi=2707738 /ug=Hs.188882 /len=7232 | AF034176 | Hs.188882 | |

| Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension | | | | | |
|--|----------|--|--------------------------|-----------------------------|-----------------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 4944 | 0.039781 | hypothetical protein FLJ20452 (FLJ20452), mRNA /cds=(15,614) /gb=NM_017828 /gi=21361660 /ug=Hs.351327 /len=1948 | NM_017828 | Hs.351327 | NP_060298 |
| 4956 | 0.011093 | hypothetical protein FLJ20671 (FLJ20671), mRNA /cds=(43,465) /gb=NM_017924 /gi=19923511 /ug=Hs.180201 /len=2855 | NM_017924 | Hs.180201 | NP_060394 |
| 4958 | 0.045456 | cDNA FLJ10235 fis, clone HEMBB1000339. /gb=AK001097 /gi=7022149 /ug=Hs.406774 /len=2530 | AK001097 | Hs.406774 | |
| 4960 | 0.03016 | hypothetical protein FLJ20958 (FLJ20958), mRNA /cds=(141,914) /gb=NM_022102 /gi=13430855 /ug=Hs.261023 /len=1842 | NM_022102 | Hs.261023 | NP_071385 |
| 4970 | 0.013076 | decorin (DCN), transcript variant A1, mRNA /cds=(200,1279) /gb=NM_001920 /gi=19743844 /ug=Hs.433989 /len=1751 | NM_001920 | Hs.433989 | NP_598014 |
| 4978 | 0.042541 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 24 (DDX24), mRNA /cds=(100,2679) /gb=NM_020414 /gi=14251213 /ug=Hs.155986 /len=2967 | NM_020414 | Hs.155986 | NP_065147 |
| 4979 | 0.004165 | ribosomal protein L6 (RPL6), mRNA /cds=(32,898) /gb=NM_000970 /gi=16753226 /ug=Hs.409045 /len=950 | NM_000970 | Hs.409045 | NP_000961 |
| 4992 | 0.03016 | tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor) (TFPI), mRNA /cds=(1,915) /gb=NM_006287 /gi=6715569 /ug=Hs.170279 /len=915 | NM_006287 | Hs.170279 | NP_006278 |
| 4994 | 0.01205 | Nedd4 binding protein 2 (N4BP2), mRNA /cds=(339,5600) /gb=NM_018177 /gi=20357506 /ug=Hs.18685 /len=6760 | NM_018177 | Hs.18685 | NP_060647 |
| 4995 | 0.013076 | S100 calcium binding protein A10 (annexin II ligand, calpactin I, light polypeptide (p11)) (S100A10), mRNA /cds=(112,405) /gb=NM_002966 /gi=4506760 /ug=Hs.400250 /len=649 | NM_002966 | Hs.400250 | NP_002957 |
| 5016 | 0.007223 | ribosomal protein L17 (RPL17), mRNA /cds=(287,841) /gb=NM_000985 /gi=14591906 /ug=Hs.82202 /len=898 | NM_000985 | Hs.82202 | NP_000976 |
| 5021 | 0.032363 | hypothetical protein MGC4368 (MGC4368), mRNA /cds=(728,1411) /gb=NM_024510 /gi=21362053 /ug=Hs.9732 /len=2250 | NM_024510 | Hs.9732 | NP_078786 |
| 5060 | 0.020917 | HIF-1 responsive RTP801 (RTP801), mRNA /cds=(198,896) /gb=NM_019058 /gi=9506686 /ug=Hs.111244 /len=1760 | NM_019058 | Hs.111244 | NP_061931 |

| Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension | | | | | |
|--|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 5069 | 0.020917 | hsp70-interacting protein (HSPBP1), mRNA /cds=(312,1400) /gb=NM_012267 /gi=21361406 /ug=Hs.53066 /len=1795 | NM_012267 | Hs.53066 | NP_036399 |
| 5098 | 0.015351 | hypothetical protein, clone MGC:12969 IMAGE:3343683, mRNA, complete cds /cds=(931,1614) /gb=BC006428 /gi=13623618 /ug=Hs.15093 /len=2632 | BC006428 | Hs.15093 | NP_057547 |
| 5102 | 0.003113 | cofilin 1 (non-muscle) (CFL1), mRNA /cds=(52,552) /gb=NM_005507 /gi=5031634 /ug=Hs.180370 /len=1059 | NM_005507 | Hs.180370 | NP_005498 |
| 5138 | 0.02428 | exostoses (multiple) 2 (EXT2), mRNA /cds=(488,2644) /gb=NM_000401 /gi=4557572 /ug=Hs.75334 /len=3781 | NM_000401 | Hs.75334 | NP_000392 |
| 5155 | 0.011093 | phosphoglycerate kinase 1 (PGK1), mRNA /cds=(70,1323) /gb=NM_000291 /gi=22095338 /ug=Hs.78771 /len=2338 | NM_000291 | Hs.78771 | NP_000282 |
| 5161 | 0.004578 | basic transcription factor 3 (BTF3), mRNA /cds=(240,728) /gb=NM_001207 /gi=20070129 /ug=Hs.101025 /len=952 | NM_001207 | Hs.101025 | NP_001198 |
| 5195 | 0.01661 | angiopoietin-like 4 (ANGPTL4), transcript variant 1, mRNA /cds=(196,1416) /gb=NM_139314 /gi=21536397 /ug=Hs.9613 /len=1967 | NM_139314 | Hs.9613 | NP_647475 |
| 5200 | 0.039781 | thrombospondin 1 (THBS1), mRNA /cds=(112,3624) /gb=NM_003246 /gi=4507484 /ug=Hs.87409 /len=5722 | NM_003246 | Hs.87409 | NP_003237 |
| 5226 | 0.034698 | mRNA; cDNA DKFZp564L2416 (from clone DKFZp564L2416) /gb=AL050385 /gi=4914588 /ug=Hs.48332 /len=5511 | AL050385 | Hs.48332 | |
| 5230 | 0.042541 | CDC28 protein kinase regulatory subunit 2 (CKS2), mRNA /cds=(96,335) /gb=NM_001827 /gi=4502858 /ug=Hs.83758 /len=627 | NM_001827 | Hs.83758 | NP_001818 |
| 5238 | 0.048529 | NRAS-related gene (D1S155E), mRNA /cds=(428,2824) /gb=NM_007158 /gi=20070240 /ug=Hs.69855 /len=4076 | NM_007158 | Hs.69855 | NP_009089 |
| 5261 | 0.011093 | replication factor C (activator 1) 4, 37kDa (RFC4), mRNA /cds=(284,1375) /gb=NM_002916 /gi=4506490 /ug=Hs.35120 /len=1446 | NM_002916 | Hs.35120 | NP_002907 |
| 5262 | 0.010202 | ALL1-fused gene from chromosome 1q (AF1Q), mRNA /cds=(353,625) /gb=NM_006818 /gi=21626459 /ug=Hs.75823 /len=1653 | NM_006818 | Hs.75823 | NP_006809 |
| 5264 | 0.045456 | small GTP-binding protein RAB1A | AF226873 | | NP_033022 |

| Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension | | | | | |
|--|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 5318 | 0.048529 | 603021120F1 NIH_MGC_114 cDNA clone IMAGE:5191733 5', mRNA sequence /clone=IMAGE:5191733 /clone_end=5' /gb=BI488592 /gi=15327820 /ug=Hs.380956 /len=988 | BI488592 | Hs.380956 | |
| 5329 | 0.032363 | dolichyl-diphosphooligosaccharide-protein glycosyltransferase (DDOST), mRNA /cds=(60,1430) /gb=NM_005216 /gi=20070196 /ug=Hs.34789 /len=2045 | NM_005216 | Hs.34789 | NP_005207 |
| 5367 | 0.026124 | hypothetical protein MGC4415 (MGC4415), mRNA /cds=(154,675) /gb=NM_031484 /gi=13899343 /ug=Hs.209614 /len=3243 | NM_031484 | Hs.209614 | NP_113672 |
| 5384 | 0.028082 | Hypothetical protein(cDNA FLJ11422 fis, clone HEMBA1001008) | AK021484 | | |
| 5400 | 0.004165 | dUTP pyrophosphatase (DUT), mRNA /cds=(20,514) /gb=NM_001948 /gi=21361335 /ug=Hs.367676 /len=1816 | NM_001948 | Hs.367676 | NP_001939 |
| 5402 | 0.039781 | brain cDNA, clone:QnpA-21421 | AB050422 | | |
| 5411 | 0.045456 | DKFZp566J2446 (from clone DKFZp566J2446) | AL050082 | | NP_008944 |
| 5420 | 0.002302 | matrilin 3 (MATN3) precursor, mRNA /cds=(64,1524) /gb=NM_002381 /gi=13518040 /ug=Hs.278461 /len=2599 | NM_002381 | Hs.278461 | NP_002372 |
| 5438 | 0.005026 | mitochondrion, complete genome | NC_001807 | | |
| 5477 | 0.007223 | lectin, galactoside-binding, soluble, 3 (galectin 3) (LGALS3), mRNA /cds=(19,771) /gb=NM_002306 /gi=4504982 /ug=Hs.621 /len=914 | NM_002306 | Hs.621 | NP_002297 |
| 5497 | 0.028082 | zinc finger, DHHC domain containing 4 (ZDHHC4), mRNA /cds=(222,1256) /gb=NM_018106 /gi=21361700 /ug=Hs.5268 /len=1704 | NM_018106 | Hs.5268 | NP_060576 |
| 5498 | 4.81E-04 | polymerase (RNA) II (DNA directed) polypeptide G (POLR2G), mRNA /cds=(107,625) /gb=NM_002696 /gi=4505946 /ug=Hs.14839 /len=828 | NM_002696 | Hs.14839 | NP_002687 |
| 5551 | 0.011093 | hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit (HADHA), mRNA /cds=(35,2326) /gb=NM_000182 /gi=20127407 /ug=Hs.75860 /len=2972 | NM_000182 | Hs.75860 | NP_000173 |
| 5594 | 0.03016 | hypothetical gene supported by U81006; NM_004800 (LOC121929), mRNA | XM_071779 | | |
| 5640 | 0.002819 | nonhistone protein HMG1 | M21683 | | |

| Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension | | | | | |
|--|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 5644 | 0.048529 | integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12) (ITGB1), transcript variant 1A, mRNA /cds=(127,2523) /gb=NM_002211 /gi=19743812 /ug=Hs.287797 /len=3700 | NM_002211 | Hs.287797 | NP_596867 |
| 5671 | 0.003784 | EPC-1 (=M76979 PEDF;U29953;M90493) | U57446 | | |
| 5672 | 0.006039 | clone IMAGE:5265581, mRNA /gb=BC035165 /gi=23272508 /ug=Hs.400548 /len=2237 | BC035165 | Hs.400548 | |
| 5717 | 0.039781 | MLL septin-like fusion (MSF), mRNA /cds=(258,1964) /gb=NM_006640 /gi=19923366 /ug=Hs.181002 /len=3929 | NM_006640 | Hs.181002 | NP_006631 |
| 5747 | 0.048529 | chromosome 20 open reading frame 14 (C20orf14), mRNA /cds=(100,2925) /gb=NM_012469 /gi=6912731 /ug=Hs.31334 /len=3060 | NM_012469 | Hs.31334 | NP_036601 |
| 5754 | 0.037168 | KIAA1360 | AB037781 | | NP_060458 |
| 5784 | 0.037168 | suppressor of cytokine signaling 2 (SOCS2), mRNA /cds=(591,1187) /gb=NM_003877 /gi=21536304 /ug=Hs.405946 /len=2210 | NM_003877 | Hs.405946 | NP_003868 |
| 5789 | 0.015351 | ribosomal protein L31 (RPL31), mRNA /cds=(28,405) /gb=NM_000993 /gi=15812219 /ug=Hs.184014 /len=442 | NM_000993 | Hs.184014 | NP_000984 |
| 5814 | 0.001216 | ribosomal protein L36a-like (RPL36AL), mRNA /cds=(95,415) /gb=NM_001001 /gi=16306559 /ug=Hs.419465 /len=537 | NM_001001 | Hs.419465 | NP_000992 |
| 5821 | 0.007223 | ribosomal protein L11 (RPL11), mRNA /cds=(21,557) /gb=NM_000975 /gi=15431289 /ug=Hs.388664 /len=609 | NM_000975 | Hs.388664 | NP_000966 |
| 5826 | 0.017954 | ribosomal protein L13a (RPL13A), mRNA /cds=(23,634) /gb=NM_012423 /gi=14591905 /ug=Hs.389335 /len=1142 | NM_012423 | Hs.389335 | NP_036555 |
| 5870 | 0.014175 | Similar to cyclin K, clone MGC:9113 IMAGE:3907416, mRNA, complete cds /cds=(110,1174) /gb=BC015935 /gi=16198507 /ug=Hs.375192 /len=1925 | BC015935 | Hs.375192 | |
| 5893 | 0.003113 | golgi phosphoprotein 2 (GOLPH2), mRNA /cds=(151,1353) /gb=NM_016548 /gi=7706084 /ug=Hs.182793 /len=3042 | NM_016548 | Hs.182793 | NP_808800 |
| 5899 | 0.006039 | Fas (TNFRSF6) associated factor 1 (FAF1), transcript variant 1, mRNA /cds=(454,2406) /gb=NM_007051 /gi=19528653 /ug=Hs.25821 /len=2610 | NM_007051 | Hs.25821 | NP_572051 |
| 5914 | 0.042541 | ribosomal protein S20 (RPS20), mRNA /cds=(128,487) /gb=NM_001023 /gi=14591915 /ug=Hs.8102 /len=539 | NM_001023 | Hs.8102 | NP_001014 |

| Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension | | | | | |
|--|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 5918 | 0.026124 | Mus musculus mitochondrion, complete genome | NC_001569 | | |
| 5934 | 0.020917 | enthoprotin (ENTH), mRNA /cds=(102,1979) /gb=NM_014666 /gi=7661967 /ug=Hs.132853 /len=3336 | NM_014666 | Hs.132853 | NP_055481 |
| 5938 | 0.039781 | chaperonin containing TCP1, subunit 3 (gamma) (CCT3), mRNA /cds=(1,1635) /gb=NM_005998 /gi=5174726 /ug=Hs.1708 /len=1901 | NM_005998 | Hs.1708 | NP_005989 |
| 5959 | 0.01661 | germline T-cell receptor beta chain | U66061 | | |
| 5974 | 0.01205 | KIAA0266 gene product (KIAA0266), mRNA /cds=(734,3034) /gb=NM_021645 /gi=11063982 /ug=Hs.127376 /len=5585 | NM_021645 | Hs.127376 | NP_067677 |
| 5989 | 0.026124 | CDA02 protein (CDA02), mRNA /cds=(3,1832) /gb=NM_032025 /gi=14042940 /ug=Hs.332404 /len=2179 | NM_032025 | Hs.332404 | NP_114414 |
| 6006 | 0.003435 | ribosomal protein L23a (RPL23A), mRNA /cds=(22,492) /gb=NM_000984 /gi=17105393 /ug=Hs.419463 /len=546 | NM_000984 | Hs.419463 | NP_000975 |
| 6009 | 0.026124 | methylmalonyl Coenzyme A mutase (MUT), nuclear gene encoding mitochondrial protein, mRNA /cds=(77,2329) /gb=NM_000255 /gi=4557766 /ug=Hs.155212 /len=2798 | NM_000255 | Hs.155212 | NP_000246 |
| 6013 | 0.039781 | Similar to hect domain and RLD 2, clone IMAGE:4830978, mRNA /gb=BC033888 /gi=21706785 /ug=Hs.429904 /len=4297 | BC033888 | Hs.429904 | |
| 6027 | 0.002549 | mesenchyme homeo box 2 (growth arrest-specific homeo box) (MEOX2), mRNA /cds=(182,1093) /gb=NM_005924 /gi=21396478 /ug=Hs.77858 /len=2284 | NM_005924 | Hs.77858 | NP_005915 |
| 6034 | 0.037168 | NRAS-related gene (D1S155E), mRNA /cds=(428,2824) /gb=NM_007158 /gi=20070240 /ug=Hs.69855 /len=4076 | NM_007158 | Hs.69855 | NP_009089 |
| 6037 | 0.028082 | splicing factor, arginine/serine-rich 2 (SFRS2), mRNA /cds=(156,821) /gb=NM_003016 /gi=4506898 /ug=Hs.73965 /len=1879 | NM_003016 | Hs.73965 | NP_003007 |
| 6042 | 0.028082 | laminin, gamma 1 (formerly LAMB2) (LAMC1), mRNA /cds=(300,5129) /gb=NM_002293 /gi=9845497 /ug=Hs.432855 /len=7923 | NM_002293 | Hs.432855 | NP_002284 |
| 6065 | 0.045456 | NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2, 14.5kDa (NDUFC2), mRNA /cds=(151,510) /gb=NM_004549 /gi=19923255 /ug=Hs.193313 /len=2168 | NM_004549 | Hs.193313 | NP_004540 |

| Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension | | | | | |
|--|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 6068 | 0.03016 | mitochondrial ribosomal protein L27 (MRPL27), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA /cds=(32,316) /gb=NM_148571 /gi=22547130 /ug=Hs.7736 /len=2472 | NM_148571 | Hs.7736 | NP_683412 |
| 6072 | 0.002819 | mRNA for KIAA0530 protein, partial cds. /cds=(1,4693) /gb=AB011102 /gi=3043583 /ug=Hs.173081 /len=6578 | AB011102 | Hs.173081 | |
| 6083 | 0.011093 | NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (NADH-coenzyme Q reductase) (NDUFS4), mRNA /cds=(9,536) /gb=NM_002495 /gi=4505368 /ug=Hs.10758 /len=668 | NM_002495 | Hs.10758 | NP_002486 |
| 6102 | 0.022547 | homer 2 (Drosophila) (HOMER2), mRNA /cds=(1,1065) /gb=NM_004839 /gi=4758547 /ug=Hs.93564 /len=1800 | NM_004839 | Hs.93564 | NP_004830 |
| 6106 | 0.003435 | EST (ym17h04.s1 clone 48282 3') | H11657 | | |
| 6139 | 0.011093 | cofilin 1 (non-muscle) (CFL1), mRNA /cds=(52,552) /gb=NM_005507 /gi=5031634 /ug=Hs.180370 /len=1059 | NM_005507 | Hs.180370 | NP_005498 |
| 6144 | 0.013076 | CSE1 chromosome segregation 1-like (yeast) (CSE1L), mRNA /cds=(124,3039) /gb=NM_001316 /gi=4503072 /ug=Hs.90073 /len=3147 | NM_001316 | Hs.90073 | NP_803185 |
| 6164 | 0.01205 | antigen NY-CO-33 (NY-CO-33) | AF039698 | | NP_005777 |
| 6166 | 0.028082 | ribosomal protein L10 (RPL10), mRNA /cds=(42,686) /gb=NM_006013 /gi=15718685 /ug=Hs.412900 /len=2188 | NM_006013 | Hs.412900 | NP_006004 |
| 6182 | 0.045456 | signal sequence receptor, gamma (translocon-associated protein gamma) (SSR3), mRNA /cds=(57,614) /gb=NM_007107 /gi=6005883 /ug=Hs.28707 /len=3061 | NM_007107 | Hs.28707 | NP_009038 |
| 6188 | 0.02428 | phosphodiesterase 10A(PDE10A) mRNA | NM_006661 | | NP_006652 |
| 6191 | 0.017954 | calsyntenin 3 (CLSTN3), mRNA /cds=(539,3445) /gb=NM_014718 /gi=7662267 /ug=Hs.107809 /len=4300 | NM_014718 | Hs.107809 | NP_055533 |
| 6200 | 0.037168 | KIAA0922 protein (KIAA0922), mRNA /cds=(123,3842) /gb=NM_015196 /gi=14149672 /ug=Hs.37892 /len=3906 | NM_015196 | Hs.37892 | NP_056011 |
| 6205 | 0.020917 | jumping translocation breakpoint (JTB), mRNA /cds=(433,873) /gb=NM_006694 /gi=5729888 /ug=Hs.6396 /len=1040 | NM_006694 | Hs.6396 | NP_006685 |
| 6268 | 0.007197 | cDNA: FLJ22008 fis, clone HEP06934. /gb=AK025661 /gi=10438250 /ug=Hs.193700 /len=2207 | AK025661 | Hs.193700 | |
| 6286 | 0.042541 | ribosomal protein S13 (RPS13), mRNA /cds=(33,488) /gb=NM_001017 /gi=14591910 /ug=Hs.165590 /len=529 | NM_001017 | Hs.165590 | NP_001008 |

| Genes Corresponding T Differentially Expressed Genes in Figure 8 - Hypertension | | | | | |
|---|----------|---|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 6309 | 0.027243 | WW domain binding protein 11 (WBP11), mRNA /cds=(162,2087) /gb=NM_016312 /gi=18375679 /ug=Hs.334811 /len=2690 | NM_016312 | Hs.334811 | NP_057396 |
| 6322 | 0.015351 | ubiquitin specific protease 9 (USP9Y) | XM_000563 | | |
| 6337 | 0.034698 | adaptor-related protein complex 2, mu 1 subunit (AP2M1), mRNA /cds=(136,1443) /gb=NM_004068 /gi=14917108 /ug=Hs.152936 /len=1936 | NM_004068 | Hs.152936 | NP_004059 |
| 6341 | 0.004165 | a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 1 (ADAMTS1), mRNA /cds=(294,3146) /gb=NM_006988 /gi=11038653 /ug=Hs.8230 /len=4459 | NM_006988 | Hs.8230 | NP_008919 |
| 6346 | 0.002819 | UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 6 (B3GNT6), mRNA /cds=(80,1327) /gb=NM_006876 /gi=5802983 /ug=Hs.8526 /len=2011 | NM_006876 | Hs.8526 | NP_006867 |
| 6352 | 0.020028 | ILK-1 gene for integrin-linked kinase 1, exons 1-13 | AJ404847 | | |
| 6359 | 0.007887 | lysyl oxidase-like 2 (LOXL2), mRNA /cds=(248,2572) /gb=NM_002318 /gi=4505010 /ug=Hs.83354 /len=3432 | NM_002318 | Hs.83354 | NP_002309 |
| 6374 | 0.045456 | alcohol dehydrogenase beta-1-subunit (ADH1-2 allele) | X03350 | | NP_000659 |
| 6402 | 0.009373 | actin, gamma 1 (ACTG1), mRNA /cds=(75,1202) /gb=NM_001614 /gi=11038618 /ug=Hs.14376 /len=1919 | NM_001614 | Hs.14376 | NP_001605 |
| 6425 | 0.02428 | insulin receptor substrate-2 (IRS2) mRNA, complete cds | AF073310 | | NP_003740 |
| 6516 | 0.004578 | ribosomal protein S27-like (RPS27L), mRNA /cds=(73,327) /gb=NM_015920 /gi=18490988 /ug=Hs.108957 /len=523 | NM_015920 | Hs.108957 | NP_057004 |
| 6546 | 0.034698 | hypothetical protein (KIAA0594) | AB011166 | | NP_055925 |
| 6554 | 0.008602 | mitochondrial ribosomal protein L13 (MRPL13), nuclear gene encoding mitochondrial protein, mRNA /cds=(287,823) /gb=NM_014078 /gi=21265072 /ug=Hs.333823 /len=1086 | NM_014078 | Hs.333823 | NP_054797 |
| 6565 | 0.032363 | PTK9 protein tyrosine kinase 9 (PTK9), mRNA /cds=(61,1113) /gb=NM_002822 /gi=4506274 /ug=Hs.82643 /len=3000 | NM_002822 | Hs.82643 | NP_002813 |
| 6577 | 0.034698 | ornithine decarboxylase antizyme 1 (OAZ1), mRNA /gb=NM_004152 /gi=9845504 /ug=Hs.281960 /len=986 | NM_004152 | Hs.281960 | NP_004143 |

| Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension | | | | | |
|--|----------|---|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 6592 | 0.003113 | methylene tetrahydrofolate dehydrogenase (NAD dependent), methenyltetrahydrofolate cyclohydrolase (MTHFD2), nuclear gene encoding mitochondrial protein, mRNA /cds=(77,1111) /gb=NM_006636 /gi=13699869 /ug=Hs.154672 /len=2154 | NM_006636 | Hs.154672 | NP_006627 |
| 6593 | 0.045456 | NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae) (NHP2L1), mRNA /cds=(95,481) /gb=NM_005008 /gi=4826859 /ug=Hs.182255 /len=1475 | NM_005008 | Hs.182255 | NP_004999 |
| 6603 | 0.002549 | tm68a09.x1 NCI_CGAP_Brn25 cDNA clone IMAGE:2163256 3', mRNA sequence /clone=IMAGE:2163256 /clone_end=3' /gb=AI498805 /gi=4390787 /ug=Hs.436349 /len=460 | AI498805 | Hs.436349 | |
| 6604 | 0.042541 | splicing factor, arginine/serine-rich 1 (splicing factor 2, alternate splicing factor) (SFRS1), mRNA /cds=(36,782) /gb=NM_006924 /gi=19923382 /ug=Hs.73737 /len=2708 | NM_006924 | Hs.73737 | NP_008855 |
| 6622 | 0.017954 | aquaporin 1 (channel-forming integral protein, 28kDa) (AQP1), mRNA /cds=(39,848) /gb=NM_000385 /gi=4755121 /ug=Hs.76152 /len=1662 | NM_000385 | Hs.76152 | NP_000376 |
| 6623 | 0.005026 | atractin (ATRN), transcript variant 1, mRNA /cds=(80,4369) /gb=NM_139321 /gi=21450860 /ug=Hs.194019 /len=8645 | NM_139321 | Hs.194019 | NP_647538 |
| 6626 | 0.022547 | tumor antigen SLP-8p (HCC8), mRNA /cds=(21,2921) /gb=NM_016516 /gi=7705396 /ug=Hs.48499 /len=3480 | NM_016516 | Hs.48499 | NP_057600 |
| 6633 | 0.02428 | HSPCO34 protein (LOC51668), mRNA, /cds=(58,402) /gb=NM_016126 /gi=7706382 /ug=Hs.46967 /len=598 | NM_016126 | Hs.46967 | NP_057210 |
| 6634 | 0.010202 | surfeit 4 (SURF4), mRNA /cds=(131,940) /gb=NM_033161 /gi=19593984 /ug=Hs.284296 /len=2985 | NM_033161 | Hs.284296 | NP_149351 |
| 6646 | 5.42E-04 | protein phosphatase 1, regulatory (inhibitor) subunit 12A (PPP1R12A), mRNA /cds=(1,3093) /gb=NM_002480 /gi=4505316 /ug=Hs.16533 /len=4613 | NM_002480 | Hs.16533 | NP_002471 |
| 6647 | 0.01205 | sterol carrier protein 2 (SCP2), mRNA /cds=(22,1665) /gb=NM_002979 /gi=19923232 /ug=Hs.75760 /len=2572 | NM_002979 | Hs.75760 | NP_002970 |
| 6650 | 0.034698 | tetratricopeptide repeat domain 1 (TTC1), mRNA /cds=(51,929) /gb=NM_003314 /gi=4507710 /ug=Hs.7733 /len=1407 | NM_003314 | Hs.7733 | NP_003305 |

| Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension | | | | | |
|--|----------|---|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 6654 | 0.009373 | pM5 protein (PM5), mRNA /cds=(1,3669) /gb=NM_014287 /gi=10947030 /ug=Hs.439182 /len=4182 | NM_014287 | Hs.439182 | NP_055102 |
| 6659 | 0.042541 | heat shock 70kDa protein 8 (HSPA8), transcript variant 1, mRNA /cds=(79,2019) /gb=NM_006597 /gi=24234684. /ug=Hs.180414 /len=2276 | NM_006597 | Hs.180414 | NP_694881 |
| 6661 | 0.020917 | stromal antigen 1 (STAG1), mRNA /cds=(401,4177) /gb=NM_005862 /gi=5032062 /ug=Hs.286148 /len=4337 | NM_005862 | Hs.286148 | NP_005853 |
| 6666 | 0.034698 | tigger transposable element derived 1 (TIGD1), mRNA /cds=(635,2410) /gb=NM_145702 /gi=22209000 /ug=Hs.351348 /len=2448 | NM_145702 | Hs.351348 | NP_663748 |
| 6677 | 0.007223 | solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA /cds=(69,965) /gb=NM_001152 /gi=4502098 /ug=Hs.79172 /len=1225 | NM_001152 | Hs.79172 | NP_001143 |
| 6682 | 0.004578 | hypothetical protein FLJ12442 (FLJ12442), mRNA /cds=(412,1974) /gb=NM_022908 /gi=12597652 /ug=Hs.84753 /len=2057 | NM_022908 | Hs.84753 | NP_075059 |
| 6683 | 2.24E-04 | lamin A/C (LMNA), transcript variant 1, mRNA /cds=(213,2207) /gb=NM_170707 /gi=27436945 /ug=Hs.377973 /len=3181 | NM_170707 | Hs.377973 | NP_733822 |
| 6717 | 0.008602 | fer-1-like 3, myoferlin (C. elegans) (FER1L3), transcript variant 1, mRNA /cds=(89,6274) /gb=NM_013451 /gi=19718757 /ug=Hs.234680 /len=6829 | NM_013451 | Hs.234680 | NP_579899 |
| 6722 | 0.037168 | syndecan 1 (SDC1), mRNA /cds=(253,1185) /gb=NM_002997 /gi=21359855 /ug=Hs.82109 /len=2484 | NM_002997 | Hs.82109 | NP_002988 |
| 6734 | 1.72E-04 | PAI-1 mRNA-binding protein (PAI-RBP1), mRNA /cds=(86,1249) /gb=NM_015640 /gi=7661625 /ug=Hs.165998 /len=2201 | NM_015640 | Hs.165998 | NP_056455 |
| 6735 | 0.007223 | DKFZp586J021 (from clone DKFZp586J021) /cds=UNKNOWN /gb=AL110197 /gi=5817115 /ug=Hs.6441 /len=1896 | AL110197 | Hs.6441 | NP_003246 |
| 6744 | 0.026124 | ribosomal protein, large, P0 (RPLP0), transcript variant 2, mRNA /cds=(111,1064) /gb=NM_053275 /gi=16933545 /ug=Hs.406511 /len=1148 | NM_053275 | Hs.406511 | NP_444505 |
| 6745 | 0.019388 | mRNA; cDNA DKFZp434A163 (from clone DKFZp434A163); partial cds /cds=(1,4964) /gb=AL110218 /gi=5817150 /ug=Hs.127401 /len=5084 | AL110218 | Hs.127401 | |

| Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension | | | | | |
|--|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 6749 | 0.034698 | histidyl-tRNA synthetase 2 (HARS2), mRNA /cds=(111,752) /gb=NM_080820 /gi=21361784 /ug=Hs.352419 /len=2396 | NM_080820 | Hs.352419 | NP_543010 |
| 6750 | 0.004165 | ADP-ribosylation-like factor 6 interacting protein 4 (ARL6IP4), mRNA /cds=(63,719) /gb=NM_016638 /gi=7706183 /ug=Hs.103561 /len=952 | NM_016638 | Hs.103561 | NP_061164 |
| 6752 | 2.56E-04 | tumor endothelial marker 6 (TEM6), mRNA /cds=(93,3710) /gb=NM_022748 /gi=17511208 /ug=Hs.12210 /len=6702 | NM_022748 | Hs.12210 | NP_073585 |
| 6770 | 0.009373 | FK506 binding protein 1A, 12kDa (FKBP1A), transcript variant 12B, mRNA /cds=(104,430) /gb=NM_000801 /gi=17149837 /ug=Hs.380080 /len=1578 | NM_000801 | Hs.380080 | NP_463460 |
| 6771 | 0.014175 | surfeit 6 (SURF6), mRNA /cds=(56,1141) /gb=NM_006753 /gi=19557701 /ug=Hs.274430 /len=2329 | NM_006753 | Hs.274430 | NP_006744 |
| 6772 | 0.003435 | hypothetical protein FLJ22301 (FLJ22301), mRNA /cds=(696,2054) /gb=NM_024836 /gi=13376246 /ug=Hs.181406 /len=2952 | NM_024836 | Hs.181406 | NP_079112 |
| 6773 | 0.003784 | hypothetical protein FLJ14834 (FLJ14834), mRNA /cds=(326,1237) /gb=NM_032849 /gi=21361885 /ug=Hs.62905 /len=2342 | NM_032849 | Hs.62905 | NP_116238 |
| 6861 | 0.02428 | mRNA; cDNA DKFZp434A012 (from clone DKFZp434A012) /gb=AL096752 /gi=5419888 /ug=Hs.306327 /len=2248 | AL096752 | Hs.306327 | |
| 6863 | 0.034698 | Sm protein F (LSM6), mRNA /cds=(82,324) /gb=NM_007080 /gi=5901997 /ug=Hs.42438 /len=596 | NM_007080 | Hs.42438 | NP_009011 |
| 6865 | 0.003435 | NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa (NDUFA4), mRNA /cds=(91,336) /gb=NM_002489 /gi=4505356 /ug=Hs.50098 /len=518 | NM_002489 | Hs.50098 | NP_002480 |
| 6881 | 0.020917 | uncharacterized hematopoietic stem/progenitor cells protein MDS029 (MDS029), mRNA /cds=(112,438) /gb=NM_018464 /gi=8923929 /ug=Hs.43549 /len=636 | NM_018464 | Hs.43549 | NP_060934 |
| 6888 | 0.017954 | enolase 1, (alpha) (ENO1), mRNA /cds=(152,1456) /gb=NM_001428 /gi=16507965 /ug=Hs.254105 /len=1812 | NM_001428 | Hs.254105 | NP_001419 |
| 6930 | 0.003113 | HMT1 hnRNP methyltransferase-like 1 (S. cerevisiae) (HRMT1L1), mRNA /cds=(166,1467) /gb=NM_001535 /gi=4504494 /ug=Hs.235887 /len=2093 | NM_001535 | Hs.235887 | NP_001526 |

| Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension | | | | | |
|--|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 6935 | 0.037168 | FtsJ 3 (E. coli) (FTSJ3), mRNA /cds=(72,2615) /gb=NM_017647 /gi=17017990 /ug=Hs.257486 /len=2999 | NM_017647 | Hs.257486 | NP_060117 |
| 6942 | 0.003435 | eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA /cds=(63,1451) /gb=NM_001402 /gi=25453469 /ug=Hs.422118 /len=1837 | NM_001402 | Hs.422118 | NP_001393 |
| 6948 | 0.048529 | putative DNA binding protein (M96), mRNA /cds=(244,2025) /gb=NM_007358 /gi=6678763 /ug=Hs.31016 /len=2648 | NM_007358 | Hs.31016 | NP_031384 |
| 6950 | 0.039781 | splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated) (SFPQ), mRNA /cds=(86,2209) /gb=NM_005066 /gi=4826997 /ug=Hs.180610 /len=3071 | NM_005066 | Hs.180610 | NP_005057 |
| 6957 | 0.003435 | ATP synthase, H transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein) (ATP5O), mRNA /cds=(37,678) /gb=NM_001697 /gi=4502302 /ug=Hs.433960 /len=772 | NM_001697 | Hs.433960 | NP_001688 |
| 6959 | 0.005026 | HLCS gene for holocarboxylase synthetase, complete cds | AB063285 | | |
| 6969 | 0.004578 | oligophrenin 1 (OPHN1), mRNA /cds=(638,3046) /gb=NM_002547 /gi=4505506 /ug=Hs.128824 /len=7350 (=FLJ11206) | NM_002547 | Hs.128824 | NP_002538 |
| 6970 | 0.007223 | neuroblastoma apoptosis-related RNA-binding protein (CUGBP2) gene, exons 10, 11a, 11b, 12, 13a, 13b, 14, and complete cds, alternatively spliced | AF295068 | | |
| 7005 | 5.42E-04 | clone MGC:24133 IMAGE:4693393, mRNA, complete cds /cds=(61,528) /gb=BC017973 /gi=22450811 /ug=Hs.288010 /len=946 | BC017973 | Hs.288010 | NP_777556 |
| 7022 | 0.048529 | ribosomal protein S29 (RPS29), mRNA /cds=(31,201) /gb=NM_001032 /gi=13904868 /ug=Hs.539 /len=346 | NM_001032 | Hs.539 | NP_001023 |
| 7048 | 0.007887 | twisted gastrulation 1 (Drosophila) (TWSG1), mRNA /cds=(106,777) /gb=NM_020648 /gi=21314788 /ug=Hs.247302 /len=3693 | NM_020648 | Hs.247302 | NP_065699 |
| 7049 | 0.045456 | C3HC4-like zinc finger protein (ZFP26), mRNA /cds=(144,836) /gb=NM_016422 /gi=21361492 /ug=Hs.44685 /len=1108 | NM_016422 | Hs.44685 | NP_057506 |

| Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension | | | | | |
|--|----------|---|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 7067 | 0.03016 | guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1 (GNB2L1), mRNA /cds=(96,1049) /gb=NM_006098 /gi=24475893 /ug=Hs.5662 /len=1093 | NM_006098 | Hs.5662 | NP_006089 |
| 7082 | 0.032363 | NCK-associated protein 1 (NCKAP1), mRNA /cds=(272,3658) /gb=NM_013436 /gi=20127530 /ug=Hs.278411 /len=4487 | NM_013436 | Hs.278411 | NP_038464 |
| 7090 | 0.02428 | eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA /cds=(63,1451) /gb=NM_001402 /gi=25453469 /ug=Hs.422118 /len=1837 | NM_001402 | Hs.422118 | NP_001393 |
| 7098 | 0.006039 | inactive progesterone receptor, 23 kD (TEBP), mRNA /cds=(107,589) /gb=NM_006601 /gi=23308578 /ug=Hs.278270 /len=1490 | NM_006601 | Hs.278270 | NP_006592 |
| 7102 | 0.003784 | survival of motor neuron protein interacting protein 1 (SIP1), mRNA /cds=(84,926) /gb=NM_003616 /gi=4506960 /ug=Hs.102456 /len=1285 | NM_003616 | Hs.102456 | NP_003607 |
| 7123 | 0.007887 | KIAA0857 protein (KIAA0857), mRNA /cds=(241,2202) /gb=NM_015470 /gi=24308074 /ug=Hs.24557 /len=4340 | NM_015470 | Hs.24557 | NP_056285 |
| 7126 | 0.015351 | ribosomal protein S18 (RPS18), mRNA /cds=(46,504) /gb=NM_022551 /gi=14165467 /ug=Hs.275865 /len=549 | NM_022551 | Hs.275865 | NP_072045 |
| 7127 | 0.014175 | actin-related protein 10 (S. cerevisiae) (ACTR10), mRNA /cds=(81,1334) /gb=NM_018477 /gi=8923711 /ug=Hs.274369 /len=1621 | NM_018477 | Hs.274369 | NP_060947 |
| 7149 | 0.017954 | solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3 (SLC25A3), nuclear gene encoding mitochondrial protein, transcript variant 1b, mRNA /cds=(49,1134) /gb=NM_002635 /gi=4505774 /ug=Hs.78713 /len=1330 | NM_002635 | Hs.78713 | NP_005879 |
| 7150 | 0.034698 | eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA /cds=(63,1451) /gb=NM_001402 /gi=25453469 /ug=Hs.422118 /len=1837 | NM_001402 | Hs.422118 | NP_001393 |
| 7187 | 0.037168 | collagen, type V, alpha 1 (COL5A1), mRNA /cds=(383,5899) /gb=NM_000093 /gi=16554578 /ug=Hs.146428 /len=6496 | NM_000093 | Hs.146428 | NP_000084 |
| 7224 | 0.028082 | hypothetical protein FLJ20312 (FLJ20312), mRNA /cds=(384,803) /gb=NM_017761 /gi=20127576 /ug=Hs.7862 /len=2382 | NM_017761 | Hs.7862 | NP_060231 |

| Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension | | | | | |
|--|----------|---|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 7236 | 0.037168 | eukaryotic translation initiation factor 3, subunit 6 48kDa (EIF3S6), mRNA /cds=(23,1360) /gb=NM_001568 /gi=4503520 /ug=Hs.106673 /len=1510 | NM_001568 | Hs.106673 | NP_001559 |
| 7238 | 0.011093 | pp11741 mRNA, complete cds /cds=(1126,2058) /gb=AF318323 /gi=18027737 /ug=Hs.382867 /len=3222 | AF318323 | Hs.382867 | |
| 7241 | 0.032363 | likely ortholog of mouse guanine nucleotide releasing protein x (GNRPX), mRNA /cds=(82,531) /gb=NM_018049 /gi=8922332 /ug=Hs.173739 /len=1215 | NM_018049 | Hs.173739 | NP_060519 |
| 7243 | 0.002302 | calcium/calmodulin-dependent protein kinase kinase 2, beta (CAMKK2), transcript variant 1, mRNA /cds=(830,2596) /gb=NM_006549 /gi=27437014 /ug=Hs.108708 /len=5620 | NM_006549 | Hs.108708 | NP_757380 |
| 7272 | 0.037168 | hypothetical protein FLJ11021 similar to splicing factor, arginine/serine-rich 4 (FLJ11021), mRNA /cds=(767,1375) /gb=NM_023012 /gi=20127619 /ug=Hs.81648 /len=1878 | NM_023012 | Hs.81648 | NP_075388 |
| 7285 | 0.045456 | MR4-ET0140-070501-014-g01 ET0140 cDNA, mRNA sequence /gb=BQ331564 /gi=20972721 /ug=Hs.442329 /len=219 | BQ331564 | Hs.442329 | |
| 7310 | 0.006608 | UI-H-BI2-agp-f-12-0-UI.s1 NCI_CGAP_Sub4 cDNA clone IMAGE:2725031 3', mRNA sequence /clone=IMAGE:2725031 /clone_end=3' /gb=AW292456 /gi=6699092 /ug=Hs.437793 /len=745 | AW292456 | Hs.437793 | |
| 7319 | 0.020917 | mRNA for KIAA0276 gene, partial cds. /cds=(1,932) /gb=D87466 /gi=1665816 /ug=Hs.240112 /len=4185 | D87466 | Hs.240112 | |
| 7361 | 0.042541 | SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4 (SMARCA4), mRNA /cds=(277,5220) /gb=NM_003072 /gi=21071055 /ug=Hs.78202 /len=5681 | NM_003072 | Hs.78202 | NP_003063 |
| 7414 | 0.004165 | tetraspanin similar to TM4SF9 (DC-TM4F2), mRNA /cds=(79,891) /gb=NM_030927 /gi=13569888 /ug=Hs.101395 /len=2556 | NM_030927 | Hs.101395 | NP_112189 |
| 7437 | 0.045456 | similar to endothelial cell-selective adhesion molecule (ESAM), mRNA /cds=(139,1311) /gb=NM_138961 /gi=20452463 /ug=Hs.173840 /len=1838 | NM_138961 | Hs.173840 | NP_620411 |
| 7450 | 0.048529 | KIAA0097 gene product (KIAA0097), mRNA /cds=(27,5945) /gb=NM_014756 /gi=24307972 /ug=Hs.76989 /len=6449 | NM_014756 | Hs.76989 | NP_055571 |

| Genes Corrsponding To Differentially Expressed Genes in Figure 8 - Hypertension | | | | | |
|---|----------|---|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 7475 | 0.048529 | mRNA; cDNA DKFZp451F056 (from clone DKFZp451F056) /gb=AL832357 /gi=21732919 /ug=Hs.118837 /len=4901 | AL832357 | Hs.118837 | |
| 7482 | 0.019388 | kinesin family member 1C (KIF1C), mRNA /cds=(114,3425) /gb=NM_006612 /gi=5729896 /ug=Hs.139648 /len=4082 | NM_006612 | Hs.139648 | NP_006603 |
| 7491 | 0.034698 | chromosome 20 open reading frame 149 (C20orf149), mRNA /cds=(150,494) /gb=NM_024299 /gi=13236523 /ug=Hs.79625 /len=803 | NM_024299 | Hs.79625 | NP_077275 |
| 7497 | 2.56E-04 | mRNA for KIAA1266 protein, partial cds. /cds=(131,1936) /gb=AB033092 /gi=6331198 /ug=Hs.58598 /len=5484 | AB033092 | Hs.58598 | |
| 7508 | 0.002819 | mRNA for RCC1-like protein (TD-60 gene) /cds=(236,1804) /gb=AJ421269 /gi=27526612 /ug=Hs.284146 /len=4114 | AJ421269 | Hs.284146 | NP_061185 |
| 7520 | 0.042541 | hypothetical protein FLJ10350 (FLJ10350), mRNA /cds=(676,2340) /gb=NM_018067 /gi=21361780 /ug=Hs.177596 /len=2811 | NM_018067 | Hs.177596 | NP_060537 |
| 7543 | 0.039781 | hypothetical protein FLJ20255 (FLJ20255), mRNA /cds=(146,1090) /gb=NM_017728 /gi=8923229 /ug=Hs.15797 /len=1769 | NM_017728 | Hs.15797 | NP_060198 |
| 7548 | 0.026124 | methionine adenosyltransferase II, beta (MAT2B), mRNA /cds=(73,1077) /gb=NM_013283 /gi=20127525 /ug=Hs.54642 /len=2054 | NM_013283 | Hs.54642 | NP_037415 |
| 7569 | 0.011093 | KIAA1601 protein, partial cds /cds=UNKNOWN /gb=AB046821 /gi=10047276 /ug=Hs.4007 /len=3851 | AB046821 | Hs.4007 | NP_009090 |
| 7574 | 0.028082 | ubiquitin-conjugating enzyme E2N (UBC13 yeast) (UBE2N), mRNA /cds=(64,522) /gb=NM_003348 /gi=4507792 /ug=Hs.75355 /len=1203 | NM_003348 | Hs.75355 | NP_003339 |
| 7576 | 0.001513 | cytochrome P450, family 1, subfamily B, polypeptide 1 (CYP1B1), mRNA /cds=(373,2004) /gb=NM_000104 /gi=13325059 /ug=Hs.154654 /len=5128 | NM_000104 | Hs.154654 | NP_000095 |
| 7587 | 0.006608 | XPA binding protein 1; putative ATP(GTP)-binding protein (NTPBP), mRNA /cds=(25,1149) /gb=NM_007266 /gi=14149628 /ug=Hs.18259 /len=1829 | NM_007266 | Hs.18259 | NP_009197 |
| 7599 | 0.01205 | fibrinogen, B beta polypeptide (FGB), mRNA /cds=(9,1484) /gb=NM_005141 /gi=11761630 /ug=Hs.7645 /len=1918 | NM_005141 | Hs.7645 | NP_005132 |

| Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension | | | | | |
|--|----------|---|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 7618 | 0.026124 | hypothetical protein FLJ11240 (FLJ11240), mRNA /cds=(26,1648) /gb=NM_018368 /gi=8922955 /ug=Hs.339833 /len=1947 | NM_018368 | Hs.339833 | NP_060838 |
| 7629 | 0.039781 | spermidine/spermine N1-acetyltransferase (SAT), mRNA /cds=(166,681) /gb=NM_002970 /gi=4506788 /ug=Hs.28491 /len=1060 | NM_002970 | Hs.28491 | NP_002961 |
| 7637 | 0.001216 | serum response factor (c-fos serum response element-binding transcription factor) (SRF), mRNA /cds=(359,1885) /gb=NM_003131 /gi=4507204 /ug=Hs.155321 /len=4201 | NM_003131 | Hs.155321 | NP_003122 |
| 7660 | 0.015351 | bladder cancer overexpressed protein (BLOV1), mRNA /cds=(72,1136) /gb=NM_018656 /gi=8922084 /ug=Hs.125830 /len=2324 | NM_018656 | Hs.125830 | NP_061126 |
| 7692 | 0.007887 | ribosomal protein, L41 (RPL41), mRNA /cds=(84,161) /gb=NM_021104 /gi=10863874 /ug=Hs.356795 /len=478 | NM_021104 | Hs.356795 | NP_066927 |
| 7694 | 0.002549 | cDNA FLJ25013 fis, clone CBL01365. /gb=AK057742 /gi=16553667 /ug=Hs.380091 /len=2200 | AK057742 | Hs.380091 | |
| 7711 | 0.017954 | death inducer with SAP domain DIS, mRNA, complete cds /cds=(120,3572) /gb=AF465616 /gi=27497117 /ug=Hs.183779 /len=3856 | AF465616 | Hs.183779 | NP_060707 |
| 7719 | 0.011093 | endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2 (EDG2), transcript variant 2, mRNA /cds=(394,1488) /gb=NM_057159 /gi=16950637 /ug=Hs.75794 /len=2732 | NM_057159 | Hs.75794 | NP_476500 |
| 7724 | 0.003784 | tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin) (TNFRSF11B), mRNA /cds=(252,1457) /gb=NM_002546 /gi=22547122 /ug=Hs.81791 /len=2291 | NM_002546 | Hs.81791 | NP_002537 |
| 7728 | 0.007887 | Down syndrome critical region gene 5 (DSCR5), transcript variant 3, mRNA /cds=(342,668) /gb=NM_016430 /gi=24497594 /ug=Hs.408790 /len=875 | NM_016430 | Hs.408790 | NP_710149 |
| 7749 | 0.039781 | mRNA; cDNA DKFZp666E058 (from clone DKFZp666E058) /gb=AL833023 /gi=21733613 /ug=Hs.379886 /len=1761 | AL833023 | Hs.379886 | |
| 7750 | 0.048529 | period 2 (Drosophila) (PER2), transcript variant 1, mRNA /cds=(123,3890) /gb=NM_022817 /gi=12707561 /ug=Hs.153405 /len=6219 | NM_022817 | Hs.153405 | NP_073728 |

| Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension | | | | | |
|--|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 7962 | 0.039781 | hypothetical protein MGC2941 (MGC2941), mRNA /cds=(172,969) /gb=NM_024297 /gi=13236519 /ug=Hs.288217 /len=2005 | NM_024297 | Hs.288217 | NP_077273 |
| 7964 | 0.022547 | CDC42 effector protein (Rho GTPase binding) 3 (CDC42EP3), mRNA /cds=(969,1733) /gb=NM_006449 /gi=19923355 /ug=Hs.260024 /len=2768 | NM_006449 | Hs.260024 | NP_006440 |
| 8020 | 0.020917 | phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase (GART), mRNA /cds=(79,3111) /gb=NM_000819 /gi=24475881 /ug=Hs.82285 /len=3291 | NM_000819 | Hs.82285 | NP_780294 |
| 8053 | 0.01661 | centromere protein C 1 (CENPC1), mRNA /cds=(157,2988) /gb=NM_001812 /gi=4502778 /ug=Hs.154207 /len=3132 | NM_001812 | Hs.154207 | NP_001803 |
| 8054 | 4.81E-04 | pyruvate dehydrogenase kinase 4 mRNA, 3' untranslated region, partial sequence /cds=UNKNOWN/gb=AF334710 /gi=12658438 /ug=Hs.8364 /len=1819 | AF334710 | Hs.8364 | NP_002603 |
| 8056 | 0.039781 | ADP-ribosyltransferase (NAD ; poly (ADP-ribose) polymerase) (ADPRT), mRNA /cds=(160,3204) /gb=NM_001618 /gi=11496989 /ug=Hs.177766 /len=3859 | NM_001618 | Hs.177766 | NP_001609 |
| 8097 | 0.010441 | mRNA for KIAA1915 protein, partial cds. /cds=(356,2536) /gb=AB067502 /gi=15620888 /ug=Hs.12915 /len=7801 | AB067502 | Hs.12915 | |
| 8151 | 0.006608 | cDNA: FLJ23115 fis, clone LNG07933. /gb=AK026768 /gi=10439696 /ug=Hs.98728 /len=1917 | AK026768 | Hs.98728 | |
| 8179 | 0.01205 | karyopherin (importin) beta 3 (KPNB3), mRNA /cds=(139,3486) /gb=NM_002271 /gi=24797085 /ug=Hs.113503 /len=5977 | NM_002271 | Hs.113503 | NP_002262 |
| 8180 | 0.039781 | wn97f10.x1 NCI_CGAP_Ut1 cDNA clone IMAGE:2453803 3' similar to TR:O76003 O76003 THIOREDOXIN-LIKE PROTEIN. ; mRNA sequence /clone=IMAGE:2453803 /clone_end=3' /gb=AI934154 /gi=5673024 /ug=Hs.215019 /len=425 | AI934154 | Hs.215019 | |
| 8341 | 0.015351 | EST(we27d09.x1 NCI_CGAP_Lu24 clone IMAGE:2342321 3') | AI797144 | | NP_002877 |
| 8355 | 0.03016 | hypothetical protein FLJ12716 (FLJ12716), mRNA /cds=(66,2513) /gb=NM_021942 /gi=21361577 /ug=Hs.5354 /len=3522 | NM_021942 | Hs.5354 | NP_068761 |

| Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension | | | | | |
|--|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 8380 | 0.02428 | yy31a11.s1 Soares melanocyte 2NbHM cDNA clone IMAGE:272828 3', mRNA sequence /clone=IMAGE:272828 /clone_end=3' /gb=N32993 /gi=1153392 /ug=Hs.149690 /len=478 | N32993 | Hs.149690 | |
| 8381 | 0.007887 | Tho2 mRNA, complete cds /cds=(1,4437) /gb=AF441770 /gi=20799317 /ug=Hs.16411 /len=4452 | AF441770 | Hs.16411 | |
| 8389 | 0.042541 | EST ov31h03.x1 Soares_testis_NHT cDNA clone IMAGE:1638965 3' | AI017329 | | |
| 8438 | 0.032363 | mRNA sequence /gb=L26969 /gi=16905391 /ug=Hs.362852 /len=1738 | L26969 | Hs.362852 | |
| 8472 | 0.039781 | cDNA FLJ14188 fis, clone NT2RP2005980. /gb=AK024250 /gi=10436579 /ug=Hs.288671 /len=2289 | AK024250 | Hs.288671 | |
| 8477 | 0.037168 | EST(EST36627 Embryo, 8 week I 5' monoamine oxidase B) | AA332652 | | NP_694587 |
| 8480 | 0.017954 | ribosomal protein L37a (RPL37A), mRNA /cds=(36,314) /gb=NM_000998 /gi=16306561 /ug=Hs.296290 /len=392 | NM_000998 | Hs.296290 | NP_000989 |
| 8492 | 0.020917 | EST CM2-BT0857-021100-470-g06 BT0857 Homo sapiens cDNA | BF745663 | | |
| 8508 | 0.01661 | 602384282F1 NIH_MGC_93 cDNA clone IMAGE:4513125 5', mRNA sequence /clone=IMAGE:4513125 /clone_end=5' /gb=BG289274 /gi=13044952 /ug=Hs.202537 /len=776 | BG289274 | Hs.202537 | |
| 8514 | 0.007887 | mRNA; cDNA DKFZp451B1818 (from clone DKFZp451B1818) /gb=AL832623 /gi=21733198 /ug=Hs.77554 /len=6240 | AL832623 | Hs.77554 | |
| 8516 | 0.011093 | EST (MR1-SN0033-100400-001-a10 SN0033) | AW867013 | | |
| 8549 | 0.034698 | EST(am82e07.s1 Stratagene schizo brain S11 cDNA clone IMAGE:1629636 3') | AA984215 | | NP_003109 |
| 8557 | 0.028082 | UI-H-ED0-awy-a-01-0-UI.s1 NCI_CGAP_ED0 cDNA clone IMAGE:5825160 3', mRNA sequence /clone=IMAGE:5825160 /clone_end=3' /gb=BQ017647 /gi=19752924 /ug=Hs.124747 /len=1445 | BQ017647 | Hs.124747 | |
| 8560 | 0.001357 | ribosomal protein L28 (RPL28), mRNA /cds=(43,456) /gb=NM_000991 /gi=13904865 /ug=Hs.356371 /len=500 | NM_000991 | Hs.356371 | NP_000982 |
| 8595 | 0.01661 | ribosomal protein L3 (RPL3), mRNA /cds=(27,1238) /gb=NM_000967 /gi=16507968 /ug=Hs.119598 /len=1311 | NM_000967 | Hs.119598 | NP_000958 |

| Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension | | | | | |
|--|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 8639 | 0.039781 | clone IMAGE:4391536, mRNA/cds=UNKNOWN /gb=BC017742 /gi=17389403 /ug=Hs.334534 /len=2651 | BC017742 | Hs.334534 | NP_002067 |
| 8668 | 0.020917 | AGENCOURT_6461316 NIH_MGC_88 cDNA clone IMAGE:5559480 5', mRNA sequence /clone=IMAGE:5559480 /clone_end=5' /gb=BM802105 /gi=19118928 /ug=Hs.48376 /len=1152 | BM802105 | Hs.48376 | |
| 8669 | 0.01661 | cDNA FLJ10190 fis, clone HEMBA1004753. /gb=AK001052 /gi=7022081 /ug=Hs.274546 /len=1318 | AK001052 | Hs.274546 | |
| 8675 | 0.001357 | UI-H-EI0-ayo-a-20-0-UI.s1 NCI_CGAP_EI0 cDNA clone IMAGE:5841307 3', mRNA sequence /clone=IMAGE:5841307 /clone_end=3' /gb=BQ004581 /gi=19729481 /ug=Hs.412459 /len=1095 | BQ004581 | Hs.412459 | |
| 8708 | 0.01661 | BX111624 NCI_CGAP_Lu5 cDNA clone IMAGp998D244068, mRNA sequence /clone=IMAGp998D244068; IMAGE:1604327 /gb=BX111624 /gi=27837123 /ug=Hs.184840 /len=808 | BX111624 | Hs.184840 | |
| 8714 | 0.02428 | eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA /cds=(63,1451) /gb=NM_001402 /gi=25453469 /ug=Hs.422118 /len=1837 | NM_001402 | Hs.422118 | NP_001393 |
| 8746 | 0.045456 | tg02e02.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:2107610 3', mRNA sequence /clone=IMAGE:2107610 /clone_end=3' /gb=AI380429 /gi=4190282 /ug=Hs.172445 /len=478 | AI380429 | Hs.172445 | |
| 8771 | 0.042541 | mitochondrion, complete genome | NC_001807 | | |
| 8782 | 0.020917 | mitochondrion, complete genome | NC_001807 | | |
| 8788 | 0.032363 | ESTs, cDNA /gb=AW978555 /gi=8169822 /ug=Hs.92448 /len=754 | AW978555 | Hs.92448 | |
| 8796 | 0.002819 | ESTs, cDNA, 3' end /clone=UI-E-EJ0-aii-I-19-0-UI /clone_end=3' /gb=BM681301 /gi=18991197 /ug=Hs.355029 /len=591 | BM681301 | Hs.355029 | |
| 8801 | 0.002549 | cDNA, 5' end /clone=IMAGE:5185850 /clone_end=5' /gb=BI759660 /gi=15751238 /ug=Hs.250691 /len=866 | BI759660 | Hs.250691 | |
| 8837 | 0.005026 | no significant match | SEQ.ID.No.39 | | |
| 8840 | 0.014175 | No significant match | SEQ.ID.No.54 | | |
| 8850 | 0.037168 | chromosome 15 clone RP11-215M5 map 15, WORKING DRAFT SEQUENCE, 6 unordered pieces | AC027467 | | |
| 8856 | 0.008602 | control | | | |

| Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension | | | | | |
|--|----------|---|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 8915 | 0.044991 | EST qh51c12.x1 Soares_fetal_liver_spleen_1NFLS_S1 H.sapiens cDNA clone IMAGE:1848214 3' | AI242874 | | |
| 8929 | 0.014175 | EST(EST92395 Skin tumor I cDNA 5' end) | AA379393 | | |
| 8931 | 0.03016 | chromosome 21 open reading frame 6 (C21orf6), mRNA /cds=(92,1051) /gb=NM_016940 /gi=8393017 /ug=Hs.34136 /len=1729 | NM_016940 | Hs.34136 | NP_058636 |
| 8942 | 0.045456 | mRNA for Sec24 protein (Sec24A isoform), partial /cds=(1,3237) /gb=AJ131244 /gi=3947687 /ug=Hs.211612 /len=5967 | AJ131244 | Hs.211612 | |
| 8946 | 0.042541 | hypothetical protein FLJ33282 (FLJ33282), mRNA /cds=(225,1523) /gb=NM_152388 /gi=22748830 /ug=Hs.346509 /len=2078 | NM_152388 | Hs.346509 | |
| 8949 | 0.008602 | tx18g05.x1 NCI_CGAP_Ut4 cDNA clone IMAGE:2269592 3', mRNA sequence /clone=IMAGE:2269592 /clone_end=3' /gb=AI612954 /gi=4622121 /ug=Hs.187303 /len=205 | AI612954 | Hs.187303 | |
| 8970 | 0.03016 | on43h10.y5 NCI_CGAP_Co8 cDNA clone IMAGE:1559491 5', mRNA sequence /clone=IMAGE:1559491 /clone_end=5' /gb=AI793153 /gi=5340869 /ug=Hs.58262 /len=521 | AI793153 | Hs.58262 | |
| 8981 | 0.002549 | AV737351 CB cDNA clone CBLALE11 5', mRNA sequence /clone=CBLALE11 /clone_end=5' /gb=AV737351 /gi=10854932 /ug=Hs.444989 /len=511 | AV737351 | Hs.444989 | |
| 8983 | 0.022547 | eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA /cds=(63,1451) /gb=NM_001402 /gi=25453469 /ug=Hs.422118 /len=1837 | NM_001402 | Hs.422118 | NP_001393 |
| 8990 | 0.011093 | hypothetical protein FLJ39514 (FLJ39514), mRNA /cds=(121,2040) /gb=NM_152540 /gi=22749126 /ug=Hs.48565 /len=2221 | NM_152540 | Hs.48565 | NP_689753 |
| 9010 | 0.015351 | 602129918F1 NIH_MGC_56 cDNA clone IMAGE:4286549 5', mRNA sequence /clone=IMAGE:4286549 /clone_end=5' /gb=BF697934 /gi=11983259 /ug=Hs.162812 /len=820 | BF697934 | Hs.162812 | |
| 9020 | 0.034698 | Similar to hypothetical protein FLJ31322, clone IMAGE:5296647, mRNA /gb=BC045189 /gi=28277118 /ug=Hs.350001 /len=2971 | BC045189 | Hs.350001 | NP_787112 |

| Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension | | | | | |
|--|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 9021 | 0.028082 | EST (zs08a07.r1 NCI_CGAP_GCB1 cDNA clone IMAGE:684564 5') | AA251433 | | |
| 9036 | 0.045456 | BX115055 Soares infant brain 1NIB cDNA clone IMAGp998A16174, mRNA sequence /clone=IMAGp998A16174_ IMAGE:41580 /gb=BX115055 /gi=27839210 /ug=Hs.443738 /len=490 | BX115055 | Hs.443738 | |
| 9057 | 0.015351 | glycosyltransferase (LOC83468), mRNA /cds=(408,1457) /gb=NM_031302 /gi=21314737 /ug=Hs.159993 /len=1908 | NM_031302 | Hs.159993 | NP_112592 |
| 9061 | 0.03016 | cDNA FLJ33960 fis, clone CTONG2018843. /gb=AK091279 /gi=21749612 /ug=Hs.126465 /len=2849 | AK091279 | Hs.126465 | |
| 9072 | 0.001683 | clone MGC:20469 IMAGE:4554554, mRNA, complete cds /cds=(208,1149) /gb=BC012182 /gi=15082546 /ug=Hs.82508 /len=1862 | BC012182 | Hs.82508 | |
| 9087 | 0.026124 | EST370944 MAGE resequences, MAGE cDNA, mRNA sequence /gb=AW958874 /gi=8148558 /ug=Hs.403977 /len=504 | AW958874 | Hs.403977 | |
| 9096 | 0.03016 | C1q and tumor necrosis factor related protein 7 (C1QTNF7), mRNA /cds=(234,1103) /gb=NM_031911 /gi=21314748 /ug=Hs.153714 /len=3959 | NM_031911 | Hs.153714 | NP_114117 |
| 9108 | 0.005512 | UI-H-EI0-aye-c-17-0-UI.s1 NCI_CGAP_EI0 cDNA clone UI-H-EI0-aye-c-17-0-UI 3', mRNA sequence /clone=UI-H-EI0-aye-c-17-0-UI /clone_end=3' /gb=CA447385 /gi=24811805 /ug=Hs.420740 /len=812 | CA447385 | Hs.420740 | |
| 9110 | 0.045456 | UI-E-CR1-adz-a-04-0-UI.r1 UI-E-CR1 cDNA clone UI-E-CR1-adz-a-04-0-UI 5', mRNA sequence /clone=UI-E-CR1-adz-a-04-0-UI /clone_end=5' /gb=BM706524 /gi=19019782 /ug=Hs.421063 /len=1149 | BM706524 | Hs.421063 | |
| 9124 | 0.019388 | UI-H-EZ1-bbf-l-14-0-UI.s1 NCI_CGAP_Ch2 cDNA clone UI-H-EZ1-bbf-l-14-0-UI 3', mRNA sequence /clone=UI-H-EZ1-bbf-l-14-0-UI /clone_end=3' /gb=BQ575680 /gi=21478997 /ug=Hs.257044 /len=1036 | BQ575680 | Hs.257044 | |
| 9138 | 0.022547 | mRNA full length insert cDNA clone EUROIMAGE 1287006 /cds=UNKNOWN /gb=AJ420423 /gi=17066287 /ug=Hs.23703 /len=1742 | AJ420423 | Hs.23703 | NP_003349 |

| Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension | | | | | |
|--|----------|---|--------------------|----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigen Accession No. | Protein Accession No. |
| 9200 | 0.011093 | 602387746F1 NIH_MGC_93 cDNA clone IMAGE:4516739 5', mRNA sequence /clone=IMAGE:4516739 /clone_end=5' /gb=BG287971 /gi=13042340 /ug=Hs.303110 /len=749 | BG287971 | Hs.303110 | |
| 9244 | 0.009373 | Mus musculus mitochondrion, complete genome | NC_001569 | | |
| 9253 | 0.007223 | 603390782F1 NIH_MGC_87 cDNA clone IMAGE:5399756 5', mRNA sequence /clone=IMAGE:5399756 /clone_end=5' /gb=BI860842 /gi=16001577 /ug=Hs.112472 /len=917 | BI860842 | Hs.112472 | |
| 9274 | 5.42E-04 | mRNA; cDNA DKFZp586G2120 (from clone DKFZp586G2120); complete cds /cds=(19,2604) /gb=AL136924/gi=12053342 /ug=Hs.62349 /len=4137 | AL136924 | Hs.62349 | NP_061866 |
| 9275 | 0.037168 | ESTs, cDNA, 5' end /clone=IMAGE:3857750 /clone_end=5' /gb=BF035134 /gi=10742846 /ug=Hs.195789 /len=847 | BF035134 | Hs.195789 | |
| 9310 | 0.001683 | No significant match | SEQ.ID.No.71 | | |
| 9317 | 0.042541 | No significant match, ORF+1(37~252,298~399) | SEQ.ID.No.95 | | |
| 9383 | 0.048529 | phosphoinositide-3-kinase, regulatory subunit, polypeptide 2 (p85 beta) (PIK3R2), mRNA /cds=(242,2428) /gb=NM_005027 /gi=4826907 /ug=Hs.211586 /len=3201 | NM_005027 | Hs.211586 | NP_005018 |
| 9440 | 0.042541 | ATP citrate lyase (ACLY), mRNA /cds=(85,3402) /gb=NM_001096 /gi=4501864 /ug=Hs.174140 /len=4297 | NM_001096 | Hs.174140 | NP_001087 |
| 9446 | 0.037168 | hypothetical protein RP1-317E23 (LOC56181), mRNA /cds=(311,1189) /gb=NM_019557 /gi=24475811 /ug=Hs.323396 /len=2119 | NM_019557 | Hs.323396 | NP_062457 |
| 9459 | 0.01205 | ubiquinol-cytochrome c reductase binding protein (UQCRB), mRNA /cds=(54,389) /gb=NM_006294 /gi=20070231 /ug=Hs.131255 /len=965 | NM_006294 | Hs.131255 | NP_006285 |
| 9461 | 0.005512 | thioredoxin-like protein p19 (TLP19), mRNA /cds=(280,798) /gb=NM_015913 /gi=23943808 /ug=Hs.241489 /len=1616 | NM_015913 | Hs.241489 | NP_056997 |
| 9468 | 0.005026 | hypothetical protein MGC13159 (MGC13159), mRNA /cds=(592,1017) /gb=NM_032927 /gi=14249719 /ug=Hs.12845 /len=1759 | NM_032927 | Hs.12845 | NP_116316 |

| Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension | | | | | |
|--|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 9473 | 0.037168 | mRNA; cDNA DKFZp564D152 (from clone DKFZp564D152); complete cds /cds=(99,1415) /gb=AL136629 /gi=12052783 /ug=Hs.278479 /len=3229 | AL136629 | Hs.278479 | |
| 9489 | 0.001216 | similar to putative (H. sapiens) (LOC129641), mRNA | XM_059369 | | |
| 9498 | 0.032363 | PFTAIRE protein kinase 1 (PFTK1), mRNA /cds=(145,1500) /gb=NM_012395 /gi=6912583 /ug=Hs.57856 /len=4957 | NM_012395 | Hs.57856 | NP_036527 |
| 9513 | 0.042541 | hypothetical gene supported by AY007122 (LOC92719), mRNA | XM_046853 | | |
| 9530 | 0.002302 | hypothetical protein FLJ10856 (FLJ10856), mRNA /cds=(148,1233) /gb=NM_018247 /gi=8922719 /ug=Hs.108530 /len=3720 | NM_018247 | Hs.108530 | NP_060717 |
| 9541 | 0.037168 | alcohol dehydrogenase IB (class I), beta polypeptide (ADH1B), mRNA /cds=(71,1198) /gb=NM_000668 /gi=11496887 /ug=Hs.4 /len=2534 | NM_000668 | Hs.4 | NP_000659 |
| 9545 | 0.01205 | mRNA; cDNA DKFZp686C117 (from clone DKFZp686C117) /gb=AL832773 /gi=21733355 /ug=Hs.433512 /len=5984 | AL832773 | Hs.433512 | |
| 9595 | 0.013076 | hypothetical protein MGC4701 (MGC4701), mRNA /cds=(149,1585) /gb=NM_024511 /gi=24308290 /ug=Hs.421054 /len=1686 | NM_024511 | Hs.421054 | NP_078787 |
| 9596 | 0.003113 | vimentin (VIM), mRNA /cds=(123,1523) /gb=NM_003380 /gi=4507894 /ug=Hs.297753 /len=1851 | NM_003380 | Hs.297753 | NP_000995 |
| 9610 | 0.048529 | nuclear DNA-binding protein (C1D), transcript variant 1, mRNA /cds=(64,489) /gb=NM_006333 /gi=27894371 /ug=Hs.15164 /len=1200 | NM_006333 | Hs.15164 | NP_775269 |
| 9627 | 0.019388 | hypothetical protein DKFZp564B1162 (DKFZp564B1162), mRNA /cds=(661,2628) /gb=NM_031305 /gi=13775229 /ug=Hs.93589 /len=4593 | NM_031305 | Hs.93589 | NP_112595 |
| 9632 | 0.03016 | clone MGC:9947 IMAGE:3876105, mRNA, complete cds /cds=(51,2216) /gb=BC013590 /gi=15488925 /ug=Hs.2437 /len=2651 | BC013590 | Hs.2437 | |
| 9648 | 0.002549 | Similar to RIKEN cDNA 1500009M05 gene, clone MGC:40370 IMAGE:5105935, mRNA, complete cds /cds=(45,452) /gb=BC032300 /gi=21619026 /ug=Hs.295953 /len=1617 | BC032300 | Hs.295953 | |

| Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension | | | | | |
|--|----------|---|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 9682 | 0.007887 | BX091044 Soares retina N2b4HR cDNA clone IMAGp998D18828 ; IMAGE:360161, mRNA sequence /clone=IMAGp998D18828 ; IMAGE:360161 /gb=BX091044 /gi=27826224 /ug=Hs.435655 /len=644 | BX091044 | Hs.435655 | |
| 9741 | 0.032363 | EST UI-H-BI0p-aau-a-05-0-UI.s1 NCI_CGAP_Sub2 Human sapiens cDNA clone IMAGE:2710544 3' | AW015507 | | NP_037442 |
| 9758 | 0.022547 | UI-E-DX0-agr-j-18-0-UI.s1 UI-E-DX0 cDNA clone UI-E-DX0-agr-j-18-0-UI 3', mRNA sequence /clone=UI-E-DX0-agr-j-18-0-UI /clone_end=3' /gb=BM667357 /gi=18975188 /ug=Hs.436172 /len=983 | BM667357 | Hs.436172 | |
| 9774 | 0.039781 | cDNA FLJ36605 fis, clone TRACH2015316, highly similar to VIMENTIN. /cds=(631,1317) /gb=AK093924 /gi=21752883 /ug=Hs.379100 /len=2665 | AK093924 | Hs.379100 | |
| 9886 | 0.004165 | mRNA; cDNA DKFZp451F1910 (from clone DKFZp451F1910) /gb=AL833265 /gi=21733898 /ug=Hs.332030 /len=5254 | AL833265 | Hs.332030 | |
| 9972 | 0.005026 | caldesmon 1 (CALD1), transcript variant 1, mRNA /cds=(230,2611) /gb=NM_033138 /gi=15149460 /ug=Hs.325474 /len=3610 | NM_033138 | Hs.325474 | NP_149347 |
| 9985 | 0.026124 | mRNA from chromosome 5q21-22, clone:843Ex. /gb=AB002449 /gi=2943812 /ug=Hs.182723 /len=1228 | AB002449 | Hs.182723 | |
| 10002 | 0.022547 | synaptotagmin-like 4 (granuphilin-a) (SYTL4), mRNA /cds=(333,2348) /gb=NM_080737 /gi=18152766 /ug=Hs.247525 /len=3914 | NM_080737 | Hs.247525 | NP_542775 |
| 10041 | 0.01661 | COP9 constitutive photomorphogenic subunit 4 (Arabidopsis) (COPS4), mRNA /cds=(7,1224) /gb=NM_016129 /gi=7705844 /ug=Hs.6671 /len=1613 | NM_016129 | Hs.6671 | NP_057213 |
| 10060 | 0.048529 | roundabout, axon guidance receptor, 1 (Drosophila) (ROBO1), transcript variant 2, mRNA /cds=(964,5802) /gb=NM_133631 /gi=19743805 /ug=Hs.301198 /len=7475 | NM_133631 | Hs.301198 | NP_598334 |
| 10092 | 0.039781 | hypothetical protein MGC14376 (MGC14376), mRNA /cds=(185,256) /gb=NM_032895 /gi=14249657 /ug=Hs.417157 /len=1263 | NM_032895 | Hs.417157 | NP_116284 |
| 10146 | 0.042541 | EST qz90a06.x1 Soares_pregnant_uterus_NbHPU cDNA clone IMAGE:2041810 3' | AI493872 | | NP_008878 |

| Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension | | | | | |
|--|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 10151 | 0.003784 | cDNA FLJ36605 fis, clone TRACH2015316, highly similar to VIMENTIN. /cds=(631,1317) /gb=AK093924 /gi=21752883 /ug=Hs.379100 /len=2665 | AK093924 | Hs.379100 | |
| 10192 | 0.019388 | hypothetical protein clone 25242 mRNA | AF131854 | | |
| 10205 | 0.011093 | EST (ol74f05.s1 NCI_CGAP_Kid3 cDNA clone IMAGE:1535361 3') | AA919165 | | |
| 10208 | 0.007887 | cDNA FLJ33503 fis, clone BRAMY2004521. /cds=(367,750) /gb=AK090822 /gi=21749052 /ug=Hs.356719 /len=2339 | AK090822 | Hs.356719 | NP_787089 |
| 10228 | 0.028082 | hypothetical protein FLJ10342 (FLJ10342), mRNA /cds=(534,1145) /gb=Nm_018064 /gi=14149717 /ug=Hs.101514 /len=1506 | Nm_018064 | Hs.101514 | NP_060534 |
| 10247 | 6.88E-04 | vimentin (VIM) gene | M18895 | | |
| 10277 | 0.037168 | likely ortholog of mouse embryonic epithelial gene 1 (EEG1), mRNA /cds=(319,1794) /gb=Nm_017611 /gi=18252046 /ug=Hs.274453 /len=2630 | Nm_017611 | Hs.274453 | NP_060081 |
| 10293 | 0.037168 | BX102130 NCI_CGAP_Pr3 cDNA clone IMAGp998P072795, mRNA sequence /clone=IMAGp998P072795; IMAGE:1115766 /gb=BX102130 /gi=27831621 /ug=Hs.433046 /len=450 | BX102130 | Hs.433046 | |
| 10323 | 0.03016 | mRNA; cDNA DKFZp434K1115 (from clone DKFZp434K1115); complete cds /cds=(97,2877) /gb=AL136764 /gi=12053044 /ug=Hs.42676 /len=4868 | AL136764 | Hs.42676 | |
| 10342 | 0.048529 | hypothetical protein FLJ38725 (FLJ38725), mRNA /cds=(322,1614) /gb=Nm_153218 /gi=23397476 /ug=Hs.210586 /len=2468 | Nm_153218 | Hs.210586 | NP_694950 |
| 10358 | 0.006039 | cDNA, 5' end /clone=IMAGE:4148900 /clone_end=5' /gb=BF342391 /gi=11289392 /ug=Hs.30469 /len=803 | BF342391 | Hs.30469 | NP_055313 |
| 10385 | 0.042541 | chondroitin sulfate GalNAcT-2 (GALNAcT-2), mRNA /cds=(336,1964) /gb=Nm_018590 /gi=24429591 /ug=Hs.180758 /len=3745 | Nm_018590 | Hs.180758 | NP_061060 |
| 10392 | 0.006608 | ribosomal protein, large, P1 (RPLP1), mRNA /cds=(130,474) /gb=Nm_001003 /gi=16905511 /ug=Hs.424299 /len=512 | Nm_001003 | Hs.424299 | NP_000994 |

| Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension | | | | | |
|--|----------|---|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 10432 | 0.02428 | UI-H-BW0-ajd-b-12-0-UI.s1 NCI_CGAP_Sub6 cDNA clone. IMAGE:2731343 3', mRNA sequence /clone=IMAGE:2731343 /clone_end=3' /gb=AW297162 /gi=6703808 /ug=Hs.438076 /len=690 | AW297162 | Hs.438076 | |
| 10438 | 0.045456 | we90c07.x1 Soares_NFL_T_GBC_S1 cDNA clone IMAGE:2348364 3', mRNA sequence /clone=IMAGE:2348364 /clone_end=3' /gb=AI797677 /gi=5363149 /ug=Hs.199882 /len=554 | AI797677 | Hs.199882 | |
| 10456 | 0.037168 | mRNA; cDNA DKFZp451D112 (from clone DKFZp451D112); complete cds /cds=(316,4719) /gb=AL831962 /gi=21732493 /ug=Hs.202949 /len=5391 | AL831962 | Hs.202949 | |
| 10475 | 0.013076 | solute carrier family 25 (mitochondrial carrier; citrate transporter), member 1 (SLC25A1), mRNA /cds=(100,1035) /gb=NM_005984 /gi=21389314 /ug=Hs.111024 /len=1619 | NM_005984 | Hs.111024 | NP_005975 |
| 10485 | 0.013076 | cDNA FLJ36429 fis, clone THYMU2011573. /gb=AK093748 /gi=21752675 /ug=Hs.378821 /len=1901 | AK093748 | Hs.378821 | |
| 10527 | 0.03016 | clone MGC:26123 IMAGE:4823171, mRNA, complete cds /cds=(279,1991) /gb=BC030580 /gi=21040474 /ug=Hs.374951 /len=2464 | BC030580 | Hs.374951 | |
| 10531 | 0.042541 | mRNA; cDNA DKFZp686J172 (from clone DKFZp686J172) /gb=AL832206 /gi=21732751 /ug=Hs.56896 /len=6055 | AL832206 | Hs.56896 | |
| 10536 | 0.001254 | nascent-polypeptide-associated complex alpha polypeptide (NACA), mRNA /cds=(26,673) /gb=NM_005594 /gi=5031930 /ug=Hs.32916 /len=797 | NM_005594 | Hs.32916 | NP_005585 |
| 10559 | 0.042541 | UI-E-CL1-afg-c-18-0-UI.r1 UI-E-CL1 cDNA clone UI-E-CL1-afg-c-18-0-UI 5', mRNA sequence /clone=UI-E-CL1-afg-c-18-0-UI /clone_end=5' /gb=BM691757 /gi=19005015 /ug=Hs.11355 /len=1234 | BM691757 | Hs.11355 | |
| 10565 | 0.019388 | clone IMAGE:5284350, mRNA /gb=BC037924 /gi=23138690 /ug=Hs.143061 /len=2659 | BC037924 | Hs.143061 | |
| 10601 | 0.009373 | EST(cDNA clone IMAGE:3566688 3') | BF110315 | | NP_002154 |
| 10603 | 0.028082 | eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA /cds=(63,1451) /gb=NM_001402 /gi=25453469 /ug=Hs.422118 /len=1837 | NM_001402 | Hs.422118 | NP_001393 |

| Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension | | | | | |
|--|----------|---|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 10612 | 0.048529 | cDNA FLJ39382 fis, clone PERIC2000473. /gb=AK096701 /gi=21756253 /ug=Hs.293799 /len=2425 | AK096701 | Hs.293799 | |
| 10632 | 0.009373 | UI-H-EI1-aze-g-21-0-UI.s1 NCI_CGAP_EI1 cDNA clone IMAGE:5847596 3', mRNA sequence /clone=IMAGE:5847596 /clone_end=3' /gb=BQ003542 /gi=19728442 /ug=Hs.190642 /len=1086 | BQ003542 | Hs.190642 | |
| 10779 | 0.026124 | EST (ADB cDNA clone ADBAKA02 5') | AV704531 | | |
| 10780 | 0.048529 | hypothetical protein FLJ10300 (FLJ10300), mRNA /cds=(1710,3359) /gb=NM_018051 /gi=21361686 /ug=Hs.42233 /len=3785 | NM_018051 | Hs.42233 | NP_060521 |
| 10788 | 0.028082 | yg45f12.s1 Soares infant brain 1NIB cDNA clone IMAGE:35625 3', mRNA sequence /clone=IMAGE:35625 /clone_end=3' /gb=R45691 /gi=822137 /ug=Hs.268774 /len=574 | R45691 | Hs.268774 | |
| 10789 | 0.017954 | cDNA FLJ14374 fis, clone HEMBA1001635, weakly similar to TESTIS SPECIFIC PROTEIN A. /cds=(185,1464) /gb=AK027280 /gi=14041858 /ug=Hs.400618 /len=1464 | AK027280 | Hs.400618 | |
| 10794 | 0.004578 | FSHD region gene 1 (FRG1), mRNA /cds=(192,968) /gb=NM_004477 /gi=4758403 /ug=Hs.203772 /len=1042 | NM_004477 | Hs.203772 | NP_004468 |
| 10853 | 0.001088 | EST(zf89c05.r1 Soares testis NHT clone 729512 5') | AA398038 | | NP_004632 |
| 10862 | 0.006608 | mitochondrion, complete genome | NC_001807 | | |
| 10888 | 1.14E-04 | UI-H-DH0-aui-j-10-0-UI.s1 NCI_CGAP_DH0 cDNA clone IMAGE:5871081 3', mRNA sequence /clone=IMAGE:5871081 /clone_end=3' /gb=BM994461 /gi=19719362 /ug=Hs.434057 /len=2059 | BM994461 | Hs.434057 | |
| 10906 | 0.034698 | cDNA FLJ39740 fis, clone SMINT2016477. /gb=AK097059 /gi=21756705 /ug=Hs.432907 /len=1987 | AK097059 | Hs.432907 | NP_444269 |
| 10972 | 0.042541 | fetal liver cDNA library Human cDNA | AI132941 | | |
| 10975 | 0.034698 | FLJ30021 fis, clone 3NB692000973 | AK054583 | | |
| 10991 | 0.042541 | ribosomal protein L12 (RPL12), mRNA /cds=(89,586) /gb=NM_000976 /gi=15431291 /ug=Hs.405042 /len=632 | NM_000976 | Hs.405042 | NP_000967 |

| Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension | | | | | |
|--|----------|---|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 10996 | 0.010202 | BX118052 Soares breast 2NbHBst cDNA clone IMAGp998C21252, mRNA sequence /clone=IMAGp998C21252_ IMAGE:158156 /gb=BX118052 /gi=27840946 /ug=Hs.32250 /len=612 | BX118052 | Hs.32250 | |
| 11003 | 0.007887 | cDNA FLJ14832 fis, clone OVARC1001169. /gb=AK027738 /gi=14042638 /ug=Hs.235860 /len=2350 | AK027738 | Hs.235860 | |
| 11011 | 0.028082 | EST(cDNA clone IMAGE:2686869 3') | AW197394 | | |
| 11016 | 0.014175 | mitochondrion, complete genome | NC_001807 | | |
| 11026 | 0.022547 | EST(cDNA clone IMAGE:4663252 5') | BG534476 | | |
| 11032 | 0.037168 | nj38c05.s1 NCI_CGAP_AA1 cDNA clone IMAGE:994760 3' similar to gb:M62424 THROMBIN RECEPTOR PRECURSOR mRNA sequence /clone=IMAGE:994760 /clone_end=3' /gb=AA548630 /gi=2318912 /ug=Hs.105848 /len=555 | AA548630 | Hs.105848 | |
| 11085 | 0.013076 | EST(cDNA clone IMAGE:2126419 3') | AI435109 | | |
| 11115 | 0.032363 | basic transcription factor 3 (BTF3), mRNA /cds=(240,728) /gb=NM_001207 /gi=20070129 /ug=Hs.101025 /len=952 | NM_001207 | Hs.101025 | NP_001198 |
| 11136 | 0.01661 | clone IMAGE:3138608, mRNA /cds=UNKNOWN /gb=BC007266 /gi=13938277 /ug=Hs.334566 /len=1635 | BC007266 | Hs.334566 | |
| 11148 | 0.02428 | ij23g01.x1 Melton Normalized Islet 4 N4-HIS 1 cDNA clone IMAGE:6135721 3', mRNA sequence /clone=IMAGE:6135721 /clone_end=3' /gb=BQ100789 /gi=20133773 /ug=Hs.372964 /len=568 | BQ100789 | Hs.372964 | |
| 11161 | 0.037168 | ESTs, cDNA /gb=AW975851 /gi=8167072 /ug=Hs.361171 /len=684 | AW975851 | Hs.361171 | |
| 11167 | 0.037168 | cDNA FLJ31063 fis, clone HSYRA2001105 | AK055625 | | |
| 11237 | 0.004165 | vesicle-associated membrane protein 2 (synaptobrevin 2) (VAMP2), mRNA /cds=(95,445) /gb=NM_014232 /gi=7657674 /ug=Hs.25348 /len=2159 | NM_014232 | Hs.25348 | NP_055047 |
| 11243 | 0.014175 | apoA polymorphism Kringle IV gene, exons 1 and 2 | L14005 | | |
| 11257 | 0.032363 | mRNA for FLJ00086 protein, partial cds. /cds=(1951,3150) /gb=AK024487 /gi=10440487 /ug=Hs.343828 /len=4456 | AK024487 | Hs.343828 | NP_835461 |
| 11266 | 0.004165 | B-cell translocation gene 1, anti-proliferative (BTG1), mRNA /cds=(309,824) /gb=NM_001731 /gi=4502472 /ug=Hs.77054 /len=1783 | NM_001731 | Hs.77054 | NP_001722 |

| Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension | | | | | |
|--|----------|---|--------------------|----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigen Accession No. | Protein Accession No. |
| 11293 | 0.042541 | hypothetical protein (FLJ20485), mRNA /cds=(112,729) /gb=NM_019042 /gi=9506680 /ug=Hs.98806 /len=2021 | NM_019042 | Hs.98806 | NP_061915 |
| 11305 | 0.007223 | tousled-like kinase 2 (TLK2), mRNA /cds=(147,2396) /gb=NM_006852 /gi=11140818 /ug=Hs.57553 /len=3327 | NM_006852 | Hs.57553 | NP_006843 |
| 11321 | 0.020917 | transient receptor potential cation channel, subfamily C, member 1 (TRPC1), mRNA /cds=(138,2417) /gb=NM_003304 /gi=27545448 /ug=Hs.250687 /len=4085 | NM_003304 | Hs.250687 | NP_003295 |
| 11329 | 0.023405 | similar to CG9578 gene product (MGC3794), mRNA /cds=(146,964) /gb=NM_152902 /gi=23097249 /ug=Hs.137576 /len=1314 | NM_152902 | Hs.137576 | NP_690866 |
| 11332 | 0.026124 | polyadenylate binding protein-interacting protein 1 (PAIP1), mRNA /cds=(188,1627) /gb=NM_006451 /gi=17511254 /ug=Hs.109643 /len=2764 | NM_006451 | Hs.109643 | NP_006442 |
| 11334 | 0.022547 | clone alpha_est218/52C1 mRNA sequence /gb=AF001542 /gi=2529714 /ug=Hs.356442 /len=2992 | AF001542 | Hs.356442 | |
| 11355 | 0.034698 | chondroitin sulfate proteoglycan 6 (bamacan) (CSPG6), mRNA /cds=(92,3745) /gb=NM_005445 /gi=24475891 /ug=Hs.24485 /len=4096 | NM_005445 | Hs.24485 | NP_005436 |
| 11362 | 0.034698 | mitochondrial ribosomal protein L35 (MRPL35), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA /cds=(35,601) /gb=NM_016622 /gi=22035591 /ug=Hs.93814 /len=2805 | NM_016622 | Hs.93814 | NP_663619 |
| 11364 | 0.01661 | NAD(P)H dehydrogenase, quinone 1 (NQO1), mRNA /cds=(51,875) /gb=NM_000903 /gi=4505414 /ug=Hs.406515 /len=2447 | NM_000903 | Hs.406515 | NP_000894 |
| 11365 | 0.027243 | Rho-specific guanine-nucleotide exchange factor 164 kDa (P164RHOGF), mRNA /cds=(16,6207) /gb=NM_014786 /gi=21361457 /ug=Hs.45180 /len=7540 | NM_014786 | Hs.45180 | NP_055601 |
| 11382 | 0.039781 | GTP cyclohydrolase 1 (dopa-responsive dystonia) (GCH1), mRNA /cds=(149,901) /gb=NM_000161 /gi=4503948 /ug=Hs.86724 /len=2921 | NM_000161 | Hs.86724 | NP_000152 |
| 11398 | 0.022547 | CGI-147 protein (CGI-147), mRNA /cds=(128,667) /gb=NM_016077 /gi=7706350 /ug=Hs.12677 /len=806 | NM_016077 | Hs.12677 | NP_057161 |

| Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension | | | | | |
|--|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | UniGene Accession No. | Protein Accession No. |
| 11402 | 0.037168 | cytochrome c, somatic (CYCS), mRNA /cds=(61,378) /gb=NM_018947 /gi=21361707 /ug=Hs.169248 /len=3990 | NM_018947 | Hs.169248 | NP_061820 |
| 11446 | 0.006039 | ornithine decarboxylase antizyme 1 (OAZ1), mRNA /gb=NM_004152 /gi=9845504 /ug=Hs.281960 /len=986 | NM_004152 | Hs.281960 | NP_004143 |
| 11454 | 0.01205 | similar to protein tyrosine phosphatase, receptor type, E; Protein tyrosine phosphatase, receptor type, epsilon; protein tyrosine phosphatase, receptor type, epsilon polypeptide (H. sapiens) (LOC119466), mRNA | XM_005781 | | |
| 11466 | 0.034698 | chemokine (C-C motif) ligand 13 (CCL13), mRNA /cds=(76,372) /gb=NM_005408 /gi=22538799 /ug=Hs.11383 /len=861 | NM_005408 | Hs.11383 | NP_005399 |
| 11475 | 0.02428 | mitogen-activated protein kinase kinase kinase 8 (MAP3K8), mRNA /cds=(697,2100) /gb=NM_005204 /gi=22035597 /ug=Hs.248 /len=3096 | NM_005204 | Hs.248 | NP_005195 |
| 11479 | 0.042541 | B lymphocyte activation-related protein BC-2048 | AAL26788 | | |
| 11482 | 0.005026 | clone IMAGE:5271722, mRNA /gb=BC038786 /gi=24270905 /ug=Hs.190456 /len=1535 | BC038786 | Hs.190456 | |
| 11501 | 0.019388 | RAB34, member RAS oncogene family (RAB34), mRNA /cds=(206,985) /gb=NM_031934 /gi=21361998 /ug=Hs.301853 /len=1340 | NM_031934 | Hs.301853 | NP_114140 |
| 11519 | 0.045456 | mRNA; cDNA DKFZp761O0611 (from clone DKFZp761O0611) /gb=AL834155 /gi=21739631 /ug=Hs.22969 /len=4502 | AL834155 | Hs.22969 | |
| 11536 | 0.011093 | EST(yh89e10.r1 cDNA clone 136938 5') 8e06 match | R38461 | | NP_001002 |
| 11543 | 0.037168 | UI-H-BI1-adj-f-10-0-UI.s1 NCI_CGAP_Sub3 cDNA clone IMAGE:2716963 3', mRNA sequence /clone=IMAGE:2716963 /clone_end=3' /gb=AW137857 /gi=6142175 /ug=Hs.437502 /len=612 | AW137857 | Hs.437502 | |
| 11545 | 0.003784 | UI-H-CO0-aqn-g-08-0-UI.s1 NCI_CGAP_Sub9 cDNA clone IMAGE:3104798 3', mRNA sequence /clone=IMAGE:3104798 /clone_end=3' /gb=BM987319 /gi=19706708 /ug=Hs.445870 /len=655 | BM987319 | Hs.445870 | |
| 11553 | 0.034698 | EST(yv89b04.s1 clone 249871 3') | H96982 | | NP_775876 |

| Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hyp ertension | | | | | |
|---|----------|---|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 11596 | 0.019388 | hypothetical protein cDNA DKFZp761K1115 (from clone DKFZp761K1115); partial cds | AL162046 | | NP_060717 |
| 11597 | 0.03016 | EST HUM517A08B Clontech human placenta polyA mRNA (#6572) Human sapiens cDNA clone GEN-517A08 5' | D63277 | | |
| 11608 | 0.009373 | EST(MR0-HT0407-140300-013-h01 HT0407) | BE159552 | | NP_003751 |
| 11616 | 0.044991 | EST qz49d11.x1 NCI_CGAP_Kid11 IMAGE:2030229 3' | AI493076 | | |
| 11634 | 0.003113 | hypothetical protein FLJ12118 (FLJ12118), mRNA /cds=(24,1718) /gb=NM_024537 /gi=13375694 /ug=Hs.381043 /len=1843 | NM_024537 | Hs.381043 | NP_078813 |
| 11643 | 0.010441 | cDNA FLJ14388 fis, clone HEMBA1002716. /gb=AK027294 /gi=14041878 /ug=Hs.9812 /len=1673 | AK027294 | Hs.9812 | |
| 11646 | 0.004578 | df117a11.w1 Morton Fetal Cochlea cDNA clone IMAGE:2539676 3', mRNA sequence /clone=IMAGE:2539676 /clone_end=3' /gb=BI495331 /gi=15334675 /ug=Hs.347861 /len=405 | BI495331 | Hs.347861 | |
| 11650 | 0.010202 | EST IL3-CT0214-040400-108-C01 CT0214 H.sapiens cDNA | AW849070 | | |
| 11691 | 2.24E-04 | cDNA sequence cDNA sequence DKFZp434D0935 (from clone cDNA sequence DKFZp434D0935) | AL117502 | | NP_149107 |
| 11692 | 0.007887 | KIAA0874 protein (KIAA0874), mRNA /cds=(1,6189) /gb=NM_015208 /gi=14140237 /ug=Hs.27973 /len=6189 | NM_015208 | Hs.27973 | NP_056023 |
| 11706 | 0.034698 | KIAA1887 protein (KIAA1887), mRNA /cds=(259,3270) /gb=NM_052897 /gi=24308373 /ug=Hs.348428 /len=3592 | NM_052897 | Hs.348428 | NP_443129 |
| 11710 | 0.039781 | translocase of outer mitochondrial membrane 20 (yeast) (KIAA0016), mRNA /cds=(102,539) /gb=NM_014765 /gi=7657256 /ug=Hs.75187 /len=3259 | NM_014765 | Hs.75187 | NP_055580 |
| 11721 | 0.042541 | Wolf-Hirschhorn syndrome candidate 1 (WHSC1), transcript variant 4, mRNA /cds=(495,2903) /gb=NM_014919 /gi=19913345 /ug=Hs.110457 /len=8458 | NM_014919 | Hs.110457 | NP_579891 |
| 11724 | 0.037168 | chromosome 14 open reading frame 2 (C14orf2), mRNA /cds=(61,237) /gb=NM_004894 /gi=4758939 /ug=Hs.109052 /len=627 | NM_004894 | Hs.109052 | NP_004885 |
| 11732 | 0.007223 | hypothetical protein FLJ20699 (FLJ20699), mRNA /cds=(33,1043) /gb=NM_017931 /gi=8923627 /ug=Hs.15125 /len=2594 | NM_017931 | Hs.15125 | NP_060401 |

| Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension | | | | | |
|--|----------|---|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 11742 | 0.048529 | prolactin regulatory element binding (PREB), mRNA /cds=(132,1385) /gb=NM_013388 /gi=7019502 /ug=Hs.279784 /len=2059 | NM_013388 | Hs.279784 | NP_037520 |
| 11765 | 0.03016 | ribosomal protein L12 (RPL12), mRNA /cds=(89,586) /gb=NM_000976 /gi=15431291 /ug=Hs.405042 /len=632 | NM_000976 | Hs.405042 | NP_000967 |
| 11775 | 0.01661 | UI-E-CQ1-acq-f-05-0-UI.r1 UI-E-CQ1 cDNA clone UI-E-CQ1-acq-f-05-0-UI 5', mRNA sequence /clone=UI-E-CQ1-acq-f-05-0-UI /clone_end=5' /gb=BM688680 /gi=19001938 /ug=Hs.406520 /len=934 | BM688680 | Hs.406520 | |
| 11781 | 0.01661 | serum/glucocorticoid regulated kinase-like (SGKL), transcript variant 1, mRNA /cds=(416,1705) /gb=NM_013257 /gi=25168264 /ug=Hs.380877 /len=4155 | NM_013257 | Hs.380877 | NP_733827 |
| 11783 | 0.011093 | cDNA FLJ20709 fis, clone KAIA1124, highly similar to D86324 mRNA for CMP-N-acetylneuraminic acid. /gb=AK000716 /gi=7020978 /ug=Hs.24697 /len=3488 | AK000716 | Hs.24697 | |
| 11784 | 0.001683 | sperm associated antigen 9 (SPAG9), transcript variant 1, mRNA /cds=(79,4002) /gb=NM_003971 /gi=27436919 /ug=Hs.129872 /len=4663 | NM_003971 | Hs.129872 | NP_758853 |
| 11788 | 0.032363 | Bardet-Biedl syndrome 2 (BBS2), mRNA /cds=(422,2587) /gb=NM_031885 /gi=22208996 /ug=Hs.332633 /len=2978 | NM_031885 | Hs.332633 | NP_114091 |
| 11805 | 0.03016 | tryptophanyl-tRNA synthetase (WARS), mRNA /cds=(188,1603) /gb=NM_004184 /gi=7710155 /ug=Hs.82030 /len=2693 | NM_004184 | Hs.82030 | NP_004175 |
| 11811 | 2.91E-04 | FLJ11481 fis, clone HEMBA1001803 /cds=UNKNOWN /gb=AK021543 /gi=10432744 /ug=Hs.135159 /len=1539 | AK021543 | Hs.135159 | |
| 11816 | 0.020917 | likely ortholog of rat V-1 protein (V-1), mRNA /cds=(229,585) /gb=NM_145808 /gi=21956644 /ug=Hs.21321 /len=3770 | NM_145808 | Hs.21321 | NP_665807 |
| 11822 | 0.037168 | protein phosphatase 2, regulatory subunit B (B56), gamma isoform (PPP2R5C), mRNA /cds=(89,1633) /gb=NM_002719 /gi=4506022 /ug=Hs.171734 /len=4064 | NM_002719 | Hs.171734 | NP_848703 |
| 11830 | 0.014175 | DKFZp564P2064_s1 564 (synonym: hfbr2) cDNA clone DKFZp564P2064 3', mRNA sequence /clone=DKFZp564P2064 /clone_end=3' /gb=AL037172 /gi=5406623 /ug=Hs.328612 /len=682 | AL037172 | Hs.328612 | |
| 11851 | 0.037168 | mitochondrion, complete genome | NC_001807 | | |

| Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension | | | | | |
|--|----------|---|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 11897 | 0.007887 | hypothetical protein FLJ20701 (FLJ20701), mRNA /cds=(39,938) /gb=NM_017933 /gi=8923631 /ug=Hs.424598 /len=2284 | NM_017933 | Hs.424598 | NP_060403 |
| 11927 | 0.009373 | CCR4-NOT transcription complex, subunit 8 (CNOT8), mRNA /cds=(245,1123) /gb=NM_004779 /gi=24496777 /ug=Hs.26703 /len=2489 | NM_004779 | Hs.26703 | NP_004770 |
| 11958 | 0.03016 | mRNA; cDNA DKFZp686D143 (from clone DKFZp686D143) /gb=AL833539 /gi=21734184 /ug=Hs.56340 /len=8318 | AL833539 | Hs.56340 | |
| 11967 | 0.034698 | TNF receptor-associated factor 5 (TRAF5), transcript variant 1, mRNA /cds=(194,1867) /gb=NM_004619 /gi=22027625 /ug=Hs.29736 /len=4132 | NM_004619 | Hs.29736 | NP_665702 |
| 12041 | 0.034698 | kelch-like protein C3IP1 (C3IP1), mRNA /cds=(201,1907) /gb=NM_021633 /gi=21361889 /ug=Hs.3826 /len=3338 | NM_021633 | Hs.3826 | NP_067646 |
| 12066 | 0.037168 | chromosome 1 open reading frame 19 (C1orf19), mRNA /cds=(51,566) /gb=NM_052965 /gi=24308389 /ug=Hs.32058 /len=1943 | NM_052965 | Hs.32058 | NP_443197 |
| 12072 | 0.015351 | EST(ta04f03.x1 Soares_pregnant_uterus_NbHPU clone IMAGE:2043101 3') | AI580773 | | |
| 12080 | 0.019388 | AGENCOURT_8899857 NIH_MGC_142 cDNA clone IMAGE:6451082 5', mRNA sequence /clone=IMAGE:6451082 /clone_end=5' /gb=BU595281 /gi=23247040 /ug=Hs.5250 /len=1163 | BU595281 | Hs.5250 | |
| 12083 | 0.044991 | EST on95c11.s1 Soares_NFL_T_GBC_S1 IMAGE:1564436 3' | AA934121 | | NP_057174 |
| 12085 | 0.008602 | retinoic acid induced 14 (RAI14), mRNA /cds=(112,3054) /gb=NM_015577 /gi=13470085 /ug=Hs.15165 /len=4925 | NM_015577 | Hs.15165 | NP_056392 |
| 12117 | 0.045456 | EST(tj90g04.x1 Soares_NSF_F8_9W_OT_PA_P_S1 cDNA clone | AI470101 | | |
| 12123 | 0.028082 | UI-H-BI0-aaa-f-10-0-UI.s1 NCI_CGAP_Sub1 cDNA clone IMAGE:2708874 3', mRNA sequence /clone=IMAGE:2708874 /clone_end=3' /gb=AW014102 /gi=5862859 /ug=Hs.304671 /len=654 | AW014102 | Hs.304671 | |
| 12200 | 0.026124 | hypothetical protein FLJ10159 (FLJ10159), mRNA /cds=(1,807) /gb=NM_018013 /gi=8922262 /ug=Hs.22505 /len=2070 | NM_018013 | Hs.22505 | NP_060483 |

| Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension | | | | | |
|--|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 12210 | 0.026124 | cDNA FLJ38039 fis, clone CTONG2013934. /gb=AK095358 /gi=21754600 /ug=Hs.46506 /len=2956 | AK095358 | Hs.46506 | |
| 12222 | 0.007887 | GRB2-associated binding protein 3 (GAB3), mRNA /cds=(33,1793) /gb=NM_080612 /gi=18079322 /ug=Hs.102630 /len=4731 | NM_080612 | Hs.102630 | NP_542179 |
| 12252 | 0.045456 | UI-E-CL1-afb-k-21-0-UI.s1 UI-E-CL1.cDNA clone UI-E-CL1-afb-k-21-0-UI 3', mRNA sequence /clone=UI-E-CL1-afb-k-21-0-UI /clone_end=3' /gb=BM665519 /gi=18972482 /ug=Hs.159501 /len=1100 | BM665519 | Hs.159501 | |
| 12257 | 0.01661 | EST390958 MAGE resequences, MAGP cDNA, mRNA sequence /gb=AW978849 /gi=8170126 /ug=Hs.124977 /len=678 | AW978849 | Hs.124977 | |
| 12271 | 0.048529 | EST(ne86c04.s1 NCI_CGAP_Kid1 clone IMAGE:911142 contains L1.t1 L1 repeat) | AA480776 | | |
| 12310 | 0.007887 | 602644358F1 NIH_MGC_61 cDNA clone IMAGE:4775006 5', mRNA sequence /clone=IMAGE:4775006 /clone_end=5' /gb=BG615069 /gi=13666440 /ug=Hs.190422 /len=770 | BG615069 | Hs.190422 | |
| 12313 | 0.02428 | EST ya88e03.r1 Stratagene placenta(#937225) cDNA clone IMAGE:68764 5' | T53373 | | |
| 12320 | 0.037168 | EST(EST178403 Colon carcinoma (HCC) cell line cDNA 5' end similar to similar to ribosomal protein L30) | AA307521 | | NP_000980 |
| 12346 | 0.005512 | selenoprotein H (SELH), mRNA /cds=(243,611) /gb=NM_170746 /gi=25014108 /ug=Hs.290874 /len=834 | NM_170746 | Hs.290874 | NP_734467 |
| 12399 | 0.017954 | UI-E-CK1-afb-b-14-0-UI.r1 UI-E-CK1 cDNA clone UI-E-CK1-afb-b-14-0-UI 5', mRNA sequence /clone=UI-E-CK1-afb-b-14-0-UI /clone_end=5' /gb=BM702699 /gi=19015957 /ug=Hs.446508 /len=1088 | BM702699 | Hs.446508 | |
| 12403 | 0.042541 | mRNA; cDNA DKFZp564D2071 (from clone DKFZp564D2071) /gb=AL110232 /gi=5817171 /ug=Hs.279243 /len=1077 | AL110232 | Hs.279243 | |
| 12412 | 0.001357 | cDNA / IL3-NT0294-060401-533-D04 NT0294 | BI041924 | | |
| 12440 | 0.048529 | clone IMAGE:5286019, mRNA /gb=BC042960 /gi=27693187 /ug=Hs.5724 /len=3174 | BC042960 | Hs.5724 | |
| 12465 | 0.006039 | ESTs, cDNA, 5' end /clone=IMAGE:3922401 /clone_end=5' /gb=BE894201 /gi=10356330 /ug=Hs.176376 /len=916 | BE894201 | Hs.176376 | |

| Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension | | | | | |
|--|----------|---|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 12470 | 0.034698 | cDNA: FLJ22930 fis, clone KAT07255. /gb=AK026583 /gi=10439467 /ug=Hs.90790 /len=1600 | AK026583 | Hs.90790 | |
| 12500 | 0.039781 | EST(cDNA clone IMAGE:2974964 3') | AW628675 | | NP_006274 |
| 12501 | 0.032363 | EST(cDNA clone IMAGE:4693130 5') | BG539987 | | NP_005397 |
| 12510 | 0.011093 | hypothetical protein DKFZp564F013 (DKFZP564F013), mRNA /cds=(107,2194) /gb=NM_020432 /gi=24308192 /ug=Hs.128653 /len=4572 | NM_020432 | Hs.128653 | NP_065165 |
| 12571 | 0.009373 | EST, clone IMAGE:4127796, mRNA | BC007799 | | NP_443107 |
| 12574 | 0.002077 | UI-H-ED0-awx-b-15-0-UI.s1 NCI_CGAP_ED0 cDNA clone IMAGE:5824814 3', mRNA sequence /clone=IMAGE:5824814 /clone_end=3' /gb=BQ020068 /gi=19755345 /ug=Hs.396278 /len=1351 | BQ020068 | Hs.396278 | |
| 12580 | 0.009373 | No significant match | SEQ.ID.No.34 | | |
| 12604 | 2.91E-04 | EST(IL3-HT0618-120500-138-D11 HT0618 cDNA, MRNA sequence) | BE179957 | | |
| 12608 | 0.034698 | mRNA; cDNA DKFZp586L081 (from clone DKFZp586L081) /gb=AL080234 /gi=5262727 /ug=Hs.432862 /len=2159 | AL080234 | Hs.432862 | |
| 12609 | 0.019388 | Similar to hypothetical protein FLJ31322, clone IMAGE:5296647, mRNA /gb=BC045189 /gi=28277118 /ug=Hs.350001 /len=2971 | BC045189 | Hs.350001 | NP_787112 |
| 12626 | 0.032363 | Novel | SEQ.ID.No.85 | | |
| 12676 | 0.034698 | UI-E-EJ0-aij-i-12-0-UI.r1 UI-E-EJ0 cDNA clone UI-E-EJ0-aij-i-12-0-UI 5', mRNA sequence /clone=UI-E-EJ0-aij-i-12-0-UI /clone_end=5' /gb=BM726397 /gi=19047730 /ug=Hs.232059 /len=973 | BM726397 | Hs.232059 | |
| 12688 | 0.039781 | myxoid liposarcoma associated protein 4 (MLAT4), mRNA /cds=(199,2325) /gb=NM_018192 /gi=27764881 /ug=Hs.42824 /len=3396 | NM_018192 | Hs.42824 | NP_060662 |
| 12689 | 0.045456 | hypothetical protein MGC3077 (MGC3077), mRNA /cds=(137,703) /gb=NM_024051 /gi=13129017 /ug=Hs.433404 /len=1195 | NM_024051 | Hs.433404 | NP_076956 |
| 12696 | 0.026124 | cDNA, 3' end /clone=IMAGE:2369618 /clone_end=3' /gb=AI819052 /gi=5438216 /ug=Hs.50918 /len=540 | AI819052 | Hs.50918 | |
| 12705 | 0.032363 | hypothetical protein FLJ31121 (FLJ31121), mRNA /cds=(15,614) /gb=NM_144723 /gi=21389510 /ug=Hs.350194 /len=1512 | NM_144723 | Hs.350194 | NP_653324 |

| Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension | | | | | |
|--|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 12708 | 0.042541 | nz86f07.s1 NCI_CGAP_GCB1 cDNA clone IMAGE:1302373 3', mRNA sequence /clone=IMAGE:1302373 /clone_end=3' /gb=AA731386 /gi=2753542 /ug=Hs.120251 /len=295 | AA731386 | Hs.120251 | |
| 12715 | 0.026124 | cDNA FLJ31753 fis, clone NT2RI2007468. /gb=AK056315 /gi=16551681 /ug=Hs.349283 /len=2361 | AK056315 | Hs.349283 | |
| 12720 | 0.034698 | mRNA; cDNA DKFZp667O1616 (from clone DKFZp667O1616) /gb=AL713722 /gi=19584452 /ug=Hs.365655 /len=1773 | AL713722 | Hs.365655 | |
| 12725 | 1.31E-04 | EST(CM3-BN0151-130400-146-f01_1 BN0151) | BE008220 | | |
| 12726 | 0.03016 | aldehyde dehydrogenase 6 family, member A1 (ALDH6A1); nuclear gene encoding mitochondrial protein, mRNA /cds=(100,1707) /gb=NM_005589 /gi=25777737 /ug=Hs.293970 /len=2183 | NM_005589 | Hs.293970 | NP_005580 |
| 12743 | 0.013076 | EST (RC3-BN0036-090200-011-h11 BN0036 cDNA) | AW994082 | | |
| 12762 | 0.034698 | wd19h11.x1 Soares_NFL_T_GBC_S1 cDNA clone IMAGE:2328645 3', mRNA sequence /clone=IMAGE:2328645 /clone_end=3' /gb=AI674745 /gi=4875225 /ug=Hs.377373 /len=347 | AI674745 | Hs.377373 | |
| 12765 | 0.042541 | EST (RC5-BT0663-050400-012-H04 BT0663 cDNA) | BE085097 | | |
| 12776 | 0.01205 | EST(cDNA clone IMAGE:4780057 5') | BG743394 | | NP_004087 |
| 12778 | 0.005512 | cDNA FLJ33834 fis, clone CTONG2004264, moderately similar to NEUROBLAST DIFFERENTIATION ASSOCIATED PROTEIN AHNAK. /cds=(6,2381) /gb=AK091153 /gi=21749455 /ug=Hs.378738 /len=2712 | AK091153 | Hs.378738 | |
| 12797 | 0.034698 | EST(xu17f02.x1 NCI_CGAP_Co14 cDNA clone IMAGE:2800443 3') | AW272306 | | NP_002201 |
| 12798 | 0.008602 | UI-H-DF0-bem-a-10-0-UI.s1 NCI_CGAP_DF0 cDNA clone UI-H-DF0-bem-a-10-0-UI 3', mRNA sequence /clone=UI-H-DF0-bem-a-10-0-UI /clone_end=3' /gb=CA425521 /gi=24788247 /ug=Hs.411829 /len=1131 | CA425521 | Hs.411829 | |
| 12811 | 0.048529 | EST(UI-CF-EC1-aec-j-17-0-UI.s1 UI-CF-EC1 cDNA clone UI-CF-EC1-aec-j-17-0-UI 3') | BM977996 | | |
| 12843 | 0.028082 | cDNA clone IMAGE:123789 3' similar to contains Alu repetitive element; contains THR repetitive element ; Soares fetal liver spleen 1NFLS | R01434 | | |

| Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension | | | | | |
|--|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | D scription | Gene Accession No. | Unigene Acc ssion No. | Protein Accession No. |
| 12847 | 0.019388 | EST(cDNA clone IMAGE:4472298 5') | BG251774 | | NP_598001 |
| 12848 | 0.014175 | cDNA: FLJ23165 fis, clone LNG09846. /gb=AK026818 /gi=10439763 /ug=Hs.279898 /len=2117 | AK026818 | Hs.279898 | |
| 12851 | 0.009373 | FLJ11311 fis, clone PLACE1010102/cds=UNKNOWN /gb=AK002173 /gi=7023889 /ug=Hs.5518 /len=1839 | AK002173 | Hs.5518 | NP_689971 |
| 12871 | 0.034698 | wg97c03.x1 NCI_CGAP_Kid11 cDNA clone IMAGE:2379172 3' similar to contains L1.b1 L1 repetitive element ;, mRNA sequence /clone=IMAGE:2379172 /clone_end=3' /gb=AI762342 /gi=5178009 /ug=Hs.304298 /len=531 | AI762342 | Hs.304298 | |
| 12878 | 0.039781 | cDNA PSEC0152 fis, clone PLACE1007885. /cds=(20,1144) /gb=AK075459 /gi=22761560 /ug=Hs.350475 /len=2130 | AK075459 | Hs.350475 | |
| 12892 | 8.68E-04 | ESTs, cDNA, 5' end /clone=IMAGE:1554245 /clone_end=5' /gb=AI792925 /gi=5340641 /ug=Hs.137097 /len=585 | AI792925 | Hs.137097 | |
| 12905 | 0.031589 | UI-H-BI3-ako-d-10-0-UI.s1 NCI_CGAP_Sub5 cDNA clone IMAGE:2734914 3', mRNA sequence /clone=IMAGE:2734914 /clone_end=3' /gb=AW450461 /gi=6991237 /ug=Hs.440730 /len=755 | AW450461 | Hs.440730 | |
| 13007 | 0.014175 | EST(cDNA clone GKCAHD03 5') | AV696986 | | NP_072179 |
| 13042 | 0.010202 | EST(cDNA clone IMAGE:4717063 5') | BG569807 | | |
| 13065 | 0.045456 | control | | | |
| 13079 | 0.03649 | DKFZp686H0168_r1 686 (synonym: hlcc3) cDNA clone DKFZp686H0168 5', mRNA sequence /clone=DKFZp686H0168 /clone_end=5' /gb=AL710266 /gi=19693621 /ug=Hs.123224 /len=839 | AL710266 | Hs.123224 | |
| 13109 | 0.026124 | cDNA FLJ13752 fis, clone PLACE3000352. /gb=AK023814 /gi=10435863 /ug=Hs.144871 /len=3904 | AK023814 | Hs.144871 | |
| 13110 | 7.74E-04 | hypothetical protein P1 p373c6 (P1P373C6), mRNA /cds=(254,1891) /gb=NM_019110 /gi=17738284 /ug=Hs.44720 /len=2316 | NM_019110 | Hs.44720 | NP_061983 |
| 13134 | 0.007887 | sine oculis homeobox 2 (Drosophila) (SIX2), mRNA /cds=(283,1158) /gb=NM_016932 /gi=21314676 /ug=Hs.101937 /len=2141 | NM_016932 | Hs.101937 | NP_058628 |

| Genes Corresponding To Differentially Expressed Genes in Figur 8 - Hypertension | | | | | |
|---|----------|--|--------------------|----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigen Accession No. | Protein Accession No. |
| 13139 | 0.002077 | chromosome 1 open reading frame 8 (C1orf8), mRNA /cds=(251,1222) /gb=NM_004872 /gi=27545320 /ug=Hs.416495 /len=1709 | NM_004872 | Hs.416495 | NP_004863 |
| 13151 | 0.034698 | cell division cycle associated 4 (CDCA4), transcript variant 1, mRNA /cds=(164,889) /gb=NM_017955 /gi=22027508 /ug=Hs.34045 /len=2171 | NM_017955 | Hs.34045 | NP_663747 |
| 13152 | 0.003435 | cDNA FLJ13545 fis, clone PLACE1006867. /gb=AK023607 /gi=10435587 /ug=Hs.421529 /len=1887 | AK023607 | Hs.421529 | |
| 13159 | 0.034698 | enoyl Coenzyme A hydratase, short chain, 1, mitochondrial (ECHS1), nuclear gene encoding mitochondrial protein, mRNA /cds=(72,944) /gb=NM_004092 /gi=12707569 /ug=Hs.76394 /len=1326 | NM_004092 | Hs.76394 | NP_004083 |
| 13180 | 0.005512 | F-box only protein 7 (FBXO7), mRNA /cds=(281,1849) /gb=NM_012179 /gi=15812192 /ug=Hs.5912 /len=2165 | NM_012179 | Hs.5912 | NP_036311 |
| 13182 | 0.037168 | mRNA for KIAA1564 protein, partial cds. /cds=(1,6016) /gb=AB046784 /gi=20521943 /ug=Hs.173421 /len=6143 | AB046784 | Hs.173421 | |
| 13184 | 0.017954 | KIAA1903 protein, partial cds /cds=UNKNOWN /gb=AB067490 /gi=15620864 /ug=Hs.89278 /len=4382 | AB067490 | Hs.89278 | NP_060823 |
| 13188 | 2.14E-05 | hypothetical protein PRO2013 (PRO2013), mRNA /cds=(136,381) /gb=NM_021243 /gi=24308272 /ug=Hs.238205 /len=876 | NM_021243 | Hs.238205 | |
| 13190 | 0.020917 | membrane-spanning 4-domains, subfamily A, member 6A (MS4A6A), transcript variant 1, mRNA /cds=(239,985) /gb=NM_152852 /gi=23238237 /ug=Hs.17914 /len=1564 | NM_152852 | Hs.17914 | NP_690591 |
| 13199 | 0.02428 | HSKM-B protein (HSKM-B), mRNA /cds=(23,1324) /gb=NM_020197 /gi=9910273 /ug=Hs.66170 /len=1694 | NM_020197 | Hs.66170 | NP_064582 |
| 13200 | 0.017954 | FLJ12726 fis, clone NT2RP2000001, highly similar to Human mRNA for KIAA1111 protein | AK022788 | | |
| 13206 | 0.009373 | spinal cord-derived growth factor-B (SCDGF-B), transcript variant 1, mRNA /cds=(176,1288) /gb=NM_025208 /gi=15451919 /ug=Hs.112885 /len=3808 | NM_025208 | Hs.112885 | NP_149126 |
| 13207 | 0.006039 | ARP8 actin-related protein 8 (yeast) (ACTR8), mRNA /cds=(5,1129) /gb=NM_022899 /gi=12597636 /ug=Hs.124219 /len=2797 | NM_022899 | Hs.124219 | NP_075050 |

| Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension | | | | | |
|--|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 13210 | 0.034698 | hypothetical protein FLJ13188 (FLJ13188), mRNA /cds=(247,948) /gb=NM_022063 /gi=11545770 /ug=Hs.11859 /len=2746 | NM_022063 | Hs.11859 | NP_071346 |
| 13212 | 0.01661 | hypothetical protein FLJ20060 (FLJ20060), mRNA /cds=(72,2078) /gb=NM_017645 /gi=24431978 /ug=Hs.54617 /len=2884 | NM_017645 | Hs.54617 | NP_060115 |
| 13222 | 0.039781 | yf95a11.s1 Soares infant brain 1NIB cDNA clone IMAGE:30037 3', mRNA sequence /clone=IMAGE:30037 /clone_end=3' /gb=R41424 /gi=816727 /ug=Hs.387904 /len=396 | R41424 | Hs.387904 | |
| 13227 | 0.028082 | cysteine dioxygenase, type I (CDO1), mRNA /cds=(255,857) /gb=NM_001801 /gi=4502754 /ug=Hs.3229 /len=1556 | NM_001801 | Hs.3229 | NP_001792 |
| 13233 | 0.002453 | synovial sarcoma translocation gene on chromosome 18-like 2 (SS18L2), mRNA /cds=(99,332) /gb=NM_016305 /gi=10047103 /ug=Hs.9774 /len=817 | NM_016305 | Hs.9774 | NP_057389 |
| 13291 | 0.014175 | actin related protein 2/3 complex, subunit 5, 16kDa (ARPC5), mRNA /cds=(192,647) /gb=NM_005717 /gi=23238212 /ug=Hs.82425 /len=2000 | NM_005717 | Hs.82425 | NP_005708 |
| 13304 | 0.010202 | wl27d01.x1 NCI_CGAP_Ut1 cDNA clone IMAGE:2426113 3', mRNA sequence /clone=IMAGE:2426113 /clone_end=3' /gb=AI866216 /gi=5530323 /ug=Hs.413738 /len=133 | AI866216 | Hs.413738 | |
| 13305 | 0.03016 | apoptosis inhibitor 5 (API5), mRNA /cds=(133,1647) /gb=NM_006595 /gi=5729729 /ug=Hs.227913 /len=3739 | NM_006595 | Hs.227913 | NP_006586 |
| 13309 | 0.014175 | nuclear receptor subfamily 3, group C, member 2 (NR3C2), mRNA /cds=(217,3171) /gb=NM_000901 /gi=4505198 /ug=Hs.1790 /len=5749 | NM_000901 | Hs.1790 | NP_000892 |
| 13316 | 0.039781 | ring finger protein 19 (RNF19), mRNA /cds=(318,2834) /gb=NM_015435 /gi=19923421 /ug=Hs.48320 /len=4357 | NM_015435 | Hs.48320 | NP_056250 |
| 13319 | 0.007887 | cDNA FLJ33540 fis, clone BRAMY2007613. /gb=AK090859 /gi=21749098 /ug=Hs.21213 /len=2030 | AK090859 | Hs.21213 | |
| 13330 | 0.008602 | bridging integrator 2 (BIN2), mRNA /cds=(39,1736) /gb=NM_016293 /gi=7706486 /ug=Hs.14770 /len=2206 | NM_016293 | Hs.14770 | NP_057377 |
| 13335 | 0.004165 | hypothetical protein FLJ12118 (FLJ12118), mRNA /cds=(24,1718) /gb=NM_024537 /gi=13375694 /ug=Hs.381043 /len=1843 | NM_024537 | Hs.381043 | NP_078813 |

| Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension | | | | | |
|--|----------|---|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 13339 | 0.022547 | mRNA for KIAA1133 protein, partial cds. /cds=(1,2676) /gb=AB051436 /gi=13195720 /ug=Hs.318584 /len=6542 | AB051436 | Hs.318584 | |
| 13388 | 0.014175 | fos-related antigen DNA, exon 4 | X98050 | | |
| 13391 | 0.045456 | chondroitin sulfate GalNAcT-2 (GALNACT-2), mRNA /cds=(336,1964) /gb=NM_018590 /gi=24429591 /ug=Hs.180758 /len=3745 | NM_018590 | Hs.180758 | NP_061060 |
| 13425 | 0.02428 | EST(wk79e07.x1 NCI_CGAP_Pan1 clone IMAGE:2421636 3') | AI813780 | | |
| 13457 | 0.045456 | translin (TSN), mRNA /cds=(236,922) /gb=NM_004622 /gi=20302160 /ug=Hs.75066 /len=3408 | NM_004622 | Hs.75066 | NP_004613 |
| 13459 | 0.005026 | N-ethylmaleimide-sensitive factor (NSF), mRNA /cds=(61,2295) /gb=NM_006178 /gi=11079227 /ug=Hs.108802 /len=3960 | NM_006178 | Hs.108802 | NP_006169 |
| 13467 | 0.006047 | EST(zf04d06.r1 NCI_CGAP_GCB1 clone IMAGE:712139 5') | AA280235 | | NP_005728 |
| 13469 | 0.02428 | clone IMAGE:5299642, mRNA /gb=BC041913 /gi=27469540 /ug=Hs.17132 /len=2227 | BC041913 | Hs.17132 | |
| 13507 | 0.020917 | ho25d05.x1 NCI_CGAP_Co14 cDNA clone IMAGE:3038409 3', mRNA sequence /clone=IMAGE:3038409 /clone_end=3' /gb=BE042545 /gi=8359683 /ug=Hs.276275 /len=448 | BE042545 | Hs.276275 | |
| 13520 | 0.005026 | EST(tz32c11.x1 NCI_CGAP_Ut2 clone IMAGE:2290292 3') | AI631079 | | NP_079436 |
| 13523 | 0.02428 | UI-H-DIO-auw-o-12-0-UI.s1 NCI_CGAP_DIO cDNA clone IMAGE:5875427 3', mRNA sequence /clone=IMAGE:5875427 /clone_end=3' /gb=BM997944 /gi=19722845 /ug=Hs.444026 /len=753 | BM997944 | Hs.444026 | |
| 13577 | 0.019388 | DKFZP586L2024 protein (NESHBP), mRNA /cds=(364,1824) /gb=NM_015429 /gi=14149685 /ug=Hs.58419 /len=3023 | NM_015429 | Hs.58419 | NP_056244 |
| 13599 | 0.03016 | mRNA; cDNA DKFZp313E1012 (from clone DKFZp313E1012) /gb=AL832661 /gi=21733237 /ug=Hs.94694 /len=3233 | AL832661 | Hs.94694 | |
| 13601 | 0.002549 | similar to rat myomegalin (LOC64182), mRNA /cds=(336,1268) /gb=NM_022359 /gi=21314705 /ug=Hs.333512 /len=1717 | NM_022359 | Hs.333512 | NP_071754 |
| 13602 | 4.81E-04 | UI-1-BC1p-asi-a-02-0-UI.s1 NCI_CGAP_PI3 cDNA clone UI-1-BC1p-asi-a-02-0-UI 3', mRNA sequence /clone=UI-1-BC1p-asi-a-02-0-UI /clone_end=3' /gb=BQ011545 /gi=19736446 /ug=Hs.361171 /len=1143 | BQ011545 | Hs.361171 | |

| Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension | | | | | |
|--|----------|---|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 13619 | 0.045456 | FLJ30633 fis, clone CTONG2002418, weakly similar to Homo sapiens scaffold attachment factor B (SAF-B) mRNA (AK055195.1) | AK055195 | Hs.331328 | NP_079031 |
| 13642 | 0.045456 | calpastatin (CAST), transcript variant 2, mRNA /cds=(155,2215) /gb=NM_173060 /gi=27765084 /ug=Hs.359682 /len=4296 | NM_173060 | Hs.359682 | NP_775085 |
| 13670 | 0.009373 | hypothetical protein FLJ11506 (FLJ11506), mRNA /cds=(16,963) /gb=NM_024666 /gi=20070334 /ug=Hs.77703 /len=2774 | NM_024666 | Hs.77703 | NP_078942 |
| 13702 | 0.02428 | mRNA for KIAA0551 protein, partial cds. /cds=(192,4349) /gb=AB011123 /gi=20521082 /ug=Hs.170204 /len=5727 | AB011123 | Hs.170204 | |
| 13713 | 0.022547 | heterogeneous nuclear ribonucleoprotein H2 (H') (HNRPH2), mRNA /cds=(79,1428) /gb=NM_019597 /gi=14141155 /ug=Hs.278857 /len=2220 | NM_019597 | Hs.278857 | NP_062543 |
| 13716 | 0.03016 | chromosome 15 open reading frame 12 (C15orf12), nuclear gene encoding mitochondrial protein, mRNA /cds=(48,602) /gb=NM_018285 /gi=8922793 /ug=Hs.6118 /len=1115 | NM_018285 | Hs.6118 | NP_060755 |
| 13747 | 0.022547 | hypothetical protein MGC23401 (MGC23401), mRNA /cds=(258,1334) /gb=NM_144982 /gi=21450672 /ug=Hs.245383 /len=1510 | NM_144982 | Hs.245383 | NP_659419 |
| 13750 | 0.022547 | heterogeneous nuclear ribonucleoprotein D like (HNRPDL), transcript variant 1, mRNA /cds=(581,1843) /gb=NM_005463 /gi=14110410 /ug=Hs.372673 /len=3514 | NM_005463 | Hs.372673 | NP_112740 |
| 13751 | 0.037168 | hypothetical protein MGC17330 (MGC17330), mRNA /cds=(148,939) /gb=NM_052880 /gi=16418388 /ug=Hs.26670 /len=2427 | NM_052880 | Hs.26670 | NP_443112 |
| 13755 | 0.039781 | cyclin H (CCNH), mRNA /cds=(233,1204) /gb=NM_001239 /gi=17738313 /ug=Hs.514 /len=1398 | NM_001239 | Hs.514 | NP_001230 |
| 13768 | 0.018499 | likely ortholog of mouse hypoxia induced gene 1 (HIG1), mRNA /cds=(93,374) /gb=NM_014056 /gi=7661619 /ug=Hs.7917 /len=1362 | NM_014056 | Hs.7917 | NP_054775 |
| 13786 | 0.019388 | mitochondrion, complete genome | NC_001807 | | |
| 13797 | 0.02428 | 603041572T1 NIH_MGC_116 cDNA clone IMAGE:5163112 3', mRNA sequence /clone=IMAGE:5163112 /clone_end=3' /gb=BI517954 /gi=15342746 /ug=Hs.398211 /len=964 | BI517954 | Hs.398211 | |

| Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension | | | | | |
|--|----------|---|--------------------|-----------------------|-----------------------|
| Spot | p-value | D scription | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 13807 | 0.026124 | solute carrier family 16 (monocarboxylic acid transporters), member 1 (SLC16A1), mRNA /cds=(194,1696) /gb=NM_003051 /gi=19923752 /ug=Hs.75231 /len=3410 | NM_003051 | Hs.75231 | NP_003042 |
| 13826 | 0.032363 | C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 12 (CLECSF12), mRNA /cds=(72,677) /gb=NM_022570 /gi=13384603 /ug=Hs.161786 /len=2354 | NM_022570 | Hs.161786 | NP_072092 |
| 13835 | 0.006608 | mRNA for KIAA1078 protein, partial cds. /cds=(1,4098) /gb=AB029001 /gi=20521755 /ug=Hs.23585 /len=6740 | AB029001 | Hs.23585 | |
| 13839 | 0.02428 | TEA domain family member 1 (SV40 transcriptional enhancer factor) mRNA; cDNA DKFZp434N1435 (from clone DKFZp434N1435) /cds=UNKNOWN /gb=AL133574 /gi=6599153 /ug=Hs.42458 /len=4459 | AL133574 | Hs.42458 | NP_068780 |
| 13844 | 0.01661 | zinc finger protein 11b (KOX 2) (ZNF11B), mRNA /cds=(116,2452) /gb=NM_006955 /gi=24307874 /ug=Hs.378077 /len=5958 | NM_006955 | Hs.378077 | NP_008886 |
| 13856 | 0.010202 | myeloid differentiation primary response gene (88) (MYD88), mRNA /cds=(40,930) /gb=NM_002468 /gi=19923143 /ug=Hs.82116 /len=2678 | NM_002468 | Hs.82116 | NP_002459 |
| 13927 | 0.029098 | df22c07.w1 Morton Fetal Cochlea cDNA clone IMAGE:2484085 3', mRNA sequence /clone=IMAGE:2484085 /clone_end=3' /gb=BI492292 /gi=15331636 /ug=Hs.379172 /len=359 | BI492292 | Hs.379172 | |
| 13932 | 0.041995 | EST(zr99b03.r1 NCI_CGAP_GCB1 clone IMAGE:683789 5') | AA236732 | | NP_690869 |
| 13935 | 0.01205 | CD68 antigen (CD68), mRNA /cds=(16,1080) /gb=NM_001251 /gi=4557434 /ug=Hs.246381 /len=1722 | NM_001251 | Hs.246381 | NP_001242 |
| 13950 | 0.048529 | hypothetical protein FLJ10330 (FLJ10330), mRNA /cds=(77,1717) /gb=NM_018061 /gi=8922357 /ug=Hs.342307 /len=3239 | NM_018061 | Hs.342307 | NP_060531 |
| 13961 | 0.03016 | Novel | SEQ.ID.No.90 | | |
| 13972 | 0.017954 | zo15e02.s1 Stratagene colon (#937204) cDNA clone IMAGE:586970 3' similar to contains Alu repetitive element;contains element PTR5 repetitive element ;, mRNA sequence /clone=IMAGE:586970 /clone_end=3' /gb=AA130992 /gi=1692483 /ug=Hs.426360 /len=489 | AA130992 | Hs.426360 | |

| Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension | | | | | |
|--|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 13986 | 0.039781 | phosphodiesterase 6D, cGMP-specific, rod, delta (PDE6D), mRNA /cds=(151,603) /gb=NM_002601 /gi=4505670 /ug=Hs.48291 /len=1131 | NM_002601 | Hs.48291 | NP_002592 |
| 14085 | 0.02428 | EST (np87f03.s1 NCI_CGAP_Thy1 IMAGE:1133309) | AA632677 | | |
| 14092 | 0.026124 | hypothetical protein DKFZp434K1421 (DKFZP434K1421), mRNA /cds=(29,1705) /gb=NM_032141 /gi=14149806 /ug=Hs.374609 /len=2547 | NM_032141 | Hs.374609 | NP_115517 |
| 14094 | 0.028082 | EST (wh67d04.x1 NCI_CGAP_Kid11 IMAGE:2385799 3') | AI766049 | | |
| 14132 | 0.010202 | EST (ie64h03.x1 Homo sapiens cDNA, 3' end/clone_end=3' /gb=BI963813 /gi=16338218 /ug=Hs.349015/len=555) | BI963813 | Hs.349015 | NP_116159 |
| 14175 | 0.013076 | ribosomal protein, large, P1 (RPLP1), mRNA /cds=(130,474) /gb=NM_001003 /gi=16905511 /ug=Hs.424299 /len=512 | NM_001003 | Hs.424299 | NP_000994 |
| 14209 | 0.034698 | BX109160 Soares_NhHMPu_S1 cDNA clone IMAGp998H024744, mRNA sequence /clone=IMAGp998H024744, IMAGE:1933489 /gb=BX109160 /gi=27877586 /ug=Hs.308982 /len=483 | BX109160 | Hs.308982 | |
| 14243 | 0.007223 | cDNA FLJ36574 fis, clone TRACH2012376. /gb=AK093893 /gi=21752845 /ug=Hs.356595 /len=1952 | AK093893 | Hs.356595 | |
| 14245 | 0.034698 | hypothetical protein FLJ32894 (FLJ32894), mRNA /cds=(50,550) /gb=NM_144667 /gi=21389550 /ug=Hs.350668 /len=1710 | NM_144667 | Hs.350668 | NP_653268 |
| 14255 | 0.032363 | EST wt25d05.x1 NCI_CGAP_Ut1 cDNA clone IMAGE:2508489 3' similar to contains Alu repetitive element; contains L1.t1 L1 repetitive element; | AI962961 | | |
| 14288 | 0.013076 | small acidic protein (SMAP), mRNA /cds=(137,688) /gb=NM_014267 /gi=20070245 /ug=Hs.78050 /len=1504 | NM_014267 | Hs.78050 | NP_055082 |
| 14289 | 0.003316 | clone DJ0798C17, complete sequence | AC004889 | | |
| 14291 | 0.020917 | calmodulin 2 (phosphorylase kinase, delta) (CALM2), mRNA /cds=(69,518) /gb=NM_001743 /gi=20428653 /ug=Hs.425808 /len=1128 | NM_001743 | Hs.425808 | NP_001734 |
| 14304 | 0.019388 | cDNA: FLJ23111 fis, clone LNG07835. /gb=AK026764 /gi=10439690 /ug=Hs.268231 /len=2263 | AK026764 | Hs.268231 | |

| Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension | | | | | |
|--|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 14363 | 0.037168 | ESTs, cDNA, 3' end /clone=IMAGE:2355101 /clone_end=3' /gb=AI719659 /gi=5036915 /ug=Hs.372094 /len=528 | AI719659 | Hs.372094 | |
| 14375 | 0.034482 | ESTs, cDNA, 3' end /clone=IMAGE:2402646 /clone_end=3' /gb=AI768858 /gi=5235367 /ug=Hs.157149 /len=562 | AI768858 | Hs.157149 | NP_066012 |
| 14386 | 0.007887 | UI-E-EJ0-aik-i-20-0-UI.r1 UI-E-EJ0 cDNA clone UI-E-EJ0-aik-i-20-0-UI 5', mRNA sequence /clone=UI-E-EJ0-aik-i-20-0-UI /clone_end=5' /gb=BM727413 /gi=19048746 /ug=Hs.112619 /len=1667 | BM727413 | Hs.112619 | |
| 14387 | 0.013076 | likely ortholog of rat V-1 protein (V-1), mRNA /cds=(229,585) /gb=NM_145808 /gi=21956644 /ug=Hs.21321 /len=3770 | NM_145808 | Hs.21321 | NP_665807 |
| 14452 | 0.028082 | No significant match | SEQ.ID.No.35 | | |
| 14453 | 0.048529 | No significant match, ORF+1(16~273) | SEQ.ID.No.41 | | |
| 14455 | 0.001216 | No significant match, ORF+3(135~404) | SEQ.ID.No.50 | | |
| 14475 | 0.005512 | EST, cDNA: FLJ23266 fis, clone COL06676, highly similar to HUMFRCC Homo sapiens clone s153 mRNA | AK026919 | | |
| 14524 | 0.026124 | EST (wa75f06.x1 Soares NFL T GBC S1 | AI685268 | | |
| 14528 | 0.028082 | EST (EST34421 Embryo, 6 week l cDNA 5' end similar to EST containing L1 repeat) | AA330691 | | |
| 14561 | 0.042541 | mRNA; cDNA DKFZp451B1818 (from clone DKFZp451B1818) /gb=AL832623 /gi=21733198 /ug=Hs.77554 /len=6240 | AL832623 | Hs.77554 | |
| 14600 | 0.022547 | hypothetical gene supported by AY007122 (LOC92719) | XM_046853 | | |
| 14635 | 0.008602 | hypothetical protein DKFZp434G1415 (DKFZP434G1415), mRNA /cds=(35,2140) /gb=NM_031292 /gi=13775209 /ug=Hs.151093 /len=3495 | NM_031292 | Hs.151093 | NP_112582 |
| 14637 | 0.048529 | hypothetical protein PRO1331 (PRO1331), mRNA /cds=(423,617) /gb=NM_030778 /gi=13562115 /ug=Hs.301824 /len=1634 | NM_030778 | Hs.301824 | NP_110405 |
| 14690 | 0.006608 | cDNA FLJ35033 fis, clone OCBBF2016590, weakly similar to CELL SURFACE ANTIGEN 114/A10 PRECURSOR. /cds=(407,934) /gb=AK092352 /gi=21750925 /ug=Hs.156113 /len=2884 | AK092352 | Hs.156113 | |
| 14798 | 0.039781 | EST(cDNA clone IMAGE:4731577 5') | BG621355 | | NP_002700 |

| Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension | | | | | |
|--|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 14808 | 0.045456 | ESTs, cDNA, 5' end /clone=IMAGE:3055219 /clone_end=5' /gb=AW402596 /gi=6921298 /ug=Hs.103296 /len=593 | AW402596 | Hs.103296 | NP_775767 |
| 14833 | 0.019388 | EST380251 MAGE resequences, MAGJ cDNA, mRNA sequence /gb=AW968281 /gi=8158016 /ug=Hs.319460 /len=689 | AW968281 | Hs.319460 | |
| 14842 | 0.017954 | mitochondrion, complete genome | NC_001807 | | |
| 14934 | 0.014175 | No significant match (ORF:+1:1~102[102]) | SEQ.ID.No.59 | | |

| TABLE 3B | | | | | |
|---|----------|--|--------------------|-----------------------|-----------------------|
| Genes Corresponding to Differentially Expressed Genes in Figure 9 - Obesity | | | | | |
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 1 | 0.041454 | vacuolar protein sorting 28 (yeast) (VPS28), mRNA /cds=(62,727) /gb=NM_016208 /gi=7705884 /ug=Hs.339697 /len=928 | NM_016208 | Hs.339697 | NP_057292 |
| 214 | 0.02042 | neuronal thread protein AD7c-NTP | NP_055301 | | |
| 257 | 0.005038 | KIAA0301 gene, partial cds | AB002299 | | NP_055426 |
| 288 | 0.002317 | phosphodiesterase 8B (PDE8B), mRNA /cds=(46,2703) /gb=NM_003719 /gi=26006850 /ug=Hs.78106 /len=3567 | NM_003719 | Hs.78106 | NP_003710 |
| 298 | 0.025168 | KIAA0429 gene product (KIAA0429), mRNA /cds=(2374,3444) /gb=NM_014751 /gi=7662113 /ug=Hs.77694 /len=5645 | NM_014751 | Hs.77694 | NP_055566 |
| 323 | 0.005852 | associated molecule with the SH3 domain of STAM (AMSH), mRNA /cds=(188,1462) /gb=NM_006463 /gi=17738303 /ug=Hs.12479 /len=2107 | NM_006463 | Hs.12479 | NP_006454 |
| 357 | 0.007162 | deleted in pancreatic carcinoma (DPC4) gene, exon 3 | AF045440 | | |
| 383 | 0.031506 | zinc finger protein 223 (ZNF223), mRNA /cds=(239,1687) /gb=NM_013361 /gi=7019588 /ug=Hs.279782 /len=2033 | NM_013361 | Hs.279782 | NP_037493 |
| 423 | 0.012975 | biotinidase (BTD), mRNA /cds=(36,1667) /gb=NM_000060 /gi=4557372 /ug=Hs.78885 /len=2016 | NM_000060 | Hs.78885 | NP_000051 |
| 429 | 0.026411 | NPD009 protein (NPD009), mRNA /cds=(1327,1677) /gb=NM_020686 /gi=24476005 /ug=Hs.283675 /len=2514 | NM_020686 | Hs.283675 | NP_065737 |
| 434 | 0.012537 | phosphoglycerate kinase 1 (PGK1), mRNA /cds=(70,1323) /gb=NM_000291 /gi=22095338 /ug=Hs.78771 /len=2338 | NM_000291 | Hs.78771 | NP_000282 |
| 450 | 0.028189 | nuclear factor NF-IL6 | X52560 | | |
| 453 | 0.012175 | WD repeat domain 1 (WDR1), transcript variant 1, mRNA /cds=(203,2023) /gb=NM_017491 /gi=17105397 /ug=Hs.85100 /len=3079 | NM_017491 | Hs.85100 | NP_059830 |
| 477 | 0.034563 | microfibrillar-associated protein 4 (MFAP4), mRNA /cds=(26,793) /gb=NM_002404 /gi=23111004 /ug=Hs.296049 /len=1830 | NM_002404 | Hs.296049 | NP_002395 |
| 512 | 0.001459 | myosin IXB (MYO9B), mRNA /cds=(1,6069) /gb=NM_004145 /gi=4758749 /ug=Hs.159629 /len=6069 | NM_004145 | Hs.159629 | NP_004136 |
| 565 | 0.022932 | topoisomerase (DNA) III alpha (TOP3A), mRNA /cds=(230,3235) /gb=NM_004618 /gi=20143947 /ug=Hs.91175 /len=3807 | NM_004618 | Hs.91175 | NP_004609 |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|------|----------|--|--------------------|-----------------------|-----------------------|
| 579 | 0.046542 | Rad50-interacting protein 1 (FLJ11785), mRNA /cds=(24,2489) /gb=NM_021930 /gi=19923579 /ug=Hs.44625 /len=2855 | NM_021930 | Hs.44625 | NP_068749 |
| 584 | 0.036865 | isocitrate dehydrogenase 1 (NADP), soluble (IDH1), mRNA /cds=(235,1479) /gb=NM_005896 /gi=28178824 /ug=Hs.11223 /len=2339 | NM_005896 | Hs.11223 | NP_005887 |
| 589 | 0.037157 | AGENCOURT_6640990 NIH_MGC_68 cDNA clone IMAGE:5735856 5', mRNA sequence /clone=IMAGE:5735856 /clone_end=5' /gb=BM907553 /gi=19357932 /ug=Hs.424427 /len=645 | BM907553 | Hs.424427 | |
| 613 | 0.047341 | PEF protein with a long N-terminal hydrophobic domain (peflin) (PEF), mRNA /cds=(13,867) /gb=NM_012392 /gi=6912581 /ug=Hs.241531 /len=1641 | NM_012392 | Hs.241531 | NP_036524 |
| 615 | 0.041872 | cDNA FLJ11904 fis, clone HEMBB1000048. /gb=AK021966 /gi=10433275 /ug=Hs.285519 /len=2134 | AK021966 | Hs.285519 | |
| 617 | 0.049654 | solute carrier family 2 (facilitated glucose transporter), member 10 (SLC2A10), mRNA /cds=(251,1876) /gb=NM_030777 /gi=21361923 /ug=Hs.305971 /len=4396 | NM_030777 | Hs.305971 | NP_110404 |
| 625 | 0.005892 | fragile X mental retardation 1 (FMR1), mRNA /cds=(220,2118) /gb=NM_002024 /gi=4503764 /ug=Hs.89764 /len=4362 | NM_002024 | Hs.89764 | NP_002015 |
| 627 | 0.017523 | methionine-tRNA synthetase (MARS), mRNA /cds=(24,2726) /gb=NM_004990 /gi=14043021 /ug=Hs.279946 /len=2795 | NM_004990 | Hs.279946 | NP_004981 |
| 634 | 0.020686 | mitofusin 1 (MFN1), transcript variant 1, mRNA /cds=(84,2309) /gb=NM_033540 /gi=16117784 /ug=Hs.197877 /len=3275 | NM_033540 | Hs.197877 | NP_284941 |
| 652 | 0.01004 | cDNA FLJ38331 fis, clone FCBBF3025285, moderately similar to Mus musculus peripheral benzodiazepine receptor associated protein (Pap7) mRNA. /gb=AK095650 /gi=21754954 /ug=Hs.9052 /len=3547 | AK095650 | Hs.9052 | |
| 657 | 0.00593 | FLJ30577 fis, clone BRAWH2006760 /cds=UNKNOWN /gb=AK055139 /gi=16549803 /ug=Hs.324815 /len=2353 | AK055139 | Hs.324815 | |
| 658 | 0.029283 | KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3 (KDEL3), transcript variant 1, mRNA /cds=(157,801) /gb=NM_006855 /gi=8051612 /ug=Hs.250696 /len=1705 | NM_006855 | Hs.250696 | NP_057839 |

| Spot | p-value | D scription | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|------|----------|--|--------------------|-----------------------|-----------------------|
| 662 | 0.005051 | insulin-like growth factor binding protein 5 (IGFBP5), mRNA /cds=(752,1570) /gb=NM_000599 /gi=10834981 /ug=Hs.380833 /len=1722 | NM_000599 | Hs.380833 | NP_000590 |
| 668 | 0.035062 | KIAA0391 gene product (KIAA0391), mRNA /cds=(360,2063) /gb=NM_014672 /gi=7662093 /ug=Hs.154668 /len=5677 | NM_014672 | Hs.154668 | NP_055487 |
| 670 | 0.036456 | cytidine deaminase (CDA), mRNA /cds=(118,558) /gb=NM_001785 /gi=11386156 /ug=Hs.72924 /len=892 | NM_001785 | Hs.72924 | NP_001776 |
| 691 | 0.014281 | U5 snRNP-specific protein, 200-KD (U5-200KD), mRNA /cds=(189,5624) /gb=NM_014014 /gi=24307974 /ug=Hs.246112 /len=5898 | NM_014014 | Hs.246112 | NP_054733 |
| 693 | 9.54E-04 | ubiquitin-conjugating enzyme E2L 3 (UBE2L3), mRNA /cds=(16,480) /gb=NM_003347 /gi=4507788 /ug=Hs.108104 /len=2845 | NM_003347 | Hs.108104 | NP_003338 |
| 697 | 0.044049 | interferon, alpha-inducible protein (clone IFI-6-16) (G1P3), transcript variant 3, mRNA /cds=(108,524) /gb=NM_022873 /gi=13259549 /ug=Hs.265827 /len=841 | NM_022873 | Hs.265827 | NP_075011 |
| 721 | 9.54E-04 | mitochondrion, complete genome | NC_001807 | | |
| 726 | 1.64E-04 | tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide (YWHAG), mRNA /cds=(192,935) /gb=NM_012479 /gi=21464100 /ug=Hs.25001 /len=3747 | NM_012479 | Hs.25001 | NP_036611 |
| 772 | 0.001525 | acid sphingomyelinase (ASM) gene, exons a, and alternative a (3' end), b and c (5' end). | M59917 | | |
| 787 | 0.008356 | cargo selection protein (mannose 6 phosphate receptor binding protein) (TIP47), mRNA /cds=(67,1371) /gb=NM_005817 /gi=20127485 /ug=Hs.140452 /len=2239 | NM_005817 | Hs.140452 | NP_005808 |
| 793 | 0.012175 | glyoxalase I (GLO1), mRNA /cds=(88,642) /gb=NM_006708 /gi=5729841 /ug=Hs.75207 /len=1993 | NM_006708 | Hs.75207 | NP_006699 |
| 794 | 0.004048 | zn87g06.x5 Stratagene lung carcinoma 937218 cDNA clone IMAGE:565210 3' similar to contains Alu repetitive element;contains element MER22 repetitive element ;, mRNA sequence /clone=IMAGE:565210 /clone_end=3' /gb=AI732466 /gi=5053579 /ug=Hs.193133 /len=526 | AI732466 | Hs.193133 | |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|------|----------|--|--------------------|-----------------------|-----------------------|
| 807 | 0.017281 | KIAA0102 gene product (KIAA0102), mRNA /cds=(308,679) /gb=NM_014752 /gi=7661907 /ug=Hs.77665 /len=1370 | NM_014752 | Hs.77665 | NP_055567 |
| 808 | 0.005051 | PIX1 mRNA (ORF) | AF037219 | | NP_570854 |
| 809 | 0.003193 | methylcrotonoyl-Coenzyme A carboxylase 1 (alpha) (MCCC1), mRNA /cds=(133,2310) /gb=NM_020166 /gi=13518227 /ug=Hs.47649 /len=2528 | NM_020166 | Hs.47649 | NP_064551 |
| 831 | 0.039115 | Microfibril-associated glycoprotein-2 (MAGP2), mRNA /cds=(214,735) /gb=NM_003480 /gi=4505088 /ug=Hs.300946 /len=1119 | NM_003480 | Hs.300946 | NP_003471 |
| 837 | 0.007261 | serine/arginine repetitive matrix 2 (SRRM2), mRNA /cds=(226,8484) /gb=NM_016333 /gi=19923465 /ug=Hs.197114 /len=9027 | NM_016333 | Hs.197114 | NP_057417 |
| 847 | 0.037157 | peroxisomal biogenesis factor 3 (PEX3), mRNA /cds=(64,1185) /gb=NM_003630 /gi=4505726 /ug=Hs.7277 /len=1979 | NM_003630 | Hs.7277 | NP_003621 |
| 851 | 6.22E-04 | of89c05.s1 NCI_CGAP_Li5 cDNA clone IMAGE:1437512 3' similar to contains Alu repetitive element; mRNA sequence /clone=IMAGE:1437512 /clone_end=3' /gb=AA894384 /gi=3030785 /ug=Hs.432123 /len=296 | AA894384 | Hs.432123 | |
| 865 | 0.001133 | mitochondrion, complete genome | NC_001807 | | |
| 877 | 0.006234 | ring finger protein 11 (RNF11), mRNA /cds=(128,592) /gb=NM_014372 /gi=7657519 /ug=Hs.96334 /len=2529 | NM_014372 | Hs.96334 | NP_055187 |
| 909 | 0.026411 | integral membrane protein Tmp21-l (p23) | AJ004913 | | NP_006818 |
| 918 | 0.001283 | AGENCOURT_6456859 NIH_MGC_92 cDNA clone IMAGE:5576908 5', mRNA sequence /clone=IMAGE:5576908 /clone_end=5' /gb=BM466169 /gi=18515211 /ug=Hs.439148 /len=1150 | BM466169 | Hs.439148 | |
| 921 | 0.012975 | mitochondrion, complete genome | NC_001807 | | |
| 923 | 0.013819 | eukaryotic translation initiation factor 3, subunit 3 gamma, 40kDa (EIF3S3), mRNA /cds=(6,1064) /gb=NM_003756 /gi=4503514 /ug=Hs.58189 /len=1280 | NM_003756 | Hs.58189 | NP_003747 |
| 930 | 0.008208 | FK506 binding protein 9, 63 kDa (FKBP9), mRNA /cds=(457,885) /gb=NM_007270 /gi=24307926 /ug=Hs.302749 /len=2517 | NM_007270 | Hs.302749 | NP_009201 |
| 931 | 0.041454 | signal recognition particle 54kDa (SRP54), mRNA /cds=(225,1739) /gb=NM_003136 /gi=20149548 /ug=Hs.49346 /len=2164 | NM_003136 | Hs.49346 | NP_003127 |

| Spot | p-value | Description | Gen Accession No. | Unigene Accession No. | Protein Accession No. |
|------|----------|--|-------------------------|-----------------------------|-----------------------------|
| 943 | 0.004687 | XIST, coding sequence "a" mRNA (locus DXS399E). /gb=X56199 /gi=37987 /ug=Hs.352403 /len=1614 | X56199 | Hs.352403 | |
| 954 | 0.029809 | cell cycle progression 8 protein (CPR8), mRNA /cds=(13,1140) /gb=NM_004748 /gi=4758047 /ug=Hs.82506 /len=1856 | NM_004748 | Hs.82506 | NP_004739 |
| 980 | 0.033283 | cleavage and polyadenylation specific factor 6, 68kDa (CPSF6), mRNA /cds=(35,1690) /gb=NM_007007 /gi=5901927 /ug=Hs.64542 /len=3426 | NM_007007 | Hs.64542 | NP_008938 |
| 998 | 0.017682 | down-regulator of transcription 1, TBP-binding (negative cofactor 2) (DR1), mRNA /cds=(548,1078) /gb=NM_001938 /gi=4503380 /ug=Hs.16697 /len=1375 | NM_001938 | Hs.16697 | NP_001929 |
| 1001 | 0.031506 | RAD23 B (S. cerevisiae) (RAD23B), mRNA /cds=(352,1581) /gb=NM_002874 /gi=19924138 /ug=Hs.404283 /len=2943 | NM_002874 | Hs.404283 | NP_002865 |
| 1008 | 0.039257 | Alg5, S. cerevisiae, of (ALG5), mRNA /cds=(28,1002) /gb=NM_013338 /gi=9665250 /ug=Hs.227933 /len=1125 | NM_013338 | Hs.227933 | NP_037470 |
| 1015 | 0.013819 | actinin, alpha 1 (ACTN1), mRNA /cds=(184,2862) /gb=NM_001102 /gi=12025669 /ug=Hs.119000 /len=3398 | NM_001102 | Hs.119000 | NP_001093 |
| 1021 | 0.015649 | tumor necrosis factor, alpha-induced protein 3 (TNFAIP3), mRNA /cds=(67,2439) /gb=NM_006290 /gi=26051241 /ug=Hs.211600 /len=4446 | NM_006290 | Hs.211600 | NP_006281 |
| 1023 | 0.022422 | v-fos FBJ murine osteosarcoma viral oncogene (FOS), mRNA /cds=(156,1298) /gb=NM_005252 /gi=6552332 /ug=Hs.25647 /len=2084 | NM_005252 | Hs.25647 | NP_005243 |
| 1026 | 0.023762 | methionine adenosyltransferase II, beta (MAT2B), mRNA /cds=(73,1077) /gb=NM_013283 /gi=20127525 /ug=Hs.54642 /len=2054 | NM_013283 | Hs.54642 | NP_037415 |
| 1028 | 0.025168 | ATP synthase, H transporting, mitochondrial F1 complex, epsilon subunit (ATP5E), nuclear gene encoding mitochondrial protein, mRNA /cds=(95,250) /gb=NM_006886 /gi=21327678 /ug=Hs.177530 /len=417 | NM_006886 | Hs.177530 | NP_008817 |
| 1036 | 0.031506 | mRNA for KIAA1518 protein, partial cds. /cds=(482,3112) /gb=AB040951 /gi=7959302 /ug=Hs.284208 /len=5370 | AB040951 | Hs.284208 | NP_056308 |
| 1051 | 0.029809 | HSPC133 protein (HSPC133), mRNA /cds=(83,481) /gb=NM_014168 /gi=7661791 /ug=Hs.273063 /len=963 | NM_014168 | Hs.273063 | NP_054887 |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|------|----------|--|--------------------|-----------------------|-----------------------|
| 1080 | 0.026411 | Similar to RIKEN cDNA 4833424O15 gene, clone IMAGE:4793707, mRNA /gb=BC040174 /gi=25777829 /ug=Hs.312481 /len=3745 | BC040174 | Hs.312481 | |
| 1120 | 0.046149 | clone 25032 mRNA sequence /cds=UNKNOWN /gb=AF131764 /gi=4406586 /ug=Hs.13399 /len=1798 | AF131764 | Hs.13399 | NP_071919 |
| 1168 | 0.002566 | thymosin, beta 4, X chromosome (TMSB4X), mRNA /cds=(78,212) /gb=NM_021109 /gi=11056060 /ug=Hs.75968 /len=556 | NM_021109 | Hs.75968 | NP_066932 |
| 1170 | 0.017682 | myosin, light polypeptide 6, alkali, smooth muscle and non-muscle (MYL6), transcript variant 3, mRNA /cds=(41,514) /gb=NM_079425 /gi=17986263 /ug=Hs.77385 /len=717 | NM_079425 | Hs.77385 | NP_524149 |
| 1174 | 0.025168 | eukaryotic translation initiation factor 3, subunit 6 interacting protein (EIF3S6IP), mRNA /cds=(34,1728) /gb=NM_016091 /gi=7705432 /ug=Hs.119503 /len=1901 | NM_016091 | Hs.119503 | NP_057175 |
| 1189 | 0.00181 | mRNA; cDNA DKFZp451A142 (from clone DKFZp451A142) /cds=(39,1898) /gb=AL834245 /gi=21739785 /ug=Hs.124918 /len=4902 | AL834245 | Hs.124918 | |
| 1193 | 0.031405 | CGI-100 protein (CGI-100), mRNA /cds=(113,802) /gb=NM_016040 /gi=19923441 /ug=Hs.348996 /len=3635 | NM_016040 | Hs.348996 | NP_057124 |
| 1194 | 0.013385 | proteasome (prosome, macropain) subunit, alpha type, 5 (PSMA5), mRNA /cds=(86,811) /gb=NM_002790 /gi=23110941 /ug=Hs.76913 /len=1023 | NM_002790 | Hs.76913 | NP_002781 |
| 1236 | 0.037084 | matrix metalloproteinase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV collagenase) (MMP9), mRNA /cds=(20,2143) /gb=NM_004994 /gi=4826835 /ug=Hs.151738 /len=2334 | NM_004994 | Hs.151738 | NP_004985 |
| 1267 | 0.008955 | hypothetical protein DKFZp586K0717 (DKFZP586K0717), mRNA /cds=(168,1730) /gb=NM_030917 /gi=13569873 /ug=Hs.334812 /len=1914 | NM_030917 | Hs.334812 | NP_112179 |
| 1301 | 0.003233 | actin, beta (ACTB), mRNA /cds=(74,1201) /gb=NM_001101 /gi=5016088 /ug=Hs.426930 /len=1793 | NM_001101 | Hs.426930 | NP_001092 |
| 1305 | 0.037084 | cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA /cds=(90,281) /gb=NM_001867 /gi=18105039 /ug=Hs.430075 /len=448 | NM_001867 | Hs.430075 | NP_001858 |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|------|----------|---|--------------------|-----------------------|-----------------------|
| 1306 | 0.023762 | poly(A) binding protein, cytoplasmic 1 (PABPC1), mRNA /cds=(503,2404) /gb=NM_002568 /gi=4505574 /ug=Hs.172182 /len=2848 | NM_002568 | Hs.172182 | NP_002559 |
| 1343 | 0.033283 | hypothetical protein FLJ12438 (FLJ12438), mRNA /cds=(174,1340) /gb=NM_021933 /gi=11345471 /ug=Hs.8595 /len=1575 | NM_021933 | Hs.8595 | NP_068752 |
| 1349 | 0.009309 | mRNA; cDNA DKFZp313D2314 (from clone DKFZp313D2314) /gb=AL832057 /gi=21732598 /ug=Hs.3685 /len=3141 | AL832057 | Hs.3685 | |
| 1386 | 0.034454 | AGENCOURT_6424254 NIH_MGC_67 cDNA clone IMAGE:5491531 5', mRNA sequence /clone=IMAGE:5491531 /clone_end=5' /gb=BM479954 /gi=18528996 /ug=Hs.381243 /len=1112 | BM479954 | Hs.381243 | |
| 1418 | 0.013819 | voltage-dependent anion channel 2 (VDAC2), mRNA /cds=(63,947) /gb=NM_003375 /gi=4507880 /ug=Hs.78902 /len=1404 | NM_003375 | Hs.78902 | NP_003366 |
| 1419 | 0.017682 | CD74 antigen (invariant polypeptide of major histocompatibility complex, class II antigen-associated) (CD74), mRNA /cds=(8,706) /gb=NM_004355 /gi=10835070 /ug=Hs.84298 /len=1304 | NM_004355 | Hs.84298 | NP_004346 |
| 1431 | 0.011417 | inhibitor of growth family, member 1 (ING1), mRNA /cds=(433,1701) /gb=NM_005537 /gi=19923770 /ug=Hs.46700 /len=2886 | NM_005537 | Hs.46700 | NP_005528 |
| 1450 | 0.039115 | EST384321 MAGE resequences, MAGL cDNA, mRNA sequence /gb=AW972232 /gi=8162078 /ug=Hs.152375 /len=617 | AW972232 | Hs.152375 | |
| 1455 | 0.013385 | CDC5 cell division cycle 5-like (S. pombe) (CDC5L), mRNA /cds=(260,2668) /gb=NM_001253 /gi=16357499 /ug=Hs.155174 /len=3012 | NM_001253 | Hs.155174 | NP_001244 |
| 1467 | 0.037084 | SON DNA binding protein (SON), transcript variant e, mRNA /cds=(50,6376) /gb=NM_058183 /gi=21040317 /ug=Hs.92909 /len=8482 | NM_058183 | Hs.92909 | NP_620305 |
| 1469 | 0.016639 | potassium channel modulatory factor (PCMF), mRNA /cds=(54,1199) /gb=NM_020122 /gi=10047127 /ug=Hs.5392 /len=1595 | NM_020122 | Hs.5392 | NP_064507 |
| 1497 | 0.005439 | hypothetical protein MGC45474 (MGC45474), mRNA /cds=(218,2035) /gb=NM_152369 /gi=22748794 /ug=Hs.234101 /len=2384 | NM_152369 | Hs.234101 | |
| 1500 | 0.031405 | KIAA0824 (=PCF11p homolog) | AB020631 | | NP_056969 |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|------|----------|---|--------------------|-----------------------|-----------------------|
| 1535 | 0.004048 | mRNA for KIAA0752 protein, partial cds. /cds=(1,1006) /gb=AB018295 /gi=3882224 /ug=Hs.126779 /len=4332 | AB018295 | Hs.126779 | NP_775934 |
| 1539 | 0.00295 | LENG5 protein (LENG5), mRNA /cds=(113,1285) /gb=NM_024075 /gi=13129061 /ug=Hs.15580 /len=1364 | NM_024075 | Hs.15580 | NP_076980 |
| 1574 | 0.019933 | similar to triple functional domain (PTPRF interacting) (LOC115557), mRNA /cds=(331,1755) /gb=NM_133483 /gi=19311007 /ug=Hs.61581 /len=2166 | NM_133483 | Hs.61581 | NP_597840 |
| 1577 | 0.045762 | POM121 membrane glycoprotein (rat) (POM121), mRNA /cds=(978,3932) /gb=NM_172020 /gi=26051277 /ug=Hs.295112 /len=6014 | NM_172020 | Hs.295112 | NP_742017 |
| 1651 | 0.035141 | zinc finger protein 384 (ZNF384), mRNA /cds=(499,2229) /gb=NM_133476 /gi=20143968 /ug=Hs.103315 /len=3291 | NM_133476 | Hs.103315 | NP_597733 |
| 1665 | 0.026411 | eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA /cds=(63,1451) /gb=NM_001402 /gi=25453469 /ug=Hs.422118 /len=1837 | NM_001402 | Hs.422118 | NP_001393 |
| 1673 | 0.043451 | endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1 (HERPUD1), mRNA /cds=(96,1271) /gb=NM_014685 /gi=7661869 /ug=Hs.146393 /len=1884 | NM_014685 | Hs.146393 | NP_055500 |
| 1709 | 0.048172 | KIAA0399 | AB007859 | | NP_055928 |
| 1724 | 8.74E-04 | zinc finger RNA binding protein (ZFR), mRNA /cds=(44,1300) /gb=NM_016107 /gi=7706372 /ug=Hs.173518 /len=2734 | NM_016107 | Hs.173518 | NP_057191 |
| 1751 | 0.039257 | insulin induced protein 2 (LOC51141), mRNA /cds=(141,857) /gb=NM_016133 /gi=23821030 /ug=Hs.7089 /len=1358 | NM_016133 | Hs.7089 | NP_057217 |
| 1756 | 0.013819 | uronyl-2-sulfotransferase (UST), mRNA /cds=(104,1324) /gb=NM_005715 /gi=5032218 /ug=Hs.134015 /len=4196 | NM_005715 | Hs.134015 | NP_005706 |
| 1830 | 0.033283 | calmodulin-I (CALM1) mRNA, 3'UTR, partial sequence. /gb=U16850 /gi=576644 /ug=Hs.374441 /len=2383 | U16850 | Hs.374441 | |
| 1927 | 0.036435 | EST (tg16b07.x1 NCI CGAP CLL1 clone IMAGE:2108917 3' TR:Q14526 Q14526 HIC-1 GENE FRAGMENT) | A1391567 | | NP_006488 |
| 1974 | 0.045762 | CDC20 cell division cycle 20 (S. cerevisiae) (CDC20), mRNA /cds=(111,1610) /gb=NM_001255 /gi=4557436 /ug=Hs.82906 /len=1686 | NM_001255 | Hs.82906 | NP_001246 |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Prot. in Accession No. |
|------|----------|--|--------------------|-----------------------|------------------------|
| 1988 | 0.029809 | suppression of tumorigenicity 13 (colon carcinoma) (Hsp70 interacting protein) (ST13), mRNA /cds=(144,1253) /gb=NM_003932 /gi=21237722 /ug=Hs.119222 /len=3214 | NM_003932 | Hs.119222 | NP_003923 |
| 2033 | 0.012175 | calmodulin 1 (phosphorylase kinase, delta) (CALM1), mRNA /cds=(200,649) /gb=NM_006888 /gi=5901911 /ug=Hs.282410 /len=1526 | NM_006888 | Hs.282410 | NP_008819 |
| 2036 | 0.041237 | ATPase, H transporting, lysosomal 56/58kDa, V1 subunit B, isoform 2 (ATP6V1B2), mRNA /cds=(208,1743) /gb=NM_001693 /gi=19913427 /ug=Hs.1697 /len=3054 | NM_001693 | Hs.1697 | NP_001684 |
| 2041 | 0.048653 | ribosomal protein L32 (RPL32), mRNA /cds=(51,458) /gb=NM_000994 /gi=15812220 /ug=Hs.169793 /len=521 | NM_000994 | Hs.169793 | NP_000985 |
| 2073 | 0.002372 | transcription factor B1, mitochondrial (TFB1M), mRNA /cds=(73,1113) /gb=NM_016020 /gi=7705784 /ug=Hs.279908 /len=1290 | NM_016020 | Hs.279908 | NP_057104 |
| 2074 | 0.039115 | clusterin (complement lysis inhibitor, SP-40,40, sulfated glycoprotein 2, testosterone-repressed prostate message 2, apolipoprotein J) (CLU), mRNA /cds=(48,1397) /gb=NM_001831 /gi=4502904 /ug=Hs.75106 /len=1676 | NM_001831 | Hs.75106 | NP_001822 |
| 2077 | 0.019933 | musculus exoribonuclease 1 (Xrn1) | NM_011916 | | NP_036046 |
| 2105 | 0.041237 | potassium channel, subfamily K, member 1 (KCNK1), mRNA /cds=(183,1193) /gb=NM_002245 /gi=15451900 /ug=Hs.79351 /len=1901 | NM_002245 | Hs.79351 | NP_002236 |
| 2175 | 0.025168 | clone IMAGE:4799018, mRNA /gb=BC045722 /gi=28277129 /ug=Hs.153527 /len=2587 | BC045722 | Hs.153527 | |
| 2194 | 0.011417 | monocytic leukemia zinc finger protein-related factor (MORF), mRNA /cds=(316,6537) /gb=NM_012330 /gi=6912511 /ug=Hs.27590 /len=6537 | NM_012330 | Hs.27590 | NP_036462 |
| 2211 | 0.017682 | L-isoaspartyl/D-aspartyl O-methyltransferase (PCMT1) gene, exon 1, | U49740 | | |
| 2230 | 0.041237 | PMS1 postmeiotic segregation increased 1 (S. cerevisiae) (PMS1), mRNA /cds=(81,2879) /gb=NM_000534 /gi=11496979 /ug=Hs.111749 /len=3121 | NM_000534 | Hs.111749 | NP_000525 |
| 2231 | 0.026643 | TTN gene for titin | AJ277892 | | |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|------|----------|---|--------------------|-----------------------|-----------------------|
| 2242 | 0.031506 | uncharacterized hypothalamus protein HT010 (HT010), mRNA /cds=(227,1420) /gb=NM_018471 /gi=8923807 /ug=Hs.6375 /len=2140 | NM_018471 | Hs.6375 | NP_060941 |
| 2273 | 0.033283 | Pirin (PIR), mRNA /cds=(231,1103) /gb=NM_003662 /gi=4505822 /ug=Hs.424966 /len=1318 | NM_003662 | Hs.424966 | NP_003653 |
| 2303 | 0.035141 | cDNA FLJ13446 fis, clone PLACE1002968. /gb=AK023508 /gi=10435460 /ug=Hs.201925 /len=1712 | AK023508 | Hs.201925 | |
| 2307 | 0.002773 | matrilin 3 (MATN3) precursor, mRNA /cds=(64,1524) /gb=NM_002381 /gi=13518040 /ug=Hs.278461 /len=2599 | NM_002381 | Hs.278461 | NP_002372 |
| 2309 | 0.025168 | GTPase-activating protein GAP11 | U20238 | | NP_033051 |
| 2317 | 0.006234 | mRNA for KIAA0570 protein, partial cds. /cds=(480,10718) /gb=AB011142 /gi=20521084 /ug=Hs.180948 /len=11269 | AB011142 | Hs.180948 | |
| 2318 | 0.045762 | mRNA for KIAA0611 protein, partial cds. /cds=(1,2740) /gb=AB014511 /gi=3327035 /ug=Hs.406434 /len=7176 | AB014511 | Hs.406434 | |
| 2480 | 0.025168 | topoisomerase (DNA) I (TOP1), mRNA /cds=(247,2544) /gb=NM_003286 /gi=19913404 /ug=Hs.317 /len=3734 | NM_003286 | Hs.317 | NP_003277 |
| 2506 | 0.022422 | bHLH-PAS transcription factor MOP9 (MOP9) mRNA, long form, complete cds, alternatively spliced /cds=(58,1815) /gb=AF231338 /gi=7963663 /ug=Hs.222024 /len=2008 | AF231338 | Hs.222024 | NP_064568 |
| 2542 | 0.039115 | leucyl-tRNA synthetase (LARS), mRNA /cds=(73,3603) /gb=NM_020117 /gi=24496788 /ug=Hs.6762 /len=4248 | NM_020117 | Hs.6762 | NP_064502 |
| 2557 | 0.03939 | leucine-rich PPR-motif containing (LRPPRC), mRNA /cds=(46,3867) /gb=NM_133259 /gi=18959201 /ug=Hs.182490 /len=4782 | NM_133259 | Hs.182490 | NP_573566 |
| 2625 | 0.033283 | hypothetical protein (KIAA0714) | AB018257 | | |
| 2652 | 0.013819 | membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10) (MME), transcript variant 2b, mRNA /cds=(229,2481) /gb=NM_007289 /gi=6042203 /ug=Hs.1298 /len=5725 | NM_007289 | Hs.1298 | NP_009220 |
| 2678 | 0.010023 | protein-L-isoaspartate (D-aspartate) O-methyltransferase (PCMT1), mRNA /cds=(74,757) /gb=NM_005389 /gi=4885538 /ug=Hs.79137 /len=1599 | NM_005389 | Hs.79137 | NP_005380 |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|------|----------|--|--------------------------|-----------------------------|-----------------------------|
| 2687 | 0.019933 | v-fos FBJ murine osteosarcoma viral oncogene (FOS), mRNA /cds=(156,1298) /gb=NM_005252 /gi=6552332 /ug=Hs.25647 /len=2084 | NM_005252 | Hs.25647 | NP_005243 |
| 2713 | 0.033283 | caveolin-1/-2 locus, Contig1, D7S522, genes CAV2 CAV1 | AJ133269 | | |
| 2741 | 0.010023 | golgi SNAP receptor complex member 1 (GOSR1), mRNA /cds=(13,765) /gb=NM_004871 /gi=4758455 /ug=Hs.8868 /len=999 | NM_004871 | Hs.8868 | NP_004862 |
| 2743 | 0.039115 | clone MGC:9947 IMAGE:3876105, mRNA, complete cds /cds=(51,2216) /gb=BC013590 /gi=15488925 /ug=Hs.2437 /len=2651 | BC013590 | Hs.2437 | |
| 2745 | 0.035141 | calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced | AF223391 | | |
| 2779 | 0.009383 | nuclear factor (erythroid-derived 2)-like 2 (NFE2L2), mRNA /cds=(114,1931) /gb=NM_006164 /gi=20149575 /ug=Hs.155396 /len=2439 | NM_006164 | Hs.155396 | NP_006155 |
| 2782 | 0.005811 | high mobility group 2 protein (HMG-2) | M83665 | | |
| 2797 | 0.028189 | zinc finger homeobox 1b (ZFHX1B), mRNA /cds=(445,4089) /gb=NM_014795 /gi=7662183 /ug=Hs.34871 /len=5523 | NM_014795 | Hs.34871 | NP_055610 |
| 2815 | 0.006684 | proteasome (prosome, macropain) subunit, alpha type, 6 (PSMA6), mRNA /cds=(110,850) /gb=NM_002791 /gi=23110943 /ug=Hs.410276 /len=1035 | NM_002791 | Hs.410276 | NP_002782 |
| 2843 | 0.002372 | UI-E-EJ0-ahj-n-19-0-UI.r1 UI-E-EJ0 cDNA clone UI-E-EJ0-ahj-n-19-0-UI 5', mRNA sequence /clone=UI-E-EJ0-ahj-n-19-0-UI /clone_end=5' /gb=BM701108 /gi=19014366 /ug=Hs.401941 /len=1923 | BM701108 | Hs.401941 | |
| 2848 | 0.006234 | BJ-HCC-24 tumor antigen mRNA, complete cds /cds=(2,1240) /gb=AY121805 /gi=22002585 /ug=Hs.433489 /len=1488 | AY121805 | Hs.433489 | |
| 2849 | 0.008208 | chromosome 14 open reading frame 2 (C14orf2), mRNA /cds=(61,237) /gb=NM_004894 /gi=4758939 /ug=Hs.109052 /len=627 | NM_004894 | Hs.109052 | NP_004885 |
| 2850 | 0.009383 | helicase II (RAD54L) mRNA, complete cds. /cds=(54,4979) /gb=U09820 /gi=606832 /ug=Hs.96264 /len=6115 | U09820 | Hs.96264 | NP_612115 |
| 2870 | 0.029809 | threonyl-tRNA synthetase (TARS), mRNA /cds=(135,2270) /gb=NM_152295 /gi=25054078 /ug=Hs.84131 /len=2662 | NM_152295 | Hs.84131 | NP_689508 |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|------|----------|--|--------------------|-----------------------|-----------------------|
| 2875 | 0.043451 | deubiquitinating enzyme (UNPH4)= AF153604 ubiquitin-specific protease homolog (UPH) | AF106069 | | NP_006304 |
| 2884 | 0.035141 | mitochondrial ribosomal protein S30 (MRPS30), mRNA /cds=(39,1358) /gb=NM_016640 /gi=16950598 /ug=Hs.28555 /len=1482 | NM_016640 | Hs.28555 | NP_057724 |
| 2910 | 0.026643 | Sm protein F (LSM6), mRNA /cds=(82,324) /gb=NM_007080 /gi=5901997 /ug=Hs.42438 /len=596 | NM_007080 | Hs.42438 | NP_009011 |
| 2913 | 9.20E-05 | mortality factor 4 like 1 (MORF4L1), mRNA /cds=(132,1103) /gb=NM_006791 /gi=5803101 /ug=Hs.6353 /len=1766 | NM_006791 | Hs.6353 | NP_006782 |
| 2928 | 0.022422 | ligase IV, DNA, ATP-dependent (LIG4), mRNA /cds=(274,3009) /gb=NM_002312 /gi=23199992 /ug=Hs.166091 /len=3325 | NM_002312 | Hs.166091 | NP_002303 |
| 2947 | 0.011417 | hemoglobin, alpha 2 (HBA2), mRNA /cds=(38,466) /gb=NM_000517 /gi=14043068 /ug=Hs.347939 /len=575 | NM_000517 | Hs.347939 | NP_000508 |
| 2967 | 0.016639 | matrix metalloproteinase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase) (MMP2), mRNA /cds=(290,2272) /gb=NM_004530 /gi=11342665 /ug=Hs.111301 /len=3069 | NM_004530 | Hs.111301 | NP_004521 |
| 2990 | 0.033283 | cDNA FLJ31057 fis, clone HSYRA2000787. /gb=AK055619 /gi=16550395 /ug=Hs.296261 /len=2168 | AK055619 | Hs.296261 | |
| 3011 | 0.035141 | mitochondrion, complete genome | NC_001807 | | |
| 3029 | 0.022422 | Yip1p-interacting factor (YIF1P), mRNA /cds=(116,997) /gb=NM_020470 /gi=9994168 /ug=Hs.406422 /len=1078 | NM_020470 | Hs.406422 | NP_065203 |
| 3034 | 0.043451 | serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 6 (SERPINB6), mRNA /cds=(75,1205) /gb=NM_004568 /gi=28077084 /ug=Hs.41072 /len=1361 | NM_004568 | Hs.41072 | NP_004559 |
| 3038 | 0.043451 | golgi phosphoprotein 3 (coat-protein) (GOLPH3), mRNA /cds=(241,1137) /gb=NM_022130 /gi=20149665 /ug=Hs.18271 /len=2655 | NM_022130 | Hs.18271 | NP_071413 |
| 3062 | 0.006234 | myosin, light polypeptide, regulatory, non-sarcomeric (20kD) (MLCB), mRNA /cds=(115,630) /gb=NM_006471 /gi=5453739 /ug=Hs.180224 /len=944 | NM_006471 | Hs.180224 | NP_006462 |
| 3065 | 0.041237 | KIAA0433 protein (KIAA0433), mRNA /cds=(510,4241) /gb=NM_015216 /gi=7662117 /ug=Hs.26179 /len=5814 | NM_015216 | Hs.26179 | NP_056031 |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|------|----------|--|--------------------|-----------------------|-----------------------|
| 3070 | 0.041237 | signal sequence receptor, beta (translocon-associated protein beta) (SSR2), mRNA /cds=(51,602) /gb=NM_003145 /gi=6552341 /ug=Hs.74564 /len=1093 | NM_003145 | Hs.74564 | NP_003136 |
| 3071 | 0.006234 | endothelin receptor type A (EDNRA), mRNA /cds=(485,1768) /gb=NM_001957 /gi=4503464 /ug=Hs.76252 /len=4105 | NM_001957 | Hs.76252 | NP_001948 |
| 3072 | 0.017682 | trichorhinophalangeal syndrome I (TRPS1), mRNA /cds=(639,4484) /gb=NM_014112 /gi=7657658 /ug=Hs.26102 /len=10011 | NM_014112 | Hs.26102 | NP_054831 |
| 3073 | 0.003487 | KIAA0174 gene product (KIAA0174), mRNA /cds=(64,1158) /gb=NM_014761 /gi=7661971 /ug=Hs.75824 /len=2348 | NM_014761 | Hs.75824 | NP_055576 |
| 3076 | 0.033283 | hypothetical protein FLJ20707 (FLJ20707), mRNA /cds=(83,2173) /gb=NM_032560 /gi=19923643 /ug=Hs.334657 /len=2794 | NM_032560 | Hs.334657 | NP_115949 |
| 3108 | 0.011417 | glycogen synthase 1 (muscle) (GYS1), mRNA /cds=(161,2374) /gb=NM_002103 /gi=4504232 /ug=Hs.772 /len=3531 | NM_002103 | Hs.772 | NP_002094 |
| 3113 | 0.029809 | phosphodiesterase 4D interacting protein (myomegalin) (PDE4DIP), mRNA /cds=(658,4056) /gb=NM_014644 /gi=11036643 /ug=Hs.265848 /len=5676 | NM_014644 | Hs.265848 | NP_055459 |
| 3136 | 0.015649 | splicing factor, arginine/serine-rich 5 (SFRS5), mRNA /cds=(219,542) /gb=NM_006925 /gi=5902077 /ug=Hs.166975 /len=1865 | NM_006925 | Hs.166975 | NP_008856 |
| 3137 | 0.025168 | yp24c06.s1 Soares breast 3NbHBst cDNA clone IMAGE:188362 3' similar to gb:M10942_cds1 metallothionein-le gene mRNA sequence /clone=IMAGE:188362 /clone_end=3' /gb=H43642 /gi=919694 /ug=Hs.418241 /len=452 | H43642 | Hs.418241 | |
| 3138 | 0.001342 | NCAG1 (NCAG1), mRNA /cds=(1477,5145) /gb=NM_032160 /gi=23943786 /ug=Hs.124673 /len=9528 | NM_032160 | Hs.124673 | NP_115536 |
| 3139 | 0.045762 | mRNA for KIAA0530 protein, partial cds. /cds=(1,4693) /gb=AB011102 /gi=3043583 /ug=Hs.173081 /len=6578 | AB011102 | Hs.173081 | |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|------|----------|--|--------------------|-----------------------|-----------------------|
| 3140 | 0.037084 | DKFZp451H2115_r1 451 (synonym: hlcc1) spinal cord cDNA clone DKFZp451H2115 5', mRNA sequence /clone=DKFZp451H2115 /clone_end=5' /gb=AL589315 /gi=13243087 /ug=Hs.332004 /len=517 | AL589315 | Hs.332004 | |
| 3144 | 0.00104 | solute carrier family 20 (phosphate transporter), member 1 (SLC20A1), mRNA /cds=(371,2410) /gb=NM_005415 /gi=7382462 /ug=Hs.78452 /len=3220 | NM_005415 | Hs.78452 | NP_005406 |
| 3165 | 0.031506 | SOCS box-containing WD protein SWiP-1 (WSB1), transcript variant 3, mRNA /cds=(317,1051) /gb=NM_134264 /gi=20143909 /ug=Hs.187991 /len=4243 | NM_134264 | Hs.187991 | NP_599027 |
| 3166 | 0.037084 | hypothetical protein FLJ13855 (FLJ13855), mRNA /cds=(328,1068) /gb=NM_023079 /gi=20149671 /ug=Hs.168232 /len=3053 | NM_023079 | Hs.168232 | NP_075567 |
| 3172 | 0.006684 | myocyte-specific enhancer factor 2A (MEF2A) gene, last coding exon, and complete cds | U49020 | | |
| 3174 | 1.92E-04 | lectin, galactoside-binding, soluble, 1 (galectin 1) (LGALS1), mRNA /cds=(69,476) /gb=NM_002305 /gi=6006015 /ug=Hs.382367 /len=526 | NM_002305 | Hs.382367 | NP_002296 |
| 3175 | 0.018779 | spermidine/spermine N1-acetyltransferase (SAT), mRNA /cds=(166,681) /gb=NM_002970 /gi=4506788 /ug=Hs.28491 /len=1060 | NM_002970 | Hs.28491 | NP_002961 |
| 3180 | 0.045762 | ferritin, heavy polypeptide 1 (FTH1), mRNA /cds=(92,664) /gb=NM_002032 /gi=4503794 /ug=Hs.418650 /len=801 | NM_002032 | Hs.418650 | NP_002023 |
| 3191 | 0.045762 | hypothetical protein MGC14353 (MGC14353), mRNA /cds=(77,448) /gb=NM_032731 /gi=21362103 /ug=Hs.74346 /len=728 | NM_032731 | Hs.74346 | NP_116120 |
| 3219 | 4.63E-04 | actin, alpha, cardiac muscle (ACTC), mRNA /cds=(1,1134) /gb=NM_005159 /gi=10938011 /ug=Hs.118127 /len=1294 | NM_005159 | Hs.118127 | NP_005150 |
| 3233 | 0.002995 | uncharacterized hematopoietic stem/progenitor cells protein MDS027 (MDS027), mRNA /cds=(21,248) /gb=NM_018462 /gi=27544938 /ug=Hs.421654 /len=888 | NM_018462 | Hs.421654 | NP_060932 |
| 3244 | 0.024901 | hypothetical protein FLJ13352 (FLJ13352), mRNA /cds=(97,1053) /gb=NM_024592 /gi=13375784 /ug=Hs.22972 /len=2271 | NM_024592 | Hs.22972 | NP_078868 |

| Spot | p-value | Description | Gen Accession No. | Unigene Accession No. | Protein Accession No. |
|------|----------|---|-------------------------|-----------------------------|-----------------------------|
| 3254 | 0.035141 | splicing factor, arginine/serine-rich 2 (SFRS2), mRNA /cds=(156,821) /gb=NM_003016 /gi=4506898 /ug=Hs.73965 /len=1879 | NM_003016 | Hs.73965 | NP_003007 |
| 3280 | 0.010023 | RETROVIRUS-RELATED POLYPROTEIN | P11369 | | |
| 3288 | 0.005811 | cyclin G2 (CCNG2), mRNA /cds=(136,1170) /gb=NM_004354 /gi=4757935 /ug=Hs.79069 /len=2044 | NM_004354 | Hs.79069 | NP_004345 |
| 3294 | 0.035141 | NCK adaptor protein 1 (NCK1), mRNA /cds=(117,1250) /gb=NM_006153 /gi=20070226 /ug=Hs.54589 /len=1947 | NM_006153 | Hs.54589 | NP_006144 |
| 3316 | 0.003487 | glutathione S-transferase M3 (brain) (GSTM3), mRNA /cds=(311,988) /gb=NM_000849 /gi=23065551 /ug=Hs.2006 /len=1572 | NM_000849 | Hs.2006 | NP_000840 |
| 3318 | 0.019933 | endothelial protein C receptor | AB026584 | | |
| 3327 | 0.048172 | goliath protein (GP), mRNA /cds=(428,1258) /gb=NM_018434 /gi=20127393 /ug=Hs.155718 /len=1445 | NM_018434 | Hs.155718 | NP_060904 |
| 3328 | 0.029809 | retinoblastoma-like 2 (p130) (RBL2), mRNA /cds=(70,3489) /gb=NM_005611 /gi=21361291 /ug=Hs.79362 /len=4853 | NM_005611 | Hs.79362 | NP_005602 |
| 3354 | 0.005038 | ribosomal protein L23 (RPL23), mRNA /cds=(27,449) /gb=NM_000978 /gi=14591907 /ug=Hs.234518 /len=493 | NM_000978 | Hs.234518 | NP_000969 |
| 3390 | 0.041237 | phosphoribosyl pyrophosphate synthetase associated protein 2 (PRPSAP2), mRNA /cds=(212,1321) /gb=NM_002767 /gi=22538484 /ug=Hs.13339 /len=1890 | NM_002767 | Hs.13339 | NP_002758 |
| 3405 | 0.022422 | lectin, galactoside-binding, soluble, 1 (galectin 1) (LGALS1), mRNA /cds=(69,476) /gb=NM_002305 /gi=6006015 /ug=Hs.382367 /len=526 | NM_002305 | Hs.382367 | NP_002296 |
| 3428 | 0.026643 | excision repair cross-complementing rodent repair deficiency, complementation group 3 (xeroderma pigmentosum group B complementing) (ERCC3), mRNA /cds=(96,2444) /gb=NM_000122 /gi=4557562 /ug=Hs.77929 /len=2751 | NM_000122 | Hs.77929 | NP_000113 |
| 3440 | 0.00767 | TERF1 (TRF1)-interacting nuclear factor 2 (TINF2), mRNA /cds=(263,1327) /gb=NM_012461 /gi=6912715 /ug=Hs.7797 /len=2095 | NM_012461 | Hs.7797 | NP_036593 |
| 3461 | 0.025168 | ribosomal protein S3 (RPS3), mRNA /cds=(19,750) /gb=NM_001005 /gi=15718686 /ug=Hs.414990 /len=843 | NM_001005 | Hs.414990 | NP_000996 |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|------|----------|--|--------------------|-----------------------|-----------------------|
| 3512 | 0.043451 | eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA /cds=(63,1451) /gb=NM_001402 /gi=25453469 /ug=Hs.422118 /len=1837 | NM_001402 | Hs.422118 | NP_001393 |
| 3520 | 0.016639 | mRNA; cDNA DKFZp586F2423 (from clone DKFZp586F2423) /gb=AL080209 /gi=5262698 /ug=Hs.13659 /len=4254 | AL080209 | Hs.13659 | |
| 3538 | 0.035141 | insulin-like growth factor binding protein 6 (IGFBP6), mRNA /cds=(54,776) /gb=NM_002178 /gi=11321592 /ug=Hs.274313 /len=952 | NM_002178 | Hs.274313 | NP_002169 |
| 3539 | 0.037084 | ubiquitin C (UBC), mRNA /cds=(136,2193) /gb=NM_021009 /gi=20149305 /ug=Hs.183704 /len=2309 | NM_021009 | Hs.183704 | NP_066289 |
| 3548 | 0.011417 | eukaryotic translation initiation factor 3, subunit 6 48kDa (EIF3S6), mRNA /cds=(23,1360) /gb=NM_001568 /gi=4503520 /ug=Hs.106673 /len=1510 | NM_001568 | Hs.106673 | NP_001559 |
| 3567 | 0.045762 | FUS/TLS protein gene, alternatively spliced products, exons 1 through 15 and complete cds | AF071213 | | |
| 3599 | 0.031506 | KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3 (KDEL3), transcript variant 1, mRNA /cds=(157,801) /gb=NM_006855 /gi=8051612 /ug=Hs.250696 /len=1705 | NM_006855 | Hs.250696 | NP_057839 |
| 3606 | 0.035141 | nucleolar protein family A, member 3 (H/ACA small nucleolar RNPs) (NOLA3), mRNA /cds=(98,292) /gb=NM_018648 /gi=15011920 /ug=Hs.14317 /len=556 | NM_018648 | Hs.14317 | NP_061118 |
| 3607 | 0.028189 | mitochondrion, complete genome | NC_001807 | | |
| 3609 | 0.005038 | mortality factor 4 like 1 (MORF4L1), mRNA /cds=(132,1103) /gb=NM_006791 /gi=5803101 /ug=Hs.6353 /len=1766 | NM_006791 | Hs.6353 | NP_006782 |
| 3619 | 0.043451 | cytochrome c oxidase subunit IV isoform 1 (COX4I1), nuclear gene encoding mitochondrial protein, mRNA /cds=(165,674) /gb=NM_001861 /gi=17017985 /ug=Hs.433419 /len=802 | NM_001861 | Hs.433419 | NP_001852 |
| 3641 | 1.56E-04 | hypothetical protein CL25084 (CL25084), mRNA /cds=(132,1583) /gb=NM_015701 /gi=20070263 /ug=Hs.7100 /len=2412 | NM_015701 | Hs.7100 | NP_056516 |
| 3642 | 0.001721 | chromosome 1 open reading frame 22 (C1orf22), mRNA /cds=(54,2723) /gb=NM_025191 /gi=19923618 /ug=Hs.279951 /len=6298 | NM_025191 | Hs.279951 | NP_079467 |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|------|----------|--|--------------------|-----------------------|-----------------------|
| 3643 | 0.048172 | chitinase 3-like 2 (CHI3L2), mRNA /cds=(36,1193) /gb=NM_004000 /gi=11993934 /ug=Hs.154138 /len=1418 | NM_004000 | Hs.154138 | NP_003991 |
| 3733 | 0.048172 | MAGEF1 protein (MAGEF1), mRNA /cds=(177,1103) /gb=NM_022149 /gi=11545891 /ug=Hs.306123 /len=1615 | NM_022149 | Hs.306123 | NP_071432 |
| 3751 | 0.033283 | S100 calcium binding protein A11 (calgizzarin) (S100A11), mRNA /cds=(121,438) /gb=NM_005620 /gi=5032056 /ug=Hs.417004 /len=595 | NM_005620 | Hs.417004 | NP_005611 |
| 3763 | 0.01471 | UI-E-EO1-aja-c-22-0-UI.s1 UI-E-EO1 cDNA clone UI-E-EO1-aja-c-22-0-UI 3', mRNA sequence /clone=UI-E-EO1-aja-c-22-0-UI /clone_end=3' /gb=BM680199 /gi=18990095 /ug=Hs.355581 /len=1071 | BM680199 | Hs.355581 | |
| 3787 | 0.008208 | secretory leukocyte protease inhibitor (antileukoproteinase) (SLPI), mRNA /cds=(23,421) /gb=NM_003064 /gi=15834622 /ug=Hs.251754 /len=598 | NM_003064 | Hs.251754 | NP_003055 |
| 3805 | 0.012975 | hypothetical protein FLJ10350 (FLJ10350), mRNA /cds=(676,2340) /gb=NM_018067 /gi=21361780 /ug=Hs.177596 /len=2811 | NM_018067 | Hs.177596 | NP_060537 |
| 3828 | 0.035141 | osteoblast specific factor 2 (fascilin I-like) (OSF-2), mRNA /cds=(12,2522) /gb=NM_006475 /gi=5453833 /ug=Hs.136348 /len=3213 | NM_006475 | Hs.136348 | NP_006466 |
| 3830 | 0.018779 | eukaryotic translation elongation factor 1 beta 2 (EEF1B2), transcript variant 1, mRNA /cds=(236,913) /gb=NM_001959 /gi=16519564 /ug=Hs.421608 /len=961 | NM_001959 | Hs.421608 | NP_066944 |
| 3835 | 0.018779 | NEL-like 2 (chicken) (NELL2), mRNA /cds=(97,2547) /gb=NM_006159 /gi=5453765 /ug=Hs.79389 /len=3198 | NM_006159 | Hs.79389 | NP_006150 |
| 3840 | 0.019933 | sorcin (SRI), mRNA /cds=(13,609) /gb=NM_003130 /gi=4507206 /ug=Hs.422340 /len=952 | NM_003130 | Hs.422340 | NP_003121 |
| 3856 | 0.002566 | translocase of inner mitochondrial membrane 10 (yeast) homolog (TIMM10) | NM_012456 | | NP_036588 |
| 3861 | 0.011417 | basigin (BSG), mRNA /cds=(58,867) /gb=NM_001728 /gi=4502458 /ug=Hs.74631 /len=1638 | NM_001728 | Hs.74631 | NP_001719 |
| 3872 | 0.028189 | 6-phosphogluconolactonase (PGLS), mRNA /cds=(18,794) /gb=NM_012088 /gi=6912585 /ug=Hs.100071 /len=1010 | NM_012088 | Hs.100071 | NP_036220 |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|------|----------|---|--------------------|-----------------------|-----------------------|
| 3888 | 0.041237 | SAC2 suppressor of actin mutations 2-like (yeast) (SACM2L), transcript variant 1, mRNA /cds=(245,2416) /gb=NM_080564 /gi=18379336 /ug=Hs.169407 /len=2985 | NM_080564 | Hs.169407 | NP_542131 |
| 3917 | 0.048172 | ribosomal protein L30 (RPL30), mRNA /cds=(71,418) /gb=NM_000989 /gi=15812218 /ug=Hs.334807 /len=524 | NM_000989 | Hs.334807 | NP_000980 |
| 3924 | 0.010701 | ubiquitin specific protease 10 (USP10), mRNA /cds=(114,2510) /gb=NM_005153 /gi=24307888 /ug=Hs.78829 /len=3009 | NM_005153 | Hs.78829 | NP_005144 |
| 3936 | 0.043451 | hypothetical protein AF311304 (AF311304), mRNA /cds=(21,185) /gb=NM_031214 /gi=13654285 /ug=Hs.300624 /len=1138 | NM_031214 | Hs.300624 | NP_112491 |
| 3942 | 0.010979 | spectrin, alpha, non-erythrocytic 1 (alpha-fodrin) (SPTAN1), mRNA /cds=(103,7521) /gb=NM_003127 /gi=4507190 /ug=Hs.77196 /len=7787 | NM_003127 | Hs.77196 | NP_003118 |
| 3954 | 0.002192 | esophageal cancer related gene 4 protein (ECRG4), mRNA /cds=(109,555) /gb=NM_032411 /gi=14165275 /ug=Hs.43125 /len=772 | NM_032411 | Hs.43125 | NP_115787 |
| 3970 | 0.043451 | HSPC182 protein (HSPC182), mRNA /cds=(66,650) /gb=NM_014188 /gi=7661831 /ug=Hs.30026 /len=1059 | NM_014188 | Hs.30026 | NP_054907 |
| 3976 | 0.01471 | SFRS protein kinase 2 (SRPK2), mRNA /cds=(188,2248) /gb=NM_003138 /gi=4507220 /ug=Hs.78353 /len=3745 | NM_003138 | Hs.78353 | NP_003129 |
| 3990 | 0.041237 | hypothetical protein HSPC155 (HSPC155), mRNA /cds=(241,744) /gb=NM_016406 /gi=7705480 /ug=Hs.177507 /len=1137 | NM_016406 | Hs.177507 | NP_057490 |
| 4000 | 0.028189 | KIAA1156 | AB032982 | | NP_055665 |
| 4004 | 0.001585 | bromodomain containing 2 (BRD2), mRNA /cds=(1702,4107) /gb=NM_005104 /gi=12408641 /ug=Hs.75243 /len=4693 | NM_005104 | Hs.75243 | NP_005095 |
| 4022 | 0.043451 | MDS024 protein (MDS024), mRNA /cds=(65,838) /gb=NM_021820 /gi=11141892 /ug=Hs.425659 /len=2103 | NM_021820 | Hs.425659 | NP_068592 |
| 4037 | 5.57E-04 | coagulation factor VIII | AF062515 | | |
| 4038 | 0.006234 | multiple PDZ domain protein (MPDZ), mRNA /cds=(47,6175) /gb=NM_003829 /gi=4505230 /ug=Hs.169378 /len=6582 | NM_003829 | Hs.169378 | NP_003820 |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|------|----------|--|--------------------|-----------------------|-----------------------|
| 4046 | 2.04E-05 | polymerase (RNA) II (DNA directed) polypeptide C, 33kDa (POLR2C), transcript variant gamma, mRNA /cds=(58,885) /gb=NM_032940 /gi=14702170 /ug=Hs.79402 /len=1782 | NM_032940 | Hs.79402 | NP_116558 |
| 4092 | 0.028189 | NADH dehydrogenase (ubiquinone) Fe-S protein 3, 30kDa (NADH-coenzyme Q reductase) (NDUFS3), mRNA /cds=(13,807) /gb=NM_004551 /gi=4758787 /ug=Hs.429506 /len=899 | NM_004551 | Hs.429506 | NP_004542 |
| 4093 | 0.01471 | coated vesicle membrane protein (RNP24), mRNA /cds=(24,629) /gb=NM_006815 /gi=21314646 /ug=Hs.75914 /len=2060 | NM_006815 | Hs.75914 | NP_006806 |
| 4103 | 0.001459 | protein kinase C, nu (PRKCN), mRNA /cds=(556,3228) /gb=NM_005813 /gi=6563384 /ug=Hs.143460 /len=5792 | NM_005813 | Hs.143460 | NP_005804 |
| 4118 | 0.043451 | HSPC154 protein (HSPC154), mRNA /cds=(200,946) /gb=NM_014177 /gi=7661809 /ug=Hs.7922 /len=1343 | NM_014177 | Hs.7922 | NP_054896 |
| 4121 | 0.025168 | natural killer cell enhancing factor (NKEFA) | L19184 | | NP_002565 |
| 4131 | 0.039115 | thymosin, beta 4, X chromosome (TMSB4X), mRNA /cds=(78,212) /gb=NM_021109 /gi=11056060 /ug=Hs.75968 /len=556 | NM_021109 | Hs.75968 | NP_066932 |
| 4133 | 0.00767 | vimentin (VIM), mRNA /cds=(123,1523) /gb=NM_003380 /gi=4507894 /ug=Hs.297753 /len=1851 | NM_003380 | Hs.297753 | NP_000995 |
| 4152 | 0.035141 | CG9469 gene product | AAF57414 | | |
| 4159 | 0.048172 | suppressor of Ty 3 (S. cerevisiae) (SUPT3H), mRNA /cds=(72,1025) /gb=NM_003599 /gi=4507308 /ug=Hs.304173 /len=1165 | NM_003599 | Hs.304173 | NP_003590 |
| 4189 | 9.54E-04 | fatty-acid-Coenzyme A ligase, long-chain 4 (FACL4), transcript variant 2, mRNA /cds=(507,2642) /gb=NM_022977 /gi=12669908 /ug=Hs.81452 /len=5356 | NM_022977 | Hs.81452 | NP_075266 |
| 4194 | 0.009383 | peptidase D (PEPD), mRNA /cds=(17,1498) /gb=NM_000285 /gi=4557834 /ug=Hs.73947 /len=1888 | NM_000285 | Hs.73947 | NP_000276 |
| 4200 | 0.012175 | PTD013 protein (PTD013), mRNA /cds=(87,812) /gb=NM_015952 /gi=7706269 /ug=Hs.22679 /len=982 | NM_015952 | Hs.22679 | NP_057036 |
| 4206 | 0.048172 | ring finger protein 4 (RNF4), mRNA /cds=(271,843) /gb=NM_002938 /gi=4506560 /ug=Hs.66394 /len=2918 | NM_002938 | Hs.66394 | NP_002929 |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|------|----------|--|--------------------|-----------------------|-----------------------|
| 4213 | 0.035141 | collagen, type V, alpha 2 (COL5A2), mRNA /cds=(158,4648) /gb=NM_000393 /gi=16554580 /ug=Hs.82985 /len=6217 | NM_000393 | Hs.82985 | NP_000384 |
| 4223 | 1.27E-04 | solute carrier family 25 (carnitine/acylcarnitine translocase), member 20 (SLC25A20), mitochondrial protein encoded by nuclear gene, mRNA /cds=(37,942) /gb=NM_000387 /gi=6006040 /ug=Hs.13845 /len=1219 | NM_000387 | Hs.13845 | NP_000378 |
| 4267 | 0.029809 | inhibitor of DNA binding 1, dominant negative helix-loop-helix protein (ID1), mRNA /cds=(36,500) /gb=NM_002165 /gi=4504568 /ug=Hs.75424 /len=926 | NM_002165 | Hs.75424 | NP_851998 |
| 4294 | 0.029809 | hypothetical protein FLJ20729 (FLJ20729), mRNA /cds=(135,1547) /gb=NM_017953 /gi=20149642 /ug=Hs.5111 /len=2821 | NM_017953 | Hs.5111 | NP_060423 |
| 4317 | 0.039115 | accessory protein BAP31 (DXS1357E), mRNA /cds=(137,877) /gb=NM_005745 /gi=10047078 /ug=Hs.291904 /len=1314 | NM_005745 | Hs.291904 | NP_005736 |
| 4339 | 0.043451 | lamin B receptor (LBR), mRNA /cds=(76,1923) /gb=NM_002296 /gi=4504960 /ug=Hs.152931 /len=3714 | NM_002296 | Hs.152931 | NP_002287 |
| 4364 | 0.039115 | oxysterol binding protein-like 8 (OSBPL8), mRNA /cds=(481,3150) /gb=NM_020841 /gi=22035617 /ug=Hs.109694 /len=7239 | NM_020841 | Hs.109694 | NP_065892 |
| 4369 | 0.035141 | ribosomal protein L36 (RPL36), transcript variant 2, mRNA /cds=(153,470) /gb=NM_015414 /gi=16117793 /ug=Hs.433411 /len=545 | NM_015414 | Hs.433411 | NP_378669 |
| 4390 | 0.013819 | ataxia telangiectasia and Rad3 related (ATR), mRNA /cds=(106,8040) /gb=NM_001184 /gi=20143978 /ug=Hs.77613 /len=8265 | NM_001184 | Hs.77613 | NP_001175 |
| 4407 | 0.045762 | 15 kDa selenoprotein (SEP15), mRNA /cds=(5,493) /gb=NM_004261 /gi=20127464 /ug=Hs.90606 /len=1519 | NM_004261 | Hs.90606 | NP_004252 |
| 4419 | 0.029809 | KIAA0742 | AB018285 | | NP_060903 |
| 4425 | 0.005038 | gene amplified in squamous cell carcinoma 1 (GASC1), mRNA /cds=(151,3321) /gb=NM_015061 /gi=24307986 /ug=Hs.149918 /len=4239 | NM_015061 | Hs.149918 | NP_055876 |
| 4435 | 0.010701 | clone IMAGE:3633225, mRNA /gb=BC012758 /gi=15706478 /ug=Hs.356377 /len=1914 | BC012758 | Hs.356377 | |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|------|----------|--|--------------------|-----------------------|-----------------------|
| 4440 | 0.031506 | alcohol dehydrogenase 5 (class III), chi polypeptide (ADH5), mRNA /cds=(163,1287) /gb=NM_000671 /gi=11496890 /ug=Hs.78989 /len=2496 | NM_000671 | Hs.78989 | NP_000662 |
| 4462 | 0.016639 | collagen, type I, alpha 2 (COL1A2), mRNA /cds=(138,4238) /gb=NM_000089 /gi=21536289 /ug=Hs.179573 /len=5084 | NM_000089 | Hs.179573 | NP_000080 |
| 4509 | 0.019933 | likely ortholog of mouse deleted in polyposis 1 (DP1), mRNA /cds=(38,595) /gb=NM_005669 /gi=24307896 /ug=Hs.178112 /len=3000 | NM_005669 | Hs.178112 | NP_005660 |
| 4513 | 0.029809 | hepatitis B virus x interacting protein (HBXIP), mRNA /cds=(56,331) /gb=NM_006402 /gi=5454169 /ug=Hs.433355 /len=605 | NM_006402 | Hs.433355 | NP_006393 |
| 4515 | 0.045762 | cell recognition molecule CASPR3 (CASPR3), transcript variant 1, mRNA /cds=(408,3872) /gb=NM_033655 /gi=16306508 /ug=Hs.212839 /len=5017 | NM_033655 | Hs.212839 | NP_387504 |
| 4530 | 0.00767 | I factor (complement) (IF), mRNA /cds=(15,1766) /gb=NM_000204 /gi=4504578 /ug=Hs.36602 /len=1963 | NM_000204 | Hs.36602 | NP_000195 |
| 4531 | 0.048172 | erythrocyte membrane protein band 4.1-like 2 (EPB41L2), mRNA /cds=(45,3062) /gb=NM_001431 /gi=4503578 /ug=Hs.7857 /len=4336 | NM_001431 | Hs.7857 | NP_001422 |
| 4536 | 0.035141 | splicing factor, arginine/serine-rich 2, interacting protein (SF2IP), mRNA /cds=(1211,4657) /gb=NM_004719 /gi=4759171 /ug=Hs.51957 /len=5307 | NM_004719 | Hs.51957 | NP_004710 |
| 4540 | 0.007162 | decay accelerating factor for complement (CD55, Cromer blood group system) (DAF), mRNA /cds=(66,1211) /gb=NM_000574 /gi=10835142 /ug=Hs.1369 /len=2102 | NM_000574 | Hs.1369 | NP_000565 |
| 4556 | 0.045762 | phosphorylase, glycogen; liver (Hers disease, glycogen storage disease type VI) (PYGL), mRNA /cds=(52,2595) /gb=NM_002863 /gi=4506352 /ug=Hs.771 /len=2643 | NM_002863 | Hs.771 | NP_002854 |
| 4584 | 0.008779 | Rho-associated, coiled-coil containing protein kinase 1 (ROCK1), mRNA /cds=(1,4065) /gb=NM_005406 /gi=4885582 /ug=Hs.17820 /len=4065 | NM_005406 | Hs.17820 | NP_005397 |
| 4654 | 0.041237 | RNA helicase-related protein (RNAHP), mRNA /cds=(18,2147) /gb=NM_007372 /gi=11321631 /ug=Hs.8765 /len=3347 | NM_007372 | Hs.8765 | NP_031398 |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|------|----------|---|--------------------|-----------------------|-----------------------|
| 4672 | 0.017682 | coronin, actin binding protein, 1C (CORO1C), mRNA /cds=(97,1521) /gb=NM_014325 /gi=27477119 /ug=Hs.17377 /len=3828 | NM_014325 | Hs.17377 | NP_055140 |
| 4678 | 0.002372 | hydroxysteroid (17-beta) dehydrogenase 4 (HSD17B4), mRNA /cds=(49,2259) /gb=NM_000414 /gi=4504504 /ug=Hs.75441 /len=2593 | NM_000414 | Hs.75441 | NP_000405 |
| 4693 | 0.002192 | H3 histone, family 3B (H3.3B) (H3F3B), mRNA /cds=(118,528) /gb=NM_005324 /gi=21264598 /ug=Hs.180877 /len=1662 | NM_005324 | Hs.180877 | NP_005315 |
| 4694 | 0.001459 | hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor) (HIF1A), mRNA /cds=(265,2745) /gb=NM_001530 /gi=4504384 /ug=Hs.197540 /len=3933 | NM_001530 | Hs.197540 | NP_851397 |
| 4703 | 0.013819 | leukotriene A4 hydrolase (LTA4H), mRNA /cds=(69,1904) /gb=NM_000895 /gi=4505028 /ug=Hs.81118 /len=2060 | NM_000895 | Hs.81118 | NP_000886 |
| 4720 | 0.026643 | heterogeneous nuclear ribonucleoprotein R (HNRPR), mRNA /cds=(91,1992) /gb=NM_005826 /gi=14141188 /ug=Hs.15265 /len=2663 | NM_005826 | Hs.15265 | NP_005817 |
| 4724 | 0.035141 | Niemann-Pick disease, type C1 (NPC1), mRNA /cds=(124,3960) /gb=NM_000271 /gi=4557802 /ug=Hs.76918 /len=4673 | NM_000271 | Hs.76918 | NP_000262 |
| 4736 | 0.003758 | E74-like factor 1 (ets domain transcription factor) (ELF1), mRNA /cds=(256,2115) /gb=NM_172373 /gi=27363483 /ug=Hs.154365 /len=3526 | NM_172373 | Hs.154365 | NP_758961 |
| 4741 | 0.033283 | hypothetical protein MGC21981 (MGC21981), mRNA /cds=(66,764) /gb=NM_153267 /gi=23397567 /ug=Hs.131987 /len=1727 | NM_153267 | Hs.131987 | NP_694999 |
| 4758 | 0.026643 | inhibin, beta A (activin A, activin AB alpha polypeptide) (INHBA), mRNA /cds=(86,1366) /gb=NM_002192 /gi=4504698 /ug=Hs.727 /len=1840 | NM_002192 | Hs.727 | NP_002183 |
| 4769 | 0.018779 | mitochondrial ribosomal protein L37 (MRPL37), nuclear gene encoding mitochondrial protein, mRNA /cds=(78,1349) /gb=NM_016491 /gi=22547133 /ug=Hs.4209 /len=1511 | NM_016491 | Hs.4209 | NP_057575 |
| 4774 | 0.019933 | ribosomal protein S19 (RPS19), mRNA /cds=(70,507) /gb=NM_001022 /gi=14591914 /ug=Hs.298262 /len=569 | NM_001022 | Hs.298262 | NP_001013 |
| 4778 | 0.026643 | ribosomal protein, large, P1 (RPLP1), mRNA /cds=(130,474) /gb=NM_001003 /gi=16905511 /ug=Hs.424299 /len=512 | NM_001003 | Hs.424299 | NP_000994 |

| Spot | p-value | Description | Gen Accession No. | Unigene Accession No. | Protein Accession No. |
|------|----------|--|-------------------------|-----------------------------|-----------------------------|
| 4782 | 0.01471 | CDC-like kinase1 (CLK1), mRNA /cds=(156,1610) /gb=NM_004071 /gi=4758007 /ug=Hs.2083 /len=1834 | NM_004071 | Hs.2083 | NP_004062 |
| 4794 | 0.012975 | mitochondrion, complete genome | NC_001807 | | |
| 4798 | 0.022422 | Rho-associated, coiled-coil containing protein kinase 2 (ROCK2), mRNA /cds=(455,4621) /gb=NM_004850 /gi=6633807 /ug=Hs.58617 /len=6409 | NM_004850 | Hs.58617 | NP_004841 |
| 4805 | 0.001234 | high-mobility group box 1 (HMGB1), mRNA /cds=(77,724) /gb=NM_002128 /gi=20149538 /ug=Hs.6727 /len=1207 | NM_002128 | Hs.6727 | NP_002119 |
| 4810 | 0.041237 | mRNA; cDNA DKFZp727I051 (from clone DKFZp727I051); partial cds /cds=(1,2099) /gb=AL117478 /gi=5911952 /ug=Hs.239370 /len=2480 | AL117478 | Hs.239370 | NP_056412 |
| 4814 | 0.012975 | ribosomal protein L10a (RPL10A), mRNA /cds=(16,669) /gb=NM_007104 /gi=15431287 /ug=Hs.425293 /len=700 | NM_007104 | Hs.425293 | NP_009035 |
| 4819 | 0.015649 | ribosomal protein L28 (RPL28), mRNA /cds=(43,456) /gb=NM_000991 /gi=13904865 /ug=Hs.356371 /len=500 | NM_000991 | Hs.356371 | NP_000982 |
| 4821 | 0.01471 | eukaryotic translation termination factor 1 (ETF1), mRNA /cds=(136,1449) /gb=NM_004730 /gi=4759033 /ug=Hs.77324 /len=3653 | NM_004730 | Hs.77324 | NP_004721 |
| 4823 | 0.035141 | SH3-domain GRB2-like endophilin B2 (SH3GLB2), mRNA /cds=(147,1334) /gb=NM_020145 /gi=24431995 /ug=Hs.30002 /len=2039 | NM_020145 | Hs.30002 | NP_064530 |
| 4837 | 0.041237 | UI-H-BW1-amj-g-07-0-UI.s1 NCI_CGAP_Sub7 cDNA clone IMAGE:3070261 3', mRNA sequence /clone=IMAGE:3070261 /clone_end=3' /gb=BF513214 /gi=11598393 /ug=Hs.445888 /len=620 | BF513214 | Hs.445888 | |
| 4848 | 0.005811 | aggrecan 1 (chondroitin sulfate proteoglycan 1, large aggregating proteoglycan, antigen identified by monoclonal antibody A0122) (AGC1), transcript variant 2, mRNA /cds=(61,7308) /gb=NM_013227 /gi=6995993 /ug=Hs.2159 /len=7434 | NM_013227 | Hs.2159 | NP_037359 |
| 4863 | 0.025168 | FLJ14819 fis, clone OVARC1000241, moderately similar to HYPOXIA- INDUCIBLE FACTOR 1 ALPHA | AK027725 | | NP_690009 |
| 4874 | 0.016639 | ankyrin repeat domain 10 (ANKRD10), mRNA /cds=(136,1398) /gb=NM_017664 /gi=8923103 /ug=Hs.172572 /len=2509 | NM_017664 | Hs.172572 | NP_060134 |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|------|----------|---|--------------------|-----------------------|-----------------------|
| 4877 | 0.023762 | chromosome 20 open reading frame 31 (C20orf31), mRNA /cds=(83,1819) /gb=NM_018217 /gi=8922666 /ug=Hs.93871 /len=1885 | NM_018217 | Hs.93871 | NP_060687 |
| 4878 | 0.009383 | ribosomal protein L35a (RPL35A), mRNA /cds=(74,406) /gb=NM_000996 /gi=16117790 /ug=Hs.288544 /len=511 | NM_000996 | Hs.288544 | NP_000987 |
| 4880 | 0.035141 | cDNA FLJ12776 fis, clone NT2RP2001678. /gb=AK022838 /gi=10434465 /ug=Hs.372558 /len=2629 | AK022838 | Hs.372558 | |
| 4884 | 0.006293 | geranylgeranyl diphosphate synthase 1 (GGPS1), mRNA /cds=(233,1135) /gb=NM_004837 /gi=21359876 /ug=Hs.55498 /len=1489 | NM_004837 | Hs.55498 | NP_004828 |
| 4886 | 0.026643 | proteasome (prosome, macropain) subunit, beta type, 4 (PSMB4), mRNA /cds=(24,818) /gb=NM_002796 /gi=22538466 /ug=Hs.89545 /len=925 | NM_002796 | Hs.89545 | NP_002787 |
| 4912 | 0.037157 | ATP synthase, H transporting, mitochondrial F0 complex, subunit g (ATP5L), mRNA /cds=(60,371) /gb=NM_006476 /gi=21359881 /ug=Hs.107476 /len=580 | NM_006476 | Hs.107476 | NP_006467 |
| 4915 | 0.004357 | hypothetical protein FLJ13149 (FLJ13149), mRNA /cds=(291,2585) /gb=NM_021826 /gi=11141902 /ug=Hs.112188 /len=2836 | NM_021826 | Hs.112188 | NP_068598 |
| 4916 | 0.015649 | collagen, type X, alpha 1(Schmid metaphyseal chondrodysplasia) (COL10A1), mRNA /cds=(97,2139) /gb=NM_000493 /gi=18105031 /ug=Hs.179729 /len=3285 | NM_000493 | Hs.179729 | NP_000484 |
| 4919 | 0.001459 | KIAA0436 mRNA, partial cds. /cds=(1,2070) /gb=AB007896 /gi=2662152 /ug=Hs.110 /len=4661 | AB007896 | Hs.110 | |
| 4921 | 0.025168 | cDNA FLJ10423 fis, clone NT2RP1000259. /gb=AK001285 /gi=7022444 /ug=Hs.106909 /len=1837 | AK001285 | Hs.106909 | |
| 4925 | 0.012175 | tm68a09.x1 NCI_CGAP_Brn25 cDNA clone IMAGE:2163256 3', mRNA sequence /clone=IMAGE:2163256 /clone_end=3' /gb=AI498805 /gi=4390787 /ug=Hs.436349 /len=460 | AI498805 | Hs.436349 | |
| 4926 | 0.00767 | nuclear receptor coactivator 1 (NCOA1), transcript variant 2, mRNA /cds=(202,4401) /gb=NM_147223 /gi=22538456 /ug=Hs.74002 /len=4721 | NM_147223 | Hs.74002 | NP_671766 |

| Spot | p-value | Description | Gene Accession No. | Unigene Acc ssion No. | Protein Accession No. |
|------|----------|---|--------------------|-----------------------|-----------------------|
| 4942 | 0.018779 | AF034176 mRNA (Tripodis and Ragoussis) cDNA clone ntcon5 contig /gb=AF034176 /gi=2707738 /ug=Hs.188882 /len=7232 | AF034176 | Hs.188882 | |
| 4944 | 0.005412 | hypothetical protein FLJ20452 (FLJ20452), mRNA /cds=(15,614) /gb=NM_017828 /gi=21361660 /ug=Hs.351327 /len=1948 | NM_017828 | Hs.351327 | NP_060298 |
| 4945 | 0.012975 | eukaryotic translation initiation factor 3, subunit 5 epsilon, 47kDa (EIF3S5), mRNA /cds=(7,1080) /gb=NM_003754 /gi=4503518 /ug=Hs.7811 /len=1231 | NM_003754 | Hs.7811 | NP_003745 |
| 4946 | 0.001661 | myosin, light polypeptide 6, alkali, smooth muscle and non-muscle (MYL6), transcript variant 3, mRNA /cds=(41,514) /gb=NM_079425 /gi=17986263 /ug=Hs.77385 /len=717 | NM_079425 | Hs.77385 | NP_524149 |
| 4950 | 0.045762 | mRNA for KIAA1865 protein, partial cds. /cds=(622,2793) /gb=AB058768 /gi=14017946 /ug=Hs.179260 /len=3641 | AB058768 | Hs.179260 | |
| 4956 | 0.018779 | hypothetical protein FLJ20671 (FLJ20671), mRNA /cds=(43,465) /gb=NM_017924 /gi=19923511 /ug=Hs.180201 /len=2855 | NM_017924 | Hs.180201 | NP_060394 |
| 4957 | 0.012975 | TcD37 (HTCD37), mRNA /cds=(137,1498) /gb=NM_021222 /gi=24308262 /ug=Hs.78524 /len=2995 | NM_021222 | Hs.78524 | NP_067045 |
| 4958 | 0.016639 | cDNA FLJ10235 fis, clone HEMBB1000339. /gb=AK001097 /gi=7022149 /ug=Hs.406774 /len=2530 | AK001097 | Hs.406774 | |
| 4962 | 0.027396 | mRNA for KIAA1320 protein, partial cds. /cds=(2051,3754) /gb=AB037741 /gi=7243020 /ug=Hs.117414 /len=5321 | AB037741 | Hs.117414 | |
| 4970 | 0.022422 | decorin (DCN), transcript variant A1, mRNA /cds=(200,1279) /gb=NM_001920 /gi=19743844 /ug=Hs.433989 /len=1751 | NM_001920 | Hs.433989 | NP_598014 |
| 4972 | 0.048172 | HSPC092 | AF161355 | | NP_055238 |
| 4983 | 0.035151 | F-box and leucine-rich repeat protein 3A (FBXL3A), mRNA /cds=(298,1584) /gb=NM_012158 /gi=16306583 /ug=Hs.7540 /len=3489 | NM_012158 | Hs.7540 | NP_036290 |
| 4986 | 0.003487 | adrenomedullin (ADM), mRNA /cds=(157,714) /gb=NM_001124 /gi=4501944 /ug=Hs.394 /len=1449 | NM_001124 | Hs.394 | NP_001115 |
| 4988 | 0.010701 | translocase of outer mitochondrial membrane 70 A (yeast) (TOMM70A), mRNA /cds=(92,1918) /gb=NM_014820 /gi=7662672 /ug=Hs.21198 /len=4017 | NM_014820 | Hs.21198 | NP_055635 |

| Spot | p-value | Description | Gene Accession No. | UniGene Accession No. | Protein Accession No. |
|------|----------|--|--------------------|-----------------------|-----------------------|
| 4989 | 0.045762 | chloride intracellular channel 5 (CLIC5), mRNA /cds=(298,1053) /gb=NM_016929 /gi=8393146 /ug=Hs.283021 /len=2380 | NM_016929 | Hs.283021 | NP_058625 |
| 4992 | 0.005412 | tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor) (TFPI), mRNA /cds=(1,915) /gb=NM_006287 /gi=6715569 /ug=Hs.170279 /len=915 | NM_006287 | Hs.170279 | NP_006278 |
| 4994 | 0.007162 | Nedd4 binding protein 2 (N4BP2), mRNA /cds=(339,5600) /gb=NM_018177 /gi=20357506 /ug=Hs.18685 /len=6760 | NM_018177 | Hs.18685 | NP_060647 |
| 5005 | 0.029809 | ankyrin repeat and SOCS box-containing 1 (ASB1), mRNA /cds=(87,1094) /gb=NM_016114 /gi=22208961 /ug=Hs.153489 /len=6798 | NM_016114 | Hs.153489 | NP_057198 |
| 5011 | 0.001721 | ALL1 fused gene from 5q31 (AF5Q31), mRNA /cds=(338,3829) /gb=NM_014423 /gi=7656878 /ug=Hs.231967 /len=4235 | NM_014423 | Hs.231967 | NP_055238 |
| 5016 | 0.025168 | ribosomal protein L17 (RPL17), mRNA /cds=(287,841) /gb=NM_000985 /gi=14591906 /ug=Hs.82202 /len=898 | NM_000985 | Hs.82202 | NP_000976 |
| 5060 | 5.57E-04 | HIF-1 responsive RTP801 (RTP801), mRNA /cds=(198,896) /gb=NM_019058 /gi=9506686 /ug=Hs.111244 /len=1760 | NM_019058 | Hs.111244 | NP_061931 |
| 5061 | 0.016639 | wc09c01.x1 NCI_CGAP_Pr28 cDNA clone IMAGE:2314656 3' similar to gb:J05016 PROTEIN DISULFIDE ISOMERASE-RELATED PROTEIN PRECURSOR mRNA sequence /clone=IMAGE:2314656 /clone_end=3' /gb=AI674177 /gi=4874657 /ug=Hs.200089 /len=526 | AI674177 | Hs.200089 | |
| 5069 | 0.009383 | hsp70-interacting protein (HSPBP1), mRNA /cds=(312,1400) /gb=NM_012267 /gi=21361406 /ug=Hs.53066 /len=1795 | NM_012267 | Hs.53066 | NP_036399 |
| 5090 | 0.033283 | U3 small nuclear RNA gene | M14061 | | |
| 5094 | 0.006234 | sterol regulatory element binding transcription factor 2 (SREBF2), mRNA /cds=(170,3595) /gb=NM_004599 /gi=27477112 /ug=Hs.108689 /len=4325 | NM_004599 | Hs.108689 | NP_004590 |
| 5102 | 2.35E-04 | cofilin 1 (non-muscle) (CFL1), mRNA /cds=(52,552) /gb=NM_005507 /gi=5031634 /ug=Hs.180370 /len=1059 | NM_005507 | Hs.180370 | NP_005498 |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|------|----------|---|--------------------|-----------------------|-----------------------|
| 5105 | 0.017682 | hypothetical protein FLJ20312 (FLJ20312), mRNA /cds=(384,803) /gb=NM_017761 /gi=20127576 /ug=Hs.7862 /len=2382 | NM_017761 | Hs.7862 | NP_060231 |
| 5108 | 0.005412 | calponin 2 (CNN2), mRNA /cds=(28,957) /gb=NM_004368 /gi=4758017 /ug=Hs.169718 /len=2122 | NM_004368 | Hs.169718 | NP_004359 |
| 5111 | 0.00767 | chromosome 14 open reading frame 94 (C14orf94), mRNA /cds=(211,1302) /gb=NM_017815 /gi=8923395 /ug=Hs.8886 /len=1618 | NM_017815 | Hs.8886 | NP_060285 |
| 5155 | 0.043451 | phosphoglycerate kinase 1 (PGK1), mRNA /cds=(70,1323) /gb=NM_000291 /gi=22095338 /ug=Hs.78771 /len=2338 | NM_000291 | Hs.78771 | NP_000282 |
| 5156 | 0.006684 | myosin regulatory light chain (MLC-B), mRNA /cds=(117,635) /gb=NM_033546 /gi=15809015 /ug=Hs.233936 /len=967 | NM_033546 | Hs.233936 | NP_291024 |
| 5161 | 0.018779 | basic transcription factor 3 (BTF3), mRNA /cds=(240,728) /gb=NM_001207 /gi=20070129 /ug=Hs.101025 /len=952 | NM_001207 | Hs.101025 | NP_001198 |
| 5187 | 0.012175 | zinc finger protein 281 (ZNF281), mRNA /cds=(24,2711) /gb=NM_012482 /gi=6912751 /ug=Hs.59757 /len=3029 | NM_012482 | Hs.59757 | NP_036614 |
| 5192 | 0.043451 | mRNA for KIAA0232 protein, partial cds. /cds=(435,4643) /gb=D86985 /gi=20521849 /ug=Hs.79276 /len=7840 | D86985 | Hs.79276 | |
| 5195 | 0.003233 | angiopoietin-like 4 (ANGPTL4), transcript variant 1, mRNA /cds=(196,1416) /gb=NM_139314 /gi=21536397 /ug=Hs.9613 /len=1967 | NM_139314 | Hs.9613 | NP_647475 |
| 5204 | 0.039115 | stathmin-like 3 (STMN3), mRNA /cds=(83,625) /gb=NM_015894 /gi=14670374 /ug=Hs.285753 /len=2255 | NM_015894 | Hs.285753 | NP_056978 |
| 5205 | 0.043451 | mRNA for KIAA1458 protein, partial cds. /cds=(22,1860) /gb=AB040891 /gi=7959176 /ug=Hs.27263 /len=5843 | AB040891 | Hs.27263 | |
| 5206 | 0.017682 | CAAX box 1 (CXX1), mRNA /cds=(335,964) /gb=NM_003928 /gi=4503180 /ug=Hs.250708 /len=1209 | NM_003928 | Hs.250708 | NP_003919 |
| 5234 | 0.031506 | deiodinase, iodothyronine, type II (DIO2), transcript variant 1, mRNA /cds=(707,1528) /gb=NM_013989 /gi=7549802 /ug=Hs.154424 /len=6735 | NM_013989 | Hs.154424 | NP_054644 |
| 5235 | 0.012975 | major histocompatibility complex, class II, DR beta 1 (HLA-DRB1), mRNA /cds=(63,863) /gb=NM_002124 /gi=4504410 /ug=Hs.375570 /len=1182 | NM_002124 | Hs.375570 | NP_002115 |
| 5249 | 0.026643 | Escherichia coli K-12 MG1655 section 343 of 400 of the complete genome | AE000453 | | |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|------|----------|--|--------------------|-----------------------|-----------------------|
| 5250 | 0.010023 | SFRS protein kinase 1 (SRPK1), mRNA /cds=(10,1974) /gb=NM_003137 /gi=15834623 /ug=Hs.75761 /len=4244 | NM_003137 | Hs.75761 | NP_003128 |
| 5261 | 0.031506 | replication factor C (activator 1) 4, 37kDa (RFC4), mRNA /cds=(284,1375) /gb=NM_002916 /gi=4506490 /ug=Hs.35120 /len=1446 | NM_002916 | Hs.35120 | NP_002907 |
| 5264 | 0.005412 | small GTP-binding protein RAB1A | AF226873 | | NP_033022 |
| 5283 | 0.037084 | transforming, acidic coiled-coil containing protein 2 (TACC2), mRNA /cds=(87,3167) /gb=NM_006997 /gi=11119413 /ug=Hs.272023 /len=3686 | NM_006997 | Hs.272023 | NP_008928 |
| 5287 | 0.01471 | hypothetical protein FLJ30945 fis, clone FEBRA2007613 | AK055507 | | NP_071911 |
| 5330 | 0.001234 | discs, large 7 (Drosophila) (DLG7), mRNA /cds=(218,2758) /gb=NM_014750 /gi=21361644 /ug=Hs.77695 /len=2979 | NM_014750 | Hs.77695 | NP_055565 |
| 5332 | 0.041237 | clone IMAGE:5262128, mRNA, partial cds /cds=(1,1409) /gb=BC035036 /gi=23271542 /ug=Hs.356247 /len=4728 | BC035036 | Hs.356247 | |
| 5386 | 0.037084 | ATPase, H transporting, lysosomal 9kDa, V0 subunit e (ATP6V0E), mRNA /cds=(76,321) /gb=NM_003945 /gi=19913435 /ug=Hs.415629 /len=849 | NM_003945 | Hs.415629 | NP_003936 |
| 5391 | 0.005412 | palmdelphin (PALMD), mRNA /cds=(286,1941) /gb=NM_017734 /gi=16306484 /ug=Hs.14606 /len=2581 | NM_017734 | Hs.14606 | NP_060204 |
| 5411 | 0.045762 | DKFZp566J2446 (from clone DKFZp566J2446) | AL050082 | | NP_008944 |
| 5412 | 0.026643 | SRY (sex determining region Y)-box 9 (campomelic dysplasia, autosomal sex-reversal) (SOX9), mRNA /cds=(373,1902) /gb=NM_000346 /gi=4557852 /ug=Hs.2316 /len=3936 | NM_000346 | Hs.2316 | NP_000337 |
| 5419 | 0.045321 | ATP synthase, H transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 1 (ATP5G1), mRNA /cds=(120,530) /gb=NM_005175 /gi=4885080 /ug=Hs.80986 /len=631 | NM_005175 | Hs.80986 | NP_005166 |
| 5420 | 0.001459 | matrilin 3 (MATN3) precursor, mRNA /cds=(64,1524) /gb=NM_002381 /gi=13518040 /ug=Hs.278461 /len=2599 | NM_002381 | Hs.278461 | NP_002372 |
| 5432 | 0.025168 | zinc finger protein 202 (ZNF202), mRNA /cds=(11,1957) /gb=NM_003455 /gi=10835040 /ug=Hs.9443 /len=4053 | NM_003455 | Hs.9443 | NP_003446 |
| 5433 | 0.017682 | actin related protein 2/3 complex, subunit 5, 16kDa (ARPC5), mRNA /cds=(192,647) /gb=NM_005717 /gi=23238212 /ug=Hs.82425 /len=2000 | NM_005717 | Hs.82425 | NP_005708 |

| Spot | p-value | Description | Gene Accession No. | Unigen Accession No. | Protein Accession No. |
|------|----------|--|--------------------|----------------------|-----------------------|
| 5438 | 0.010023 | mitochondrion, complete genome | NC_001807 | | |
| 5445 | 0.005051 | hypothetical protein FLJ20312 (FLJ20312), mRNA /cds=(384,803) /gb=NM_017761 /gi=20127576 /ug=Hs.7862 /len=2382 | NM_017761 | Hs.7862 | NP_060231 |
| 5448 | 0.037084 | eukaryotic translation initiation factor 4A, isoform 2 (EIF4A2), mRNA /cds=(16,1239) /gb=NM_001967 /gi=9945313 /ug=Hs.173912 /len=1864 | NM_001967 | Hs.173912 | NP_001958 |
| 5449 | 0.004357 | mRNA; cDNA DKFZp667D2123 (from clone DKFZp667D2123) /gb=AL832786 /gi=21733368 /ug=Hs.283643 /len=3000 | AL832786 | Hs.283643 | |
| 5451 | 0.035141 | tumor protein, translationally-controlled 1 (TPT1), mRNA /cds=(95,613) /gb=NM_003295 /gi=4507668 /ug=Hs.401448 /len=830 | NM_003295 | Hs.401448 | NP_003286 |
| 5476 | 0.004687 | meningioma expressed antigen 6 (coiled-coil proline-rich) (MGEA6), mRNA /cds=(315,2729) /gb=NM_005930 /gi=5174560 /ug=Hs.117242 /len=3676 | NM_005930 | Hs.117242 | NP_005921 |
| 5477 | 0.002372 | lectin, galactoside-binding, soluble, 3 (galectin 3) (LGALS3), mRNA /cds=(19,771) /gb=NM_002306 /gi=4504982 /ug=Hs.621 /len=914 | NM_002306 | Hs.621 | NP_002297 |
| 5482 | 0.023762 | proliferating cell nuclear antigen (PCNA), mRNA /cds=(119,904) /gb=NM_002592 /gi=4505640 /ug=Hs.78996 /len=1231 | NM_002592 | Hs.78996 | NP_002583 |
| 5497 | 0.033283 | zinc finger, DHHC domain containing 4 (ZDHHC4), mRNA /cds=(222,1256) /gb=NM_018106 /gi=21361700 /ug=Hs.5268 /len=1704 | NM_018106 | Hs.5268 | NP_060576 |
| 5498 | 0.045762 | polymerase (RNA) II (DNA directed) polypeptide G (POLR2G), mRNA /cds=(107,625) /gb=NM_002696 /gi=4505946 /ug=Hs.14839 /len=828 | NM_002696 | Hs.14839 | NP_002687 |
| 5499 | 0.041237 | adaptor-related protein complex 2, sigma 1 subunit (AP2S1), transcript variant AP17, mRNA /cds=(71,499) /gb=NM_004069 /gi=11038644 /ug=Hs.119591 /len=781 | NM_004069 | Hs.119591 | NP_067586 |
| 5509 | 0.019933 | brain protein 44-like (BRP44L), mRNA /cds=(123,452) /gb=NM_016098 /gi=7706368 /ug=Hs.108725 /len=988 | NM_016098 | Hs.108725 | NP_057182 |
| 5511 | 0.010023 | cytochrome c oxidase subunit IV isoform 1 (COX4I1), nuclear gene encoding mitochondrial protein, mRNA /cds=(165,674) /gb=NM_001861 /gi=17017985 /ug=Hs.433419 /len=802 | NM_001861 | Hs.433419 | NP_001852 |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|------|----------|--|--------------------|-----------------------|-----------------------|
| 5514 | 0.00767 | ribosomal protein L4 (RPL4), mRNA /cds=(57,1340) /gb=NM_000968 /gi=16579884 /ug=Hs.286 /len=1449 | NM_000968 | Hs.286 | NP_000959 |
| 5517 | 0.026643 | Hypothetical protein (cDNA FLJ20702 fis, clone KAIA2174) | AK000709 | | |
| 5550 | 0.033283 | fusion, derived from t(12;16) malignant liposarcoma (FUS), mRNA /cds=(79,1659) /gb=NM_004960 /gi=4826733 /ug=Hs.99969 /len=1824 | NM_004960 | Hs.99969 | NP_004951 |
| 5551 | 0.037084 | hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit (HADHA), mRNA /cds=(35,2326) /gb=NM_000182 /gi=20127407 /ug=Hs.75860 /len=2972 | NM_000182 | Hs.75860 | NP_000173 |
| 5584 | 0.019933 | regulator of nonsense transcripts 1. (RENT1), mRNA /cds=(232,3588) /gb=NM_002911 /gi=18375672 /ug=Hs.12719 /len=5300 | NM_002911 | Hs.12719 | NP_002902 |
| 5590 | 0.026643 | eukaryotic translation initiation factor 4E-like 3 (EIF4EL3), mRNA /cds=(15,752) /gb=NM_004846 /gi=4757701 /ug=Hs.19122 /len=974 | NM_004846 | Hs.19122 | NP_004837 |
| 5640 | 0.012175 | nonhistone protein HMG1 | M21683 | | |
| 5644 | 0.029809 | integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12) (ITGB1), transcript variant 1A, mRNA /cds=(127,2523) /gb=NM_002211 /gi=19743812 /ug=Hs.287797 /len=3700 | NM_002211 | Hs.287797 | NP_596867 |
| 5671 | 0.006684 | EPC-1 (=M76979 PEDF;U29953;M90493) | U57446 | | |
| 5672 | 0.004357 | clone IMAGE:5265581, mRNA /gb=BC035165 /gi=23272508 /ug=Hs.400548 /len=2237 | BC035165 | Hs.400548 | |
| 5752 | 0.013819 | F-box and leucine-rich repeat protein 7 (FBXL7), mRNA /cds=(482,1957) /gb=NM_012304 /gi=21071079 /ug=Hs.76798 /len=4562 | NM_012304 | Hs.76798 | NP_036436 |
| 5770 | 0.023762 | APG12 autophagy 12-like (S. cerevisiae), DKFZp761A0411 (from clone DKFZp761A0411) mRNA; cDNA /cds=UNKNOWN /gb=AL161968 /gi=7328057 /ug=Hs.264482 /len=3285 | AL161968 | Hs.264482 | NP_004698 |
| 5789 | 0.015649 | ribosomal protein L31 (RPL31), mRNA /cds=(28,405) /gb=NM_000993 /gi=15812219 /ug=Hs.184014 /len=442 | NM_000993 | Hs.184014 | NP_000984 |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|------|----------|--|--------------------|-----------------------|-----------------------|
| 5814 | 0.015649 | ribosomal protein L36a-like (RPL36AL), mRNA /cds=(95,415) /gb=NM_001001 /gi=16306559 /ug=Hs.419465 /len=537 | NM_001001 | Hs.419465 | NP_000992 |
| 5821 | 0.028189 | ribosomal protein L11 (RPL11), mRNA /cds=(21,557) /gb=NM_000975 /gi=15431289 /ug=Hs.388664 /len=609 | NM_000975 | Hs.388664 | NP_000966 |
| 5824 | 0.033283 | activated RNA polymerase II transcription cofactor 4 (PC4), mRNA /cds=(57,440) /gb=NM_006713 /gi=19923783 /ug=Hs.349506 /len=1336 | NM_006713 | Hs.349506 | NP_006704 |
| 5827 | 0.010701 | PHKB gene (exon 25) | X84930 | | |
| 5870 | 0.035141 | Similar to cyclin K, clone MGC:9113 IMAGE:3907416, mRNA, complete cds /cds=(110,1174) /gb=BC015935 /gi=16198507 /ug=Hs.375192 /len=1925 | BC015935 | Hs.375192 | |
| 5899 | 0.006684 | Fas (TNFRSF6) associated factor 1 (FAF1), transcript variant 1, mRNA /cds=(454,2406) /gb=NM_007051 /gi=19528653 /ug=Hs.25821 /len=2610 | NM_007051 | Hs.25821 | NP_572051 |
| 5918 | 0.026643 | Mus musculus mitochondrion, complete genome | NC_001569 | | |
| 5928 | 0.021147 | ubiquitin-conjugating enzyme E2B (RAD6 (UBE2B), mRNA /cds=(422,880) /gb=NM_003337 /gi=4507770 /ug=Hs.811 /len=2591 | NM_003337 | Hs.811 | NP_003328 |
| 5934 | 0.006762 | enthoprotin (ENTH), mRNA /cds=(102,1979) /gb=NM_014666 /gi=7661967 /ug=Hs.132853 /len=3336 | NM_014666 | Hs.132853 | NP_055481 |
| 5937 | 0.045762 | mitogen-activated protein kinase 9 (MAPK9), transcript variant 3, mRNA /cds=(50,1198) /gb=NM_139069 /gi=21237741 /ug=Hs.246857 /len=1947 | NM_139069 | Hs.246857 | NP_620709 |
| 5938 | 0.013819 | chaperonin containing TCP1, subunit 3 (gamma) (CCT3), mRNA /cds=(1,1635) /gb=NM_005998 /gi=5174726 /ug=Hs.1708 /len=1901 | NM_005998 | Hs.1708 | NP_005989 |
| 5939 | 0.012175 | BTAF1 RNA polymerase II, B-TFIID transcription factor-associated, 170kDa (Mot1 S. cerevisiae) (BTAF1), mRNA /cds=(118,5667) /gb=NM_003972 /gi=27477069 /ug=Hs.180930 /len=6345 | NM_003972 | Hs.180930 | NP_003963 |
| 5959 | 0.013819 | germline T-cell receptor beta chain | U66061 | | |
| 5971 | 0.008779 | UI-E-CI1-abg-f-09-0-UI.r1 UI-E-CI1 cDNA clone UI-E-CI1-abg-f-09-0-UI 5', mRNA sequence /clone=UI-E-CI1-abg-f-09-0-UI /clone_end=5' /gb=BM691540 /gi=19004798 /ug=Hs.172047 /len=1039 | BM691540 | Hs.172047 | |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|------|----------|--|--------------------------|-----------------------------|-----------------------------|
| 5974 | 0.015649 | KIAA0266 gene product (KIAA0266), mRNA /cds=(734,3034) /gb=NM_021645 /gi=11063982 /ug=Hs.127376 /len=5585 | NM_021645 | Hs.127376 | NP_067677 |
| 5976 | 0.045762 | ox06a01.s1 Soares_fetal_liver_spleen_1NFLS_S1 cDNA clone IMAGE:1655496 3' similar to gb:M86849 GAP JUNCTION BETA-2 PROTEIN mRNA sequence /clone=IMAGE:1655496 /clone_end=3' /gb=AI033469 /gi=3254422 /ug=Hs.386279 /len=551 | AI033469 | Hs.386279 | |
| 6004 | 0.048172 | UDP-glucose pyrophosphorylase 2 (UGP2), mRNA /cds=(85,1611) /gb=NM_006759 /gi=13027637 /ug=Hs.77837 /len=1832 | NM_006759 | Hs.77837 | NP_006750 |
| 6006 | 0.018779 | ribosomal protein L23a (RPL23A), mRNA /cds=(22,492) /gb=NM_000984 /gi=17105393 /ug=Hs.419463 /len=546 | NM_000984 | Hs.419463 | NP_000975 |
| 6009 | 4.63E-04 | methylmalonyl Coenzyme A mutase (MUT), nuclear gene encoding mitochondrial protein, mRNA /cds=(77,2329) /gb=NM_000255 /gi=4557766 /ug=Hs.155212 /len=2798 | NM_000255 | Hs.155212 | NP_000246 |
| 6027 | 0.025168 | mesenchyme homeo box 2 (growth arrest specific homeo box) (MEOX2), mRNA /cds=(182,1093) /gb=NM_005924 /gi=21396478 /ug=Hs.77858 /len=2284 | NM_005924 | Hs.77858 | NP_005915 |
| 6028 | 0.043451 | protein-tyrosine kinase, trkB | X75958 | | NP_006171 |
| 6034 | 0.026643 | NRAS-related gene (D1S155E), mRNA /cds=(428,2824) /gb=NM_007158 /gi=20070240 /ug=Hs.69855 /len=4076 | NM_007158 | Hs.69855 | NP_009089 |
| 6037 | 0.006234 | splicing factor, arginine/serine-rich 2 (SFRS2), mRNA /cds=(156,821) /gb=NM_003016 /gi=4506898 /ug=Hs.73965 /len=1879 | NM_003016 | Hs.73965 | NP_003007 |
| 6042 | 0.007162 | laminin, gamma 1 (formerly LAMB2) (LAMC1), mRNA /cds=(300,5129) /gb=NM_002293 /gi=9845497 /ug=Hs.432855 /len=7923 | NM_002293 | Hs.432855 | NP_002284 |
| 6068 | 0.048172 | mitochondrial ribosomal protein L27 (MRPL27), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA /cds=(32,316) /gb=NM_148571 /gi=22547130 /ug=Hs.7736 /len=2472 | NM_148571 | Hs.7736 | NP_683412 |

| Spot | p-value | Description | Gene Accession No. | Unig ne Accession No. | Protein Accession No. |
|------|----------|---|--------------------|-----------------------|-----------------------|
| 6069 | 0.022422 | stress-associated endoplasmic reticulum protein 1; ribosome associated membrane protein 4 (SERP1), mRNA /cds=(316,516) /gb=NM_014445 /gi=19923408 /ug=Hs.76698 /len=2488 | NM_014445 | Hs.76698 | NP_055260 |
| 6083 | 0.033283 | NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (NADH-coenzyme Q reductase) (NDUFS4), mRNA /cds=(9,536) /gb=NM_002495 /gi=4505368 /ug=Hs.10758 /len=668 | NM_002495 | Hs.10758 | NP_002486 |
| 6106 | 0.009383 | EST (ym17h04.s1 clone 48282 3') | H11657 | | |
| 6139 | 0.015649 | cofilin 1 (non-muscle) (CFL1), mRNA /cds=(52,552) /gb=NM_005507 /gi=5031634 /ug=Hs.180370 /len=1059 | NM_005507 | Hs.180370 | NP_005498 |
| 6159 | 0.045762 | general transCRiption factor 2-I (GTF2I) | AF038968 | | NP_127496 |
| 6182 | 0.028189 | signal sequence receptor, gamma (translocon-associated protein gamma) (SSR3), mRNA /cds=(57,614) /gb=NM_007107 /gi=6005883 /ug=Hs.28707 /len=3061 | NM_007107 | Hs.28707 | NP_009038 |
| 6185 | 0.001721 | chloride intracellular channel 4 (CLIC4), mRNA /cds=(198,959) /gb=NM_013943 /gi=7330334 /ug=Hs.25035 /len=4318 | NM_013943 | Hs.25035 | NP_039234 |
| 6205 | 0.039115 | jumping translocation breakpoint (JTB), mRNA /cds=(433,873) /gb=NM_006694 /gi=5729888 /ug=Hs.6396 /len=1040 | NM_006694 | Hs.6396 | NP_006685 |
| 6262 | 0.018779 | UDP-glucose ceramide glucosyltransferase-like 2 (UGCG2), mRNA /cds=(72,4622) /gb=NM_020121 /gi=11386200 /ug=Hs.22983 /len=4848 | NM_020121 | Hs.22983 | NP_064506 |
| 6322 | 0.006684 | ubiquitin specific protease 9 (USP9Y) | XM_000563 | | |
| 6341 | 0.005811 | a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 1 (ADAMTS1), mRNA /cds=(294,3146) /gb=NM_006988 /gi=11038653 /ug=Hs.8230 /len=4459 | NM_006988 | Hs.8230 | NP_008919 |
| 6403 | 0.004687 | glyceronephosphate O-acyltransferase (GNPAT), mRNA /cds=(158,2200) /gb=NM_014236 /gi=7657133 /ug=Hs.12482 /len=2470 | NM_014236 | Hs.12482 | NP_055051 |
| 6428 | 0.028189 | serologically defined colon cancer antigen 1 (SDCCAG1), mRNA /cds=(183,1271) /gb=NM_004713 /gi=4759077 /ug=Hs.388584 /len=2078 | NM_004713 | Hs.388584 | NP_004704 |
| 6429 | 0.033283 | ubiquitin A-52 residue ribosomal protein fusion product 1 (UBA52), mRNA /cds=(39,425) /gb=NM_003333 /gi=15451941 /ug=Hs.5308 /len=515 | NM_003333 | Hs.5308 | NP_003324 |

| Spot | p-value | Description | Gene Accession No. | Unigen Accession No. | Protein Accession No. |
|------|----------|---|--------------------|----------------------|-----------------------|
| 6442 | 0.025168 | 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3 (PFKFB3), mRNA /cds=(115,1677) /gb=NM_004566 /gi=4758899 /ug=Hs.195471 /len=4322 | NM_004566 | Hs.195471 | NP_004557 |
| 6529 | 0.00767 | nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha (NFKBIA), mRNA /cds=(95,1048) /gb=NM_020529 /gi=10092618 /ug=Hs.81328 /len=1550 | NM_020529 | Hs.81328 | NP_065390 |
| 6543 | 0.045762 | general transcription factor IIH, polypeptide 1 (62kD subunit) (GTF2H1), mRNA /cds=(161,1807) /gb=NM_005316 /gi=19923304 /ug=Hs.89578 /len=2989 | NM_005316 | Hs.89578 | NP_005307 |
| 6565 | 0.002995 | PTK9 protein tyrosine kinase 9 (PTK9), mRNA /cds=(61,1113) /gb=NM_002822 /gi=4506274 /ug=Hs.82643 /len=3000 | NM_002822 | Hs.82643 | NP_002813 |
| 6566 | 0.019933 | RAB11A, member RAS oncogene family (RAB11A), mRNA /cds=(104,754) /gb=NM_004663 /gi=20149549 /ug=Hs.75618 /len=2474 | NM_004663 | Hs.75618 | NP_004654 |
| 6570 | 0.002773 | VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa (VAPA), mRNA /cds=(25,753) /gb=NM_003574 /gi=20070155 /ug=Hs.9006 /len=1390 | NM_003574 | Hs.9006 | NP_003565 |
| 6577 | 0.012175 | ornithine decarboxylase antizyme 1 (OAZ1), mRNA /gb=NM_004152 /gi=9845504 /ug=Hs.281960 /len=986 | NM_004152 | Hs.281960 | NP_004143 |
| 6583 | 0.045762 | KIAA0170 gene product (KIAA0170), mRNA /cds=(14,6283) /gb=NM_014641 /gi=7661965 /ug=Hs.433653 /len=6940 | NM_014641 | Hs.433653 | NP_055456 |
| 6592 | 0.00767 | methylene tetrahydrofolate dehydrogenase (NAD dependent), methenyltetrahydrofolate cyclohydrolase (MTHFD2), nuclear gene encoding mitochondrial protein, mRNA /cds=(77,1111) /gb=NM_006636 /gi=13699869 /ug=Hs.154672 /len=2154 | NM_006636 | Hs.154672 | NP_006627 |
| 6593 | 0.019933 | NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae) (NHP2L1), mRNA /cds=(95,481) /gb=NM_005008 /gi=4826859 /ug=Hs.182255 /len=1475 | NM_005008 | Hs.182255 | NP_004999 |
| 6600 | 0.043451 | gonadotropin-releasing hormone 1 (leutinizing-releasing hormone) (GNRH1), mRNA /cds=(1075,1353) /gb=NM_000825 /gi=19923125 /ug=Hs.82963 /len=1512 | NM_000825 | Hs.82963 | NP_000816 |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|------|----------|--|--------------------|-----------------------|-----------------------|
| 6603 | 0.001133 | tm68a09.x1 NCI_CGAP_Brn25 cDNA clone IMAGE:2163256 3', mRNA sequence /clone=IMAGE:2163256 /clone_end=3' /gb=AI498805 /gi=4390787 /ug=Hs.436349 /len=460 | AI498805 | Hs.436349 | |
| 6612 | 0.037084 | high-mobility group box 1 (HMGB1), mRNA /cds=(77,724) /gb=NM_002128 /gi=20149538 /ug=Hs.6727 /len=1207 | NM_002128 | Hs.6727 | NP_002119 |
| 6618 | 0.022422 | eukaryotic translation elongation factor 1 gamma (EEF1G), mRNA /cds=(38,1351) /gb=NM_001404 /gi=25453475 /ug=Hs.256184 /len=1429 | NM_001404 | Hs.256184 | NP_001395 |
| 6623 | 0.048172 | atractin (ATRN), transcript variant 1, mRNA /cds=(80,4369) /gb=NM_139321 /gi=21450860 /ug=Hs.194019 /len=8645 | NM_139321 | Hs.194019 | NP_647538 |
| 6630 | 0.005038 | NADH dehydrogenase (ubiquinone) Fe-S protein 6, 13kDa (NADH-coenzyme Q reductase) (NDUFS6), mRNA /cds=(11,385) /gb=NM_004553 /gi=4758791 /ug=Hs.49767 /len=547 | NM_004553 | Hs.49767 | NP_004544 |
| 6633 | 0.019933 | HSPCO34 protein (LOC51668), mRNA /cds=(58,402) /gb=NM_016126 /gi=7706382 /ug=Hs.46967 /len=598 | NM_016126 | Hs.46967 | NP_057210 |
| 6650 | 0.043451 | tetratricopeptide repeat domain 1 (TTC1), mRNA /cds=(51,929) /gb=NM_003314 /gi=4507710 /ug=Hs.7733 /len=1407 | NM_003314 | Hs.7733 | NP_003305 |
| 6651 | 0.028189 | tumor necrosis factor (ligand) superfamily, member 10 (TNFSF10), mRNA /cds=(96,941) /gb=NM_003810 /gi=23510439 /ug=Hs.83429 /len=1776 | NM_003810 | Hs.83429 | NP_003801 |
| 6654 | 0.017682 | pM5 protein (PM5), mRNA /cds=(1,3669) /gb=NM_014287 /gi=10947030 /ug=Hs.439182 /len=4182 | NM_014287 | Hs.439182 | NP_055102 |
| 6666 | 0.01471 | tigger transposable element derived 1 (TIGD1), mRNA /cds=(635,2410) /gb=NM_145702 /gi=22209000 /ug=Hs.351348 /len=2448 | NM_145702 | Hs.351348 | NP_663748 |
| 6683 | 0.021147 | lamin A/C (LMNA), transcript variant 1, mRNA /cds=(213,2207) /gb=NM_170707 /gi=27436945 /ug=Hs.377973 /len=3181 | NM_170707 | Hs.377973 | NP_733822 |
| 6708 | 0.043451 | erythroid differentiation-related factor 1 | AF040247 | | |
| 6715 | 0.022422 | KIAA0076 gene product (KIAA0076), mRNA /cds=(87,5183) /gb=NM_014780 /gi=7661893 /ug=Hs.51039 /len=5253 | NM_014780 | Hs.51039 | NP_055595 |
| 6722 | 0.025168 | syndecan 1 (SDC1), mRNA /cds=(253,1185) /gb=NM_002997 /gi=21359855 /ug=Hs.82109 /len=2484 | NM_002997 | Hs.82109 | NP_002988 |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Prot in Accession No. |
|------|----------|---|--------------------|-----------------------|-----------------------|
| 6734 | 0.031506 | PAI-1 mRNA-binding protein (PAI-RBP1), mRNA /cds=(86,1249) /gb=NM_015640 /gi=7661625 /ug=Hs.165998 /len=2201 | NM_015640 | Hs.165998 | NP_056455 |
| 6750 | 0.033283 | ADP-ribosylation-like factor 6 interacting protein 4 (ARL6IP4), mRNA /cds=(63,719) /gb=NM_016638 /gi=7706183 /ug=Hs.103561 /len=952 | NM_016638 | Hs.103561 | NP_061164 |
| 6752 | 0.01471 | tumor endothelial marker 6 (TEM6), mRNA /cds=(93,3710) /gb=NM_022748 /gi=17511208 /ug=Hs.12210 /len=6702 | NM_022748 | Hs.12210 | NP_073585 |
| 6755 | 0.012975 | solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3 (SLC25A3), nuclear gene encoding mitochondrial protein, transcript variant 1b, mRNA /cds=(49,1134) /gb=NM_002635 /gi=4505774 /ug=Hs.78713 /len=1330 | NM_002635 | Hs.78713 | NP_005879 |
| 6760 | 0.023762 | 2-hydroxyphytanoyl-CoA lyase (HPCL2), mRNA /cds=(100,1836) /gb=NM_012260 /gi=6912417 /ug=Hs.63290 /len=1976 | NM_012260 | Hs.63290 | NP_036392 |
| 6772 | 0.029809 | hypothetical protein FLJ22301 (FLJ22301), mRNA /cds=(696,2054) /gb=NM_024836 /gi=13376246 /ug=Hs.181406 /len=2952 | NM_024836 | Hs.181406 | NP_079112 |
| 6794 | 0.037084 | chromosome 13 open reading frame 12 (C13orf12), mRNA /cds=(76,501) /gb=NM_015932 /gi=21361533 /ug=Hs.279813 /len=1352 | NM_015932 | Hs.279813 | NP_057016 |
| 6796 | 0.007162 | hypothetical protein, clone 2746033 (HSA272196), mRNA /cds=(39,593) /gb=NM_018405 /gi=24475639 /ug=Hs.8179 /len=861 | NM_018405 | Hs.8179 | NP_060875 |
| 6813 | 0.039115 | constitutive photomorphogenic protein (COP1), mRNA /cds=(1,2196) /gb=NM_022457 /gi=21359962 /ug=Hs.105737 /len=2196 | NM_022457 | Hs.105737 | NP_071902 |
| 6829 | 0.023762 | transforming growth factor, alpha (TGFA), mRNA /cds=(32,514) /gb=NM_003236 /gi=4507460 /ug=Hs.170009 /len=4119 | NM_003236 | Hs.170009 | NP_003227 |
| 6835 | 0.012975 | mRNA for KIAA0191 gene, partial cds. /cds=(1,4553) /gb=D83776 /gi=1228034 /ug=Hs.12413 /len=5203 | D83776 | Hs.12413 | |
| 6846 | 0.035141 | mitogen-activated protein kinase kinase 7 (MAP3K7), transcript variant A, mRNA /cds=(306,2045) /gb=NM_003188 /gi=21735560 /ug=Hs.7510 /len=2912 | NM_003188 | Hs.7510 | NP_663306 |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|------|----------|---|--------------------|-----------------------|-----------------------|
| 6851 | 0.013819 | Similar to expressed sequence AW111961, clone IMAGE:5268751, mRNA /gb=BC041839 /gi=27693117 /ug=Hs.237642 /len=3713 | BC041839 | Hs.237642 | |
| 6861 | 0.005811 | mRNA; cDNA DKFZp434A012 (from clone DKFZp434A012) /gb=AL096752 /gi=5419888 /ug=Hs.306327 /len=2248 | AL096752 | Hs.306327 | |
| 6880 | 0.031506 | cytochrome c oxidase subunit VIIa polypeptide 1 (muscle) (COX7A1), nuclear gene encoding mitochondrial protein, mRNA /cds=(463,702) /gb=NM_001864 /gi=18105034 /ug=Hs.421621 /len=783 | NM_001864 | Hs.421621 | NP_001855 |
| 6881 | 0.006684 | uncharacterized hematopoietic stem/progenitor cells protein MDS029 (MDS029), mRNA /cds=(112,438) /gb=NM_018464 /gi=8923929 /ug=Hs.43549 /len=636 | NM_018464 | Hs.43549 | NP_060934 |
| 6894 | 0.009383 | Werner helicase interacting protein (WHIP), transcript variant 1, mRNA /cds=(192,2189) /gb=NM_020135 /gi=18426901 /ug=Hs.236828 /len=2670 | NM_020135 | Hs.236828 | NP_569079 |
| 6920 | 0.017682 | thioredoxin (TXN), mRNA /cds=(64,381) /gb=NM_003329 /gi=4507744 /ug=Hs.432922 /len=501 | NM_003329 | Hs.432922 | NP_003320 |
| 6935 | 0.048172 | FtsJ 3 (E. coli) (FTSJ3), mRNA /cds=(72,2615) /gb=NM_017647 /gi=17017990 /ug=Hs.257486 /len=2999 | NM_017647 | Hs.257486 | NP_060117 |
| 6941 | 0.039115 | SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 2 (SMARCC2), transcript variant 1, mRNA /cds=(33,3677) /gb=NM_003075 /gi=21237804 /ug=Hs.236030 /len=4039 | NM_003075 | Hs.236030 | NP_620706 |
| 6969 | 0.010023 | oligophrenin 1 (OPHN1), mRNA /cds=(638,3046) /gb=NM_002547 /gi=4505506 /ug=Hs.128824 /len=7350 (=FLJ11206) | NM_002547 | Hs.128824 | NP_002538 |
| 6972 | 0.035141 | similar to zinc finger protein (LOC91172), mRNA (=FLJ12859,=FLJ11645) | XM_036627 | | |
| 6974 | 0.045762 | NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1, 8kDa (NDUFAB1), mRNA /cds=(25,495) /gb=NM_005003 /gi=4826851 /ug=Hs.5556 /len=663 | NM_005003 | Hs.5556 | NP_004994 |
| 6989 | 0.012175 | transmembrane 9 superfamily member 1 (TM9SF1), mRNA /cds=(35,1855) /gb=NM_006405 /gi=21361314 /ug=Hs.91586 /len=2138 | NM_006405 | Hs.91586 | NP_006396 |

| Spot | p-value | Description | Gene Accession No. | Unig ne Accession No. | Protein Accession No. |
|------|----------|---|--------------------|-----------------------|-----------------------|
| 7005 | 0.005811 | clone MGC:24133 IMAGE:4693393, mRNA, complete cds /cds=(61,528) /gb=BC017973 /gi=22450811 /ug=Hs.288010 /len=946 | BC017973 | Hs.288010 | NP_777556 |
| 7022 | 0.019933 | ribosomal protein S29 (RPS29), mRNA /cds=(31,201) /gb=NM_001032 /gi=13904868 /ug=Hs.539 /len=346 | NM_001032 | Hs.539 | NP_001023 |
| 7033 | 0.029809 | vacuolar protein sorting 35 (yeast) (VPS35), mRNA /cds=(48,2438) /gb=NM_018206 /gi=17999540 /ug=Hs.264190 /len=2707 | NM_018206 | Hs.264190 | NP_060676 |
| 7042 | 0.047799 | mRNA for KIAA0261 gene, partial cds. /cds=(1,3866) /gb=D87450 /gi=1665788 /ug=Hs.154978 /len=6155 | D87450 | Hs.154978 | |
| 7043 | 0.009383 | platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit 45kDa (PAFAH1B1), mRNA /cds=(556,1788) /gb=NM_000430 /gi=6031206 /ug=Hs.77318 /len=5581 | NM_000430 | Hs.77318 | NP_000421 |
| 7048 | 0.012975 | twisted gastrulation-1 (Drosophila) (TWSG1), mRNA /cds=(106,777) /gb=NM_020648 /gi=21314788 /ug=Hs.247302 /len=3693 | NM_020648 | Hs.247302 | NP_065699 |
| 7068 | 3.16E-04 | KIAA1128 protein (KIAA1128), mRNA /cds=(553,2253) /gb=NM_018999 /gi=24308130 /ug=Hs.81897 /len=7248 | NM_018999 | Hs.81897 | NP_061872 |
| 7097 | 0.037084 | translocating chain-associating membrane protein (TRAM), mRNA /cds=(92,1216) /gb=NM_014294 /gi=19923404 /ug=Hs.4147 /len=2722 | NM_014294 | Hs.4147 | NP_055109 |
| 7098 | 0.039115 | inactive progesterone receptor, 23 kD (TEBP), mRNA /cds=(107,589) /gb=NM_006601 /gi=23308578 /ug=Hs.278270 /len=1490 | NM_006601 | Hs.278270 | NP_006592 |
| 7102 | 0.010023 | survival of motor neuron protein interacting protein 1 (SIP1), mRNA /cds=(84,926) /gb=NM_003616 /gi=4506960 /ug=Hs.102456 /len=1285 | NM_003616 | Hs.102456 | NP_003607 |
| 7107 | 0.00767 | ectonucleotide pyrophosphatase/phosphodiesterase 4 (putative function) (ENPP4), mRNA /cds=(49,1410) /gb=NM_014936 /gi=7662357 /ug=Hs.54037 /len=4312 | NM_014936 | Hs.54037 | NP_055751 |
| 7127 | 0.026643 | actin-related protein 10 (S. cerevisiae) (ACTR10), mRNA /cds=(81,1334) /gb=NM_018477 /gi=8923711 /ug=Hs.274369 /len=1621 | NM_018477 | Hs.274369 | NP_060947 |

| Spot | p-value | Description | Gen Accession No. | Unig ne Accession No. | Protein Accession No. |
|------|----------|---|-------------------|-----------------------|-----------------------|
| 7143 | 0.041237 | benzodiazapine receptor (peripheral) (BZRP), nuclear gene encoding mitochondrial protein, transcript variant PBR, mRNA /cds=(88,597) /gb=NM_000714 /gi=21536444 /ug=Hs.202 /len=848 | NM_000714 | Hs.202 | NP_009295 |
| 7166 | 0.01471 | transducer of ERBB2, 1 (TOB1), mRNA /cds=(36,1073) /gb=NM_005749 /gi=22035666 /ug=Hs.178137 /len=1830 | NM_005749 | Hs.178137 | NP_005740 |
| 7175 | 0.029809 | AGENCOURT_6853421 NIH_MGC_99 cDNA clone IMAGE:5926418 5', mRNA sequence /clone=IMAGE:5926418 /clone_end=5' /gb=BQ064669 /gi=19893520 /ug=Hs.380699 /len=969 | BQ064669 | Hs.380699 | |
| 7176 | 0.012175 | tumor protein, translationally-controlled 1 (TPT1), mRNA /cds=(95,613) /gb=NM_003295 /gi=4507668 /ug=Hs.401448 /len=830 | NM_003295 | Hs.401448 | NP_003286 |
| 7178 | 0.005412 | supervillin (SVIL), transcript variant 2, mRNA /cds=(754,7398) /gb=NM_021738 /gi=11496981 /ug=Hs.154567 /len=8300 | NM_021738 | Hs.154567 | NP_068506 |
| 7187 | 0.015649 | collagen, type V, alpha 1 (COL5A1), mRNA /cds=(383,5899) /gb=NM_000093 /gi=16554578 /ug=Hs.146428 /len=6496 | NM_000093 | Hs.146428 | NP_000084 |
| 7201 | 0.043451 | glutathione peroxidase 1 (GPX1), mRNA /cds=(319,924) /gb=NM_000581 /gi=10834975 /ug=Hs.76686 /len=1134 | NM_000581 | Hs.76686 | NP_000572 |
| 7234 | 0.00104 | chemokine-like factor 1 (CKLF1), mRNA /cds=(148,606) /gb=NM_016951 /gi=10092593 /ug=Hs.15159 /len=689 | NM_016951 | Hs.15159 | NP_058647 |
| 7240 | 0.023762 | block of proliferation 1 (BOP1), mRNA /cds=(43,2283) /gb=NM_015201 /gi=21389316 /ug=Hs.30736 /len=2396 | NM_015201 | Hs.30736 | NP_056016 |
| 7243 | 6.11E-04 | calcium/calmodulin-dependent protein kinase kinase 2, beta (CAMKK2), transcript variant 1, mRNA /cds=(830,2596) /gb=NM_006549 /gi=27437014 /ug=Hs.108708 /len=5620 | NM_006549 | Hs.108708 | NP_757380 |
| 7244 | 0.011417 | Nedd-4-like ubiquitin-protein ligase, clone MGC:17353 IMAGE:3453212, mRNA, complete cds | BC013645.1 | Hs.333382 | AAH13645.1 |
| 7279 | 0.028189 | B double prime 1, subunit of RNA polymerase III transcription initiation factor IIIB (BDP1), mRNA /cds=(205,6969) /gb=NM_018429 /gi=21281668 /ug=Hs.272808 /len=7207 | NM_018429 | Hs.272808 | NP_060899 |

| Spot | p-value | D scription | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|------|----------|--|--------------------|-----------------------|-----------------------|
| 7283 | 0.048172 | HSPC056 protein (HSPC056), mRNA /cds=(145,972) /gb=NM_014154 /gi=7661763 /ug=Hs.422287 /len=2879 | NM_014154 | Hs.422287 | NP_054873 |
| 7284 | 0.033283 | GK003 protein (GK003), mRNA /cds=(10,690) /gb=NM_020192 /gi=21281666 /ug=Hs.83313 /len=901 | NM_020192 | Hs.83313 | NP_064577 |
| 7285 | 0.043451 | MR4-ET0140-070501-014-g01 ET0140 cDNA, mRNA sequence /gb=BQ331564 /gi=20972721 /ug=Hs.442329 /len=219 | BQ331564 | Hs.442329 | |
| 7288 | 0.022422 | KIAA0800 gene product (KIAA0800), mRNA /cds=(169,4692) /gb=NM_014703 /gi=7662315 /ug=Hs.118738 /len=5984 | NM_014703 | Hs.118738 | NP_055518 |
| 7310 | 0.023762 | UI-H-BI2-agp-f-12-0-UI.s1 NCI_CGAP_Sub4 cDNA clone IMAGE:2725031 3', mRNA sequence /clone=IMAGE:2725031 /clone_end=3' /gb=AW292456 /gi=6699092 /ug=Hs.437793 /len=745 | AW292456 | Hs.437793 | |
| 7313 | 0.048172 | translocation protein 1 (TLOC1), mRNA /cds=(613,1812) /gb=NM_003262 /gi=14602425 /ug=Hs.8146 /len=3091 | NM_003262 | Hs.8146 | NP_003253 |
| 7319 | 0.039115 | mRNA for KIAA0276 gene, partial cds. /cds=(1,932) /gb=D87466 /gi=1665816 /ug=Hs.240112 /len=4185 | D87466 | Hs.240112 | |
| 7320 | 0.006684 | RNA-binding region (RNP1, RRM) containing 4 (RNPC4), mRNA /cds=(187,1461) /gb=NM_018107 /gi=21361701 /ug=Hs.4997 /len=2442 | NM_018107 | Hs.4997 | NP_060577 |
| 7321 | 0.017682 | translocase of inner mitochondrial membrane 17 A (yeast) (TIMM17A), mRNA /cds=(8,523) /gb=NM_006335 /gi=5454119 /ug=Hs.20716 /len=1645 | NM_006335 | Hs.20716 | NP_006326 |
| 7322 | 0.031506 | BM-017 (=ALEX3) | AF208859 | | NP_808817 |
| 7331 | 0.037084 | AGENCOURT_8856629 Lupski_sciatic_nerve cDNA clone IMAGE:6200636 5', mRNA sequence /clone=IMAGE:6200636 /clone_end=5' /gb=BQ947179 /gi=22362657 /ug=Hs.356605 /len=1277 | BQ947179 | Hs.356605 | |
| 7343 | 0.007162 | hypothetical protein FLJ12619 (FLJ12619), mRNA /cds=(539,1228) /gb=NM_030939 /gi=21359961 /ug=Hs.7779 /len=2444 | NM_030939 | Hs.7779 | NP_112201 |
| 7349 | 0.005412 | dermatopontin (DPT), mRNA /cds=(7,612) /gb=NM_001937 /gi=4755134 /ug=Hs.80552 /len=717 | NM_001937 | Hs.80552 | NP_001928 |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|------|----------|---|--------------------|-----------------------|-----------------------|
| 7357 | 0.008208 | chromosome 6 open reading frame 33 (C6orf33), mRNA /cds=(165,1229) /gb=NM_133367 /gi=19115959 /ug=Hs.239388 /len=4650 | NM_133367 | Hs.239388 | NP_588608 |
| 7360 | 0.028189 | clone IMAGE:5016712, mRNA /gb=BC032119 /gi=22749564 /ug=Hs.400876 /len=1185 | BC032119 | Hs.400876 | |
| 7361 | 0.037084 | SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4 (SMARCA4), mRNA /cds=(277,5220) /gb=NM_003072 /gi=21071055 /ug=Hs.78202 /len=5681 | NM_003072 | Hs.78202 | NP_003063 |
| 7378 | 0.022422 | regulator of G-protein signalling 10 (RGS10), mRNA /cds=(44,547) /gb=NM_002925 /gi=11184225 /ug=Hs.82280 /len=664 | NM_002925 | Hs.82280 | NP_002916 |
| 7387 | 0.037157 | ribosomal protein L4 (RPL4), mRNA /cds=(57,1340) /gb=NM_000968 /gi=16579884 /ug=Hs.286 /len=1449 | NM_000968 | Hs.286 | NP_000959 |
| 7390 | 0.045762 | peptidylprolyl isomerase A (cyclophilin A) (PPIA), mRNA /cds=(45,542) /gb=NM_021130 /gi=10863926 /ug=Hs.401787 /len=753 | NM_021130 | Hs.401787 | NP_066953 |
| 7414 | 6.69E-04 | tetraspanin similar to TM4SF9 (DC-TM4F2), mRNA /cds=(79,891) /gb=NM_030927 /gi=13569888 /ug=Hs.101395 /len=2556 | NM_030927 | Hs.101395 | NP_112189 |
| 7420 | 0.029809 | UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (GalNAc-T1) (GALNT1), mRNA /cds=(32,1711) /gb=NM_020474 /gi=13124890 /ug=Hs.80120 /len=3778 | NM_020474 | Hs.80120 | NP_065207 |
| 7427 | 0.003487 | tropomyosin 3 (TPM3), mRNA /cds=(52,798) /gb=NM_153649 /gi=24119202 /ug=Hs.85844 /len=2089 | NM_153649 | Hs.85844 | NP_705935 |
| 7455 | 0.039115 | 1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltransferase, beta) (AGPAT2), mRNA /cds=(67,903) /gb=NM_006412 /gi=6041664 /ug=Hs.209119 /len=1522 | NM_006412 | Hs.209119 | NP_006403 |
| 7491 | 0.019933 | chromosome 20 open reading frame 149 (C20orf149), mRNA /cds=(150,494) /gb=NM_024299 /gi=13236523 /ug=Hs.79625 /len=803 | NM_024299 | Hs.79625 | NP_077275 |
| 7508 | 0.012175 | mRNA for RCC1-like protein (TD-60 gene) /cds=(236,1804) /gb=AJ421269 /gi=27526612 /ug=Hs.284146 /len=4114 | AJ421269 | Hs.284146 | NP_061185 |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Prot in Accession No. |
|------|----------|---|--------------------|-----------------------|-----------------------|
| 7548 | 0.015649 | methionine adenosyltransferase II, beta (MAT2B), mRNA /cds=(73,1077) /gb=NM_013283 /gi=20127525 /ug=Hs.54642 /len=2054 | NM_013283 | Hs.54642 | NP_037415 |
| 7574 | 0.039115 | ubiquitin-conjugating enzyme E2N (UBC13 yeast) (UBE2N), mRNA /cds=(64,522) /gb=NM_003348 /gi=4507792 /ug=Hs.75355 /len=1203 | NM_003348 | Hs.75355 | NP_003339 |
| 7576 | 0.002192 | cytochrome P450, family 1, subfamily B, polypeptide 1 (CYP1B1), mRNA /cds=(373,2004) /gb=NM_000104 /gi=13325059 /ug=Hs.154654 /len=5128 | NM_000104 | Hs.154654 | NP_000095 |
| 7577 | 0.00767 | chromosome 14 open reading frame 108 (C14orf108), mRNA /cds=(407,1879) /gb=NM_018229 /gi=21361775 /ug=Hs.106210 /len=3088 | NM_018229 | Hs.106210 | NP_060699 |
| 7581 | 0.017682 | FK506 binding protein 5 (FKBP5), mRNA /cds=(154,1527) /gb=NM_004117 /gi=17149847 /ug=Hs.7557 /len=3781 | NM_004117 | Hs.7557 | NP_004108 |
| 7587 | 3.83E-04 | XPA binding protein 1; putative ATP(GTP)-binding protein (NTPBP), mRNA /cds=(25,1149) /gb=NM_007266 /gi=14149628 /ug=Hs.18259 /len=1829 | NM_007266 | Hs.18259 | NP_009197 |
| 7599 | 0.012975 | fibrinogen, B beta polypeptide (FGB), mRNA /cds=(9,1484) /gb=NM_005141 /gi=11761630 /ug=Hs.7645 /len=1918 | NM_005141 | Hs.7645 | NP_005132 |
| 7600 | 0.033283 | hypothetical protein MGC45400 (MGC45400), mRNA /cds=(245,598) /gb=NM_153333 /gi=23503246 /ug=Hs.389734 /len=1290 | NM_153333 | Hs.389734 | NP_699164 |
| 7618 | 0.037084 | hypothetical protein FLJ11240 (FLJ11240), mRNA /cds=(26,1648) /gb=NM_018368 /gi=8922955 /ug=Hs.339833 /len=1947 | NM_018368 | Hs.339833 | NP_060838 |
| 7623 | 0.009969 | growth factor receptor-bound protein 10 (GRB10), mRNA /cds=(782,2548) /gb=NM_005311 /gi=19923302 /ug=Hs.81875 /len=5431 | NM_005311 | Hs.81875 | NP_005302 |
| 7637 | 0.012975 | serum response factor (c-fos serum response element-binding transcription factor) (SRF), mRNA /cds=(359,1885) /gb=NM_003131 /gi=4507204 /ug=Hs.155321 /len=4201 | NM_003131 | Hs.155321 | NP_003122 |
| 7642 | 0.048172 | actin, beta (ACTB), mRNA /cds=(74,1201) /gb=NM_001101 /gi=5016088 /ug=Hs.426930 /len=1793 | NM_001101 | Hs.426930 | NP_001092 |
| 7694 | 4.70E-05 | cDNA FLJ25013 fis, clone CBL01365. /gb=AK057742 /gi=16553667 /ug=Hs.380091 /len=2200 | AK057742 | Hs.380091 | |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|------|----------|---|--------------------|-----------------------|-----------------------|
| 7697 | 0.045762 | thioredoxin interacting protein (TXNIP), mRNA /cds=(222,1397) /gb=NM_006472 /gi=5454161 /ug=Hs.179526 /len=2704 | NM_006472 | Hs.179526 | NP_006463 |
| 7724 | 0.003233 | tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin) (TNFRSF11B), mRNA /cds=(252,1457) /gb=NM_002546 /gi=22547122 /ug=Hs.81791 /len=2291 | NM_002546 | Hs.81791 | NP_002537 |
| 7730 | 0.001342 | MTB (MTB) mRNA, complete cds /cds=(80,265) /gb=AF348994 /gi=28190031 /ug=Hs.333727 /len=408 | AF348994 | Hs.333727 | NP_783321 |
| 7731 | 0.005412 | cDNA FLJ14844 fis, clone PLACE1000133, highly similar to TRANSCRIPTION FACTOR BTF3. /cds=(91,567) /gb=AK027750 /gi=14042660 /ug=Hs.93748 /len=2203 | AK027750 | Hs.93748 | |
| 7753 | 0.017682 | SAC1 suppressor of actin mutations 1-like (yeast) (SACM1L), mRNA /cds=(70,1833) /gb=NM_014016 /gi=7662337 /ug=Hs.5867 /len=3572 | NM_014016 | Hs.5867 | NP_054735 |
| 7807 | 0.011417 | poly(A) polymerase gamma (PAPOLG), mRNA /cds=(232,2442) /gb=NM_022894 /gi=16306567 /ug=Hs.146123 /len=4252 | NM_022894 | Hs.146123 | NP_075045 |
| 7839 | 0.023762 | EST(xc43h04.x1 NCI_CGAP_Co20 clone IMAGE:2587063 3' gb:M99436 TRANSDUCIN-LIKE ENHANCER PROTEIN 2) | AW081723 | | NP_003251 |
| 7873 | 0.002024 | BX098638 Soares fetal liver spleen 1NFLS cDNA clone IMAGp998G14405, mRNA sequence /clone=IMAGp998G14405 IMAGE:208165 /gb=BX098638 /gi=27829530 /ug=Hs.435496 /len=438 | BX098638 | Hs.435496 | |
| 7908 | 0.031506 | EST EST43399 Fetal brain I cDNA 3' end | AA338448 | | NP_112577 |
| 7941 | 0.00767 | EST (EST370348 MAGE resequences, MAGE cDNA) | AW958278 | | NP_112420 |
| 7951 | 0.008208 | EST (am59f03.x1 Johnston frontal | AI124626 | | |
| 7968 | 0.031506 | low density lipoprotein receptor-related protein 5 (LRP5), mRNA /cds=(49,4896) /gb=NM_002335 /gi=4505018 /ug=Hs.6347 /len=5100 | NM_002335 | Hs.6347 | NP_002326 |
| 7985 | 0.035141 | SH3-domain GRB2-like 3 (SH3GL3), mRNA /cds=(493,1560) /gb=NM_003027 /gi=20070145 /ug=Hs.80315 /len=2015 | NM_003027 | Hs.80315 | NP_003018 |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|------|----------|--|--------------------|-----------------------|-----------------------|
| 7991 | 0.033283 | hypothetical protein FLJ20425 (LYAR), mRNA /cds=(189,1328) /gb=NM_017816 /gi=8923397 /ug=Hs.425427 /len=1598 | NM_017816 | Hs.425427 | NP_060286 |
| 8020 | 0.023762 | phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase (GART), mRNA /cds=(79,3111) /gb=NM_000819 /gi=24475881 /ug=Hs.82285 /len=3291 | NM_000819 | Hs.82285 | NP_780294 |
| 8054 | 0.011417 | pyruvate dehydrogenase kinase 4 mRNA, 3' untranslated region, partial sequence /cds=UNKNOWN/gb=AF334710 /gi=12658438 /ug=Hs.8364 /len=1819 | AF334710 | Hs.8364 | NP_002603 |
| 8056 | 0.00767 | ADP-ribosyltransferase (NAD ; poly (ADP-ribose) polymerase) (ADPRT), mRNA /cds=(160,3204) /gb=NM_001618 /gi=11496989 /ug=Hs.177766 /len=3859 | NM_001618 | Hs.177766 | NP_001609 |
| 8076 | 0.041237 | hypothetical protein PRO2577 (PRO2577), mRNA /cds=(492,665) /gb=NM_018630 /gi=8924181 /ug=Hs.241576 /len=1032 | NM_018630 | Hs.241576 | |
| 8097 | 0.027996 | mRNA for KIAA1915 protein, partial cds. /cds=(356,2536) /gb=AB067502 /gi=15620888 /ug=Hs.12915 /len=7801 | AB067502 | Hs.12915 | |
| 8191 | 0.035141 | downstream neighbor of SON (DONSON), transcript variant 1, mRNA /cds=(68,1768) /gb=NM_017613 /gi=22035582 /ug=Hs.17834 /len=2189 | NM_017613 | Hs.17834 | NP_665738 |
| 8198 | 0.039115 | PHD zinc finger protein XAP135 (XAP135), transcript variant 2, mRNA /cds=(222,1448) /gb=NM_133325 /gi=19747275 /ug=Hs.7759 /len=1583 | NM_133325 | Hs.7759 | NP_579866 |
| 8203 | 0.019933 | hypothetical protein FLJ14668 (FLJ14668), mRNA /cds=(59,475) /gb=NM_032822 /gi=14249519 /ug=Hs.334644 /len=1786 | NM_032822 | Hs.334644 | NP_116211 |
| 8230 | 0.01471 | mRNA for KIAA0592 protein, partial cds. /cds=(1,4062) /gb=AB011164 /gi=3043707 /ug=Hs.439367 /len=4623 | AB011164 | Hs.439367 | |
| 8272 | 0.043451 | EST(PM4-BT0650-010400-002-a06 BT0650) | BE083882 | | NP_060487 |
| 8308 | 0.004048 | EST(ty24e09.x1 NCI_CGAP_Ut3 clone IMAGE:2280040 3' contains Alu repeat) | AI758800 | | |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|------|----------|---|--------------------|-----------------------|-----------------------|
| 8309 | 0.002773 | hypothetical protein FLJ14906 (FLJ14906), mRNA /cds=(131,736) /gb=NM_032859 /gi=14249591 /ug=Hs.183528 /len=2492 | NM_032859 | Hs.183528 | NP_116248 |
| 8333 | 0.035141 | EST (fb12g02.x1 zebrafish fin day0 regeneration) | AI384158 | | |
| 8341 | 0.019933 | EST(we27d09.x1 NCI_CGAP_Lu24 clone IMAGE:2342321 3') | AI797144 | | NP_002877 |
| 8359 | 0.035141 | UI-H-BW1-amn-b-05-0-UI.s1 NCI_CGAP_Sub7 cDNA clone IMAGE:3070401 3', mRNA sequence /clone=IMAGE:3070401 /clone_end=3' /gb=BF513064 /gi=11598243 /ug=Hs.446233 /len=777 | BF513064 | Hs.446233 | |
| 8373 | 0.035141 | NISC_gj17d11.x1 NCI_CGAP_Pr28 cDNA clone IMAGE:3272108 3', mRNA sequence /clone=IMAGE:3272108 /clone_end=3' /gb=CB050438 /gi=27788725 /ug=Hs.435309 /len=534 | CB050438 | Hs.435309 | |
| 8381 | 0.010023 | Tho2 mRNA, complete cds /cds=(1,4437) /gb=AF441770 /gi=20799317 /ug=Hs.16411 /len=4452 | AF441770 | Hs.16411 | |
| 8411 | 0.017682 | UI-1-BB1p-aya-d-12-0-UI.s1 NCI_CGAP_PI6 cDNA clone UI-1-BB1p-aya-d-12-0-UI 3', mRNA sequence /clone=UI-1-BB1p-aya-d-12-0-UI /clone_end=3' /gb=BU754499 /gi=23713459 /ug=Hs.432873 /len=1196 | BU754499 | Hs.432873 | |
| 8435 | 0.019933 | BX099435 NCI_CGAP_Co8 cDNA clone IMAGp998M083951, mRNA sequence /clone=IMAGp998M083951 IMAGE:1559599 /gb=BX099435 /gi=27829993 /ug=Hs.126589 /len=659 | BX099435 | Hs.126589 | |
| 8438 | 0.017682 | mRNA sequence /gb=L26969 /gi=16905391 /ug=Hs.362852 /len=1738 | L26969 | Hs.362852 | |
| 8459 | 0.003487 | zs54b10.r1 NCI_CGAP_GCB1 cDNA clone IMAGE:701275 5', mRNA sequence /clone=IMAGE:701275 /clone_end=5' /gb=AA287780 /gi=1933461 /ug=Hs.369808 /len=497 | AA287780 | Hs.369808 | |
| 8472 | 0.037084 | cDNA FLJ14188 fis, clone NT2RP2005980. /gb=AK024250 /gi=10436579 /ug=Hs.288671 /len=2289 | AK024250 | Hs.288671 | |
| 8480 | 0.031506 | ribosomal protein L37a (RPL37A), mRNA /cds=(36,314) /gb=NM_000998 /gi=16306561 /ug=Hs.296290 /len=392 | NM_000998 | Hs.296290 | NP_000989 |
| 8486 | 0.043451 | cDNA, 3' end /clone=IMAGE:1935382 /clone_end=3' /gb=AI340092 /gi=4077019 /ug=Hs.327321 /len=361 | AI340092 | Hs.327321 | NP_002370 |

| Spot | p-value | D scription | Gene Accession No. | Unigene Acc ssion No. | Protein Accession No. |
|------|----------|---|--------------------------|-----------------------------|-----------------------------|
| 8492 | 0.003233 | EST CM2-BT0857-021100-470-g06 BT0857 Homo sapiens cDNA | BF745663 | | |
| 8514 | 0.041237 | mRNA; cDNA DKFZp451B1818 (from clone DKFZp451B1818) /gb=AL832623 /gi=21733198 /ug=Hs.77554 /len=6240 | AL832623 | Hs.77554 | |
| 8516 | 0.039115 | EST (MR1-SN0033-100400-001-a10 SN0033) | AW867013 | | |
| 8529 | 0.004357 | EST (602645742F1 NIH_MGC_76 clone IMAGE:4767299 5') | BG618375 | | |
| 8530 | 0.045762 | UI-E-EJ0-ahq-g-22-0-UI.s1 UI-E-EJ0 cDNA clone UI-E-EJ0-ahq-g-22-0-UI.3', mRNA sequence /clone=UI-E-EJ0-ahq-g- 22-0-UI /clone_end=3' /gb=BM674631 /gi=18984529 /ug=Hs.444500 /len=1272 | BM674631 | Hs.444500 | |
| 8546 | 0.045762 | EST(hc98c08.x1 Soares_NFL_T_GBC_S1 cDNA clone IMAGE:2908046 3' similar to TR:O14792 O14792 HEPARAN SULFATE 3-O- SULFOTRANSFERASE-1 PRECURSOR) | AW340546 | | NP_005105 |
| 8547 | 0.019933 | cDNA FLJ36837 fis, clone ASTRO2011422. /gb=AK094156 /gi=21753158 /ug=Hs.36475 /len=3302 | AK094156 | Hs.36475 | |
| 8557 | 0.018779 | UI-H-ED0-awy-a-01-0-UI.s1 NCI_CGAP_ED0 cDNA clone IMAGE:5825160 3', mRNA sequence /clone=IMAGE:5825160 /clone_end=3' /gb=BQ017647 /gi=19752924 /ug=Hs.124747 /len=1445 | BQ017647 | Hs.124747 | |
| 8560 | 0.012175 | ribosomal protein L28 (RPL28), mRNA /cds=(43,456) /gb=NM_000991 /gi=13904865 /ug=Hs.356371 /len=500 | NM_000991 | Hs.356371 | NP_000982 |
| 8564 | 0.039115 | EST(cDNA clone IMAGE:2569171 3') | AW073383 | | |
| 8595 | 0.017682 | ribosomal protein L3 (RPL3), mRNA /cds=(27,1238) /gb=NM_000967 /gi=16507968 /ug=Hs.119598 /len=1311 | NM_000967 | Hs.119598 | NP_000958 |
| 8606 | 0.011736 | hypothetical protein DKFZp451G182 (DKFZp451G182), mRNA /cds=(99,4049) /gb=NM_153610 /gi=23957703 /ug=Hs.50794 /len=4678 | NM_153610 | Hs.50794 | NP_705838 |
| 8646 | 0.001585 | cDNA FLJ39413 fis, clone PLACE6015729. /gb=AK096732 /gi=21756291 /ug=Hs.194339 /len=1957 | AK096732 | Hs.194339 | |
| 8669 | 0.005412 | cDNA FLJ10190 fis, clone HEMBA1004753. /gb=AK001052 /gi=7022081 /ug=Hs.274546 /len=1318 | AK001052 | Hs.274546 | |
| 8673 | 0.012175 | jun1.P1.D7 conorm cDNA 3', mRNA sequence /clone_end=3' /gb=AI535800 /gi=4449935 /ug=Hs.369112 /len=480 | AI535800 | Hs.369112 | |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|------|----------|--|--------------------|-----------------------|-----------------------|
| 8675 | 0.002372 | UI-H-EI0-ayo-a-20-0-UI.s1 NCI_CGAP_EI0 cDNA clone IMAGE:5841307 3', mRNA sequence /clone=IMAGE:5841307 /clone_end=3' /gb=BQ004581 /gi=19729481 /ug=Hs.412459 /len=1095 | BQ004581 | Hs.412459 | |
| 8738 | 0.041237 | tb26b01.x1 NCI_CGAP_Kid12 cDNA clone IMAGE:2055433 3' similar to contains Alu repetitive element;, mRNA sequence /clone=IMAGE:2055433 /clone_end=3' /gb=AI308217 /gi=4002852 /ug=Hs.177064 /len=421 | AI308217 | Hs.177064 | |
| 8746 | 0.018779 | tg02e02.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:2107610 3', mRNA sequence /clone=IMAGE:2107610 /clone_end=3' /gb=AI380429 /gi=4190282 /ug=Hs.172445 /len=478 | AI380429 | Hs.172445 | |
| 8769 | 0.033283 | EST(adult brain Danio rerio cDNA clone 4966301 5' similar to SW:RLA1_CHICK P18660 60S ACIDIC RIBOSOMAL PROTEIN P1. ;contains element MER22 repetitive element ;) | BI429083 | | |
| 8771 | 0.035141 | mitochondrion, complete genome | NC_001807 | | |
| 8781 | 0.011417 | cDNA: FLJ20933 fis, clone ADSE01388. /gb=AK024586 /gi=10436898 /ug=Hs.296757 /len=1567 | AK024586 | Hs.296757 | |
| 8788 | 0.012975 | ESTs, cDNA /gb=AW978555 /gi=8169822 /ug=Hs.92448 /len=754 | AW978555 | Hs.92448 | |
| 8828 | 0.037084 | cDNA FLJ13443 fis, clone PLACE1002853 | AK023505 | | NP_078968 |
| 8837 | 0.003487 | no significant match | SEQ.ID.No.39 | | |
| 8838 | 0.048172 | No significant match | SEQ.ID.No.45 | | |
| 8840 | 0.019933 | No significant match | SEQ.ID.No.54 | | |
| 8856 | 0.003233 | control | | | |
| 8874 | 0.026411 | No significant match. (ORF:+1:256~491[237]) | SEQ.ID.No.26 | | |
| 8946 | 0.018779 | hypothetical protein FLJ33282 (FLJ33282), mRNA /cds=(225,1523) /gb=NM_152388 /gi=22748830 /ug=Hs.346509 /len=2078 | NM_152388 | Hs.346509 | |
| 8949 | 0.029809 | tx18g05.x1 NCI_CGAP_Ut4 cDNA clone IMAGE:2269592 3', mRNA sequence /clone=IMAGE:2269592 /clone_end=3' /gb=AI612954 /gi=4622121 /ug=Hs.187303 /len=205 | AI612954 | Hs.187303 | |
| 8967 | 0.032562 | hypothetical protein FLJ13231 (FLJ13231), mRNA /cds=(134,1255) /gb=NM_023073 /gi=12751482 /ug=Hs.156148 /len=2642 | NM_023073 | Hs.156148 | NP_075561 |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|------|----------|---|--------------------|-----------------------|-----------------------|
| 8972 | 0.023762 | EST (ym20a08.r1 Soares infant brain 1NIB IMAGE:48353 5') | H15948 | | |
| 8981 | 0.006234 | AV737351 CB cDNA clone CBLALE11 5', mRNA sequence /clone=CBLALE11 /clone_end=5' /gb=AV737351 /gi=10854932 /ug=Hs.444989 /len=511 | AV737351 | Hs.444989 | |
| 8988 | 0.019933 | hypothetical protein FLJ36674 (FLJ36674), mRNA /cds=(26,484) /gb=NM_173622 /gi=27734737 /ug=Hs.164595 /len=2236 | NM_173622 | Hs.164595 | NP_775893 |
| 8990 | 0.028189 | hypothetical protein FLJ39514 (FLJ39514), mRNA /cds=(121,2040) /gb=NM_152540 /gi=22749126 /ug=Hs.48565 /len=2221 | NM_152540 | Hs.48565 | NP_689753 |
| 9061 | 0.037084 | cDNA FLJ33960 fis, clone CTONG2018843. /gb=AK091279 /gi=21749612 /ug=Hs.126465 /len=2849 | AK091279 | Hs.126465 | |
| 9072 | 0.035141 | clone MGC:20469 IMAGE:4554554, mRNA, complete cds /cds=(208,1149) /gb=BC012182 /gi=15082546 /ug=Hs.82508 /len=1862 | BC012182 | Hs.82508 | |
| 9096 | 0.041237 | C1q and tumor necrosis factor related protein 7 (C1QTNF7), mRNA /cds=(234,1103) /gb=NM_031911 /gi=21314748 /ug=Hs.153714 /len=3959 | NM_031911 | Hs.153714 | NP_114117 |
| 9106 | 0.023762 | yz39f06.s1 Morton Fetal Cochlea cDNA clone IMAGE:285443 3', mRNA sequence /clone=IMAGE:285443 /clone_end=3' /gb=N66393 /gi=1218518 /ug=Hs.102754 /len=618 | N66393 | Hs.102754 | |
| 9108 | 3.48E-04 | UI-H-EI0-aye-c-17-0-UI.s1 NCI_CGAP_EI0 cDNA clone UI-H-EI0-aye-c-17-0-UI 3', mRNA sequence /clone=UI-H-EI0-aye-c-17-0-UI /clone_end=3' /gb=CA447385 /gi=24811805 /ug=Hs.420740 /len=812 | CA447385 | Hs.420740 | |
| 9174 | 0.012975 | UI-E-EJ0-ahs-e-16-0-UI.r1 UI-E-EJ0 cDNA clone UI-E-EJ0-ahs-e-16-0-UI 5', mRNA sequence /clone=UI-E-EJ0-ahs-e-16-0-UI /clone_end=5' /gb=BM714718 /gi=19027976 /ug=Hs.446458 /len=1136 | BM714718 | Hs.446458 | |
| 9244 | 0.021147 | Mus musculus mitochondrion, complete genome | NC_001569 | | |
| 9266 | 0.018779 | clone FLB2932 mRNA sequence /gb=AF138859 /gi=7340965 /ug=Hs.274405 /len=2990 | AF138859 | Hs.274405 | |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|------|----------|---|--------------------|-----------------------|-----------------------|
| 9274 | 0.001585 | mRNA; cDNA DKFZp586G2120 (from clone.DKFZp586G2120); complete cds /cds=(19,2604) /gb=AL136924/gi=12053342 /ug=Hs.62349 /len=4137 | AL136924 | Hs.62349 | NP_061866 |
| 9275 | 0.003758 | ESTs, cDNA, 5' end /clone=IMAGE:3857750 /clone_end=5' /gb=BF035134 /gi=10742846 /ug=Hs.195789 /len=847 | BF035134 | Hs.195789 | |
| 9310 | 0.001585 | No significant match | SEQ.ID.No.71 | | |
| 9311 | 0.018779 | Novel, ORF+1(73~201) | SEQ.ID.No.75 | | |
| 9315 | 0.037084 | No significant match | SEQ.ID.No.89 | | |
| 9372 | 0.012175 | chromosome 17 open.reading frame 35 (C17orf35), mRNA /cds=(259,837) /gb=NM_003876 /gi=4505900 /ug=Hs.15196 /len=1211 | NM_003876 | Hs.15196 | NP_003867 |
| 9399 | 0.002773 | NPD002 protein (NPD002), mRNA /cds=(89,1954) /gb=NM_014049 /gi=21361496 /ug=Hs.7010 /len=2494 | NM_014049 | Hs.7010 | NP_054768 |
| 9407 | 0.011417 | adenylate kinase 3 like 1 (AK3L1), mRNA /cds=(141,824) /gb=NM_016282 /gi=19923436 /ug=Hs.43436 /len=2642 | NM_016282 | Hs.43436 | NP_057366 |
| 9417 | 0.00767 | Siah-interacting protein (SIP), mRNA /cds=(118,804) /gb=NM_014412 /gi=7656951 /ug=Hs.27258 /len=2435 | NM_014412 | Hs.27258 | NP_055227 |
| 9457 | 0.022422 | serine/threonine kinase 17a (apoptosis-inducing) (STK17A); mRNA /cds=(118,1362) /gb=NM_004760 /gi=4758191 /ug=Hs.9075 /len=2641 | NM_004760 | Hs.9075 | NP_004751 |
| 9459 | 0.010023 | ubiquinol-cytochrome c reductase binding protein (UQCRB), mRNA /cds=(54,389) /gb=NM_006294 /gi=20070231 /ug=Hs.131255 /len=965 | NM_006294 | Hs.131255 | NP_006285 |
| 9473 | 0.011417 | mRNA; cDNA DKFZp564D152 (from clone DKFZp564D152); complete cds /cds=(99,1415) /gb=AL136629 /gi=12052783 /ug=Hs.278479 /len=3229 | AL136629 | Hs.278479 | |
| 9485 | 0.012975 | mRNA; cDNA DKFZp434K1412 (from clone DKFZp434K1412) /gb=AL137753 /gi=6808455 /ug=Hs.12144 /len=5448 | AL137753 | Hs.12144 | |
| 9486 | 0.048172 | neural precursor cell expressed, developmentally down-regulated 5 (NEDD5), mRNA /cds=(259,1344) /gb=NM_004404 /gi=4758157 /ug=Hs.155595 /len=3433 | NM_004404 | Hs.155595 | NP_004395 |
| 9489 | 0.015649 | similar to putative (H. sapiens) (LOC129641), mRNA | XM_059369 | | |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|------|----------|---|--------------------|-----------------------|-----------------------|
| 9492 | 0.048653 | 601846634F1 NIH_MGC_55 cDNA clone IMAGE:4077632 5', mRNA sequence /clone=IMAGE:4077632 /clone_end=5' /gb=BF214729 /gi=11108315 /ug=Hs.446581 /len=835 | BF214729 | Hs.446581 | |
| 9498 | 0.048172 | PFTAIRES protein kinase 1 (PFTK1), mRNA /cds=(145,1500) /gb=NM_012395 /gi=6912583 /ug=Hs.57856 /len=4957 | NM_012395 | Hs.57856 | NP_036527 |
| 9511 | 0.028189 | emopamil binding related protein, delta8-delta7 sterol isomerase related protein (EBRP), mRNA /cds=(53,673) /gb=NM_032565 /gi=14211872 /ug=Hs.433278 /len=931 | NM_032565 | Hs.433278 | NP_115954 |
| 9513 | 0.035141 | hypothetical gene supported by AY007122 (LOC92719), mRNA | XM_046853 | | |
| 9530 | 0.004048 | hypothetical protein FLJ10856 (FLJ10856), mRNA /cds=(148,1233) /gb=NM_018247 /gi=8922719 /ug=Hs.108530 /len=3720 | NM_018247 | Hs.108530 | NP_060717 |
| 9547 | 0.048172 | mitochondrion, complete genome | NC_001807 | | |
| 9548 | 0.033283 | ubiquitin specific protease 1 (USP1), mRNA /cds=(246,2603) /gb=NM_003368 /gi=21361109 /ug=Hs.35086 /len=3379 | NM_003368 | Hs.35086 | NP_003359 |
| 9561 | 0.037084 | phosphatidylinositol transfer protein, beta (PITPNB), mRNA /cds=(40,855) /gb=NM_012399 /gi=19923401 /ug=Hs.7370 /len=2906 | NM_012399 | Hs.7370 | NP_036531 |
| 9595 | 0.001459 | hypothetical protein MGC4701 (MGC4701), mRNA /cds=(149,1585) /gb=NM_024511 /gi=24308290 /ug=Hs.421054 /len=1686 | NM_024511 | Hs.421054 | NP_078787 |
| 9596 | 0.001867 | vimentin (VIM), mRNA /cds=(123,1523) /gb=NM_003380 /gi=4507894 /ug=Hs.297753 /len=1851 | NM_003380 | Hs.297753 | NP_000995 |
| 9610 | 0.017682 | nuclear DNA-binding protein (C1D), transcript variant 1, mRNA /cds=(64,489) /gb=NM_006333 /gi=27894371 /ug=Hs.15164 /len=1200 | NM_006333 | Hs.15164 | NP_775269 |
| 9648 | 0.025168 | Similar to RIKEN cDNA 1500009M05 gene, clone MGC:40370 IMAGE:5105935, mRNA, complete cds /cds=(45,452) /gb=BC032300 /gi=21619026 /ug=Hs.295953 /len=1617 | BC032300 | Hs.295953 | |
| 9712 | 0.026643 | w154c05.x1 NCI_CGAP_Brn25 cDNA clone IMAGE:2428712 3', mRNA sequence /clone=IMAGE:2428712 /clone_end=3' /gb=AI864553 /gi=5528660 /ug=Hs.371597 /len=474 | AI864553 | Hs.371597 | |

| Sp t | p-value | Description | Gen Accession No. | Unigene Accession No. | Protein Accession No. |
|-------|----------|--|-------------------------|-----------------------------|-----------------------------|
| 9721 | 0.045762 | EST(yj01e06.r1 clone 147490 5') | R81297 | | NP_057707 |
| 9730 | 0.035141 | 601862578F1 NIH_MGC_53 cDNA clone IMAGE:4082082 5', mRNA sequence /clone=IMAGE:4082082 /clone_end=5' /gb=BF207870 /gi=11101456 /ug=Hs.396179 /len=756 | BF207870 | Hs.396179 | |
| 9769 | 0.043451 | AGENCOURT_6445786 NIH_MGC_92 cDNA clone IMAGE:5587250 5', mRNA sequence /clone=IMAGE:5587250 /clone_end=5' /gb=BM468951 /gi=18517993 /ug=Hs.275340 /len=967 | BM468951 | Hs.275340 | |
| 9774 | 0.031506 | cDNA FLJ36605 fis, clone TRACH2015316, highly similar to VIMENTIN. /cds=(631,1317) /gb=AK093924 /gi=21752883 /ug=Hs.379100 /len=2665 | AK093924 | Hs.379100 | |
| 9833 | 0.004687 | AGENCOURT_6861057 NIH_MGC_99 cDNA clone IMAGE:5931113 5', mRNA sequence /clone=IMAGE:5931113 /clone_end=5' /gb=BQ066467 /gi=19895513 /ug=Hs.446485 /len=1029 | BQ066467 | Hs.446485 | |
| 9886 | 0.005811 | mRNA; cDNA DKFZp451F1910 (from clone DKFZp451F1910) /gb=AL833265 /gi=21733898 /ug=Hs.332030 /len=5254 | AL833265 | Hs.332030 | |
| 9921 | 0.033283 | hypothetical protein FLJ10477 (FLJ10477), mRNA /cds=(232,873) /gb=NM_018105 /gi=8922445 /ug=Hs.7432 /len=2167 | NM_018105 | Hs.7432 | NP_060575 |
| 9965 | 0.039115 | hypothetical protein DKFZp434K1421 (DKFZP434K1421), mRNA /cds=(29,1705) /gb=NM_032141 /gi=14149806 /ug=Hs.374609 /len=2547 | NM_032141 | Hs.374609 | NP_115517 |
| 9972 | 0.035141 | caldesmon 1 (CALD1), transcript variant 1, mRNA /cds=(230,2611) /gb=NM_033138 /gi=15149460 /ug=Hs.325474 /len=3610 | NM_033138 | Hs.325474 | NP_149347 |
| 10011 | 0.045762 | v-ral simian leukemia viral oncogene homolog B (ras related; GTP binding protein), clone MGC:9025 IMAGE:3880116, mRNA, complete cds (BC018163.1) | BC018163 | Hs.348024 | NP_002872 |
| 10054 | 0.028189 | similar to hypothetical protein FLJ10883 (LOC115294), mRNA /cds=(98,1171) /gb=NM_052937 /gi=24308385 /ug=Hs.60293 /len=3967 | NM_052937 | Hs.60293 | NP_443169 |
| 10080 | 0.015649 | hypothetical protein DKFZp761N0624 (DKFZp761N0624), mRNA /cds=(113,1444) /gb=NM_032295 /gi=14150046 /ug=Hs.21893 /len=2973 | NM_032295 | Hs.21893 | NP_115671 |

| Spot | p-value | Description | Gene Accession No. | Unigen Accession No. | Protein Accession No. |
|-------|----------|--|--------------------|----------------------|-----------------------|
| 10100 | 0.025168 | hypothetical protein FLJ22662 (FLJ22662), mRNA /cds=(66,1586) /gb=NM_024829 /gi=13376231 /ug=Hs.178470 /len=1707 | NM_024829 | Hs.178470 | NP_079105 |
| 10143 | 0.043451 | phospholipase A2 receptor 1, 180kDa (PLA2R1), mRNA /cds=(207,4604) /gb=NM_007366 /gi=19923388 /ug=Hs.171945 /len=5633 | NM_007366 | Hs.171945 | NP_031392 |
| 10146 | 0.037084 | EST qz90a06.x1 Soares_pregnant_uterus_NbHPU cDNA clone IMAGE:2041810 3' | AI493872 | | NP_008878 |
| 10151 | 0.006684 | cDNA FLJ36605 fis, clone TRACH2015316, highly similar to VIMENTIN. /cds=(631,1317) /gb=AK093924 /gi=21752883 /ug=Hs.379100 /len=2665 | AK093924 | Hs.379100 | |
| 10205 | 0.003193 | EST (ql74f05.s1 NCI_CGAP_Kid3 cDNA clone IMAGE:1535361 3') | AA919165 | | |
| 10208 | 0.004048 | cDNA FLJ33503 fis, clone BRAMY2004521. /cds=(367,750) /gb=AK090822 /gi=21749052 /ug=Hs.356719 /len=2339 | AK090822 | Hs.356719 | NP_787089 |
| 10228 | 0.004357 | hypothetical protein FLJ10342 (FLJ10342), mRNA /cds=(534,1145) /gb=NM_018064 /gi=14149717 /ug=Hs.101514 /len=1506 | NM_018064 | Hs.101514 | NP_060534 |
| 10247 | 0.002773 | vimentin (VIM) gene | M18895 | | |
| 10277 | 0.039115 | likely ortholog of mouse embryonic epithelial gene 1 (EEG1), mRNA /cds=(319,1794) /gb=NM_017611 /gi=18252046 /ug=Hs.274453 /len=2630 | NM_017611 | Hs.274453 | NP_060081 |
| 10315 | 0.035141 | EST (MR0-HT0407-010200-008-g12 HT0407) | BE159321 | | |
| 10323 | 0.006234 | mRNA; cDNA DKFZp434K1115 (from clone DKFZp434K1115); complete cds /cds=(97,2877) /gb=AL136764 /gi=12053044 /ug=Hs.42676 /len=4868 | AL136764 | Hs.42676 | |
| 10351 | 0.021147 | EST (IL2-UM0076-070400-061-F10 UM0076) | AW802800 | | |
| 10358 | 0.033283 | cDNA, 5' end /clone=IMAGE:4148900 /clone_end=5' /gb=BF342391 /gi=11289392 /ug=Hs.30469 /len=803 | BF342391 | Hs.30469 | NP_055313 |
| 10385 | 0.045762 | chondroitin sulfate GalNAcT-2 (GALNAcT-2), mRNA /cds=(336,1964) /gb=NM_018590 /gi=24429591 /ug=Hs.180758 /len=3745 | NM_018590 | Hs.180758 | NP_061060 |
| 10392 | 0.012175 | ribosomal protein, large, P1 (RPLP1), mRNA /cds=(130,474) /gb=NM_001003 /gi=16905511 /ug=Hs.424299 /len=512 | NM_001003 | Hs.424299 | NP_000994 |

| Spot | p-value | D scription | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|-------|----------|---|--------------------|-----------------------|-----------------------|
| 10430 | 0.017682 | EST(ha63a03.x1 NCI_CGAP_Pan1 cDNA clone IMAGE:2878348 3') | AW338626 | | NP_006826 |
| 10432 | 0.010023 | UI-H-BW0-ajd-b-12-0-UI.s1 NCI_CGAP_Sub6 cDNA clone IMAGE:2731343 3', mRNA sequence /clone=IMAGE:2731343 /clone_end=3' /gb=AW297162 /gi=6703808 /ug=Hs.438076 /len=690 | AW297162 | Hs.438076 | |
| 10456 | 0.045762 | mRNA; cDNA DKFZp451D112 (from clone DKFZp451D112); complete cds /cds=(316,4719) /gb=AL831962 /gi=21732493 /ug=Hs.202949 /len=5391 | AL831962 | Hs.202949 | |
| 10503 | 0.003487 | thymosin, beta 4, X chromosome (TMSB4X), mRNA /cds=(78,212) /gb=NM_021109 /gi=11056060 /ug=Hs.75968 /len=556 | NM_021109 | Hs.75968 | NP_066932 |
| 10536 | 0.005658 | nascent-polypeptide-associated complex alpha polypeptide (NACA), mRNA /cds=(26,673) /gb=NM_005594 /gi=5031930 /ug=Hs.32916 /len=797 | NM_005594 | Hs.32916 | NP_005585 |
| 10565 | 0.048172 | clone IMAGE:5284350, mRNA /gb=BC037924 /gi=23138690 /ug=Hs.143061 /len=2659 | BC037924 | Hs.143061 | |
| 10566 | 0.023762 | actin, beta (ACTB), mRNA /cds=(74,1201) /gb=NM_001101 /gi=5016088 /ug=Hs.426930 /len=1793 | NM_001101 | Hs.426930 | NP_001092 |
| 10601 | 0.004048 | EST(cDNA clone IMAGE:3566688 3') | BF110315 | | NP_002154 |
| 10627 | 0.013819 | 602584221F1 NIH_MGC_76 cDNA clone IMAGE:4712140 5', mRNA sequence /clone=IMAGE:4712140 /clone_end=5' /gb=BG564543 /gi=13572195 /ug=Hs.105449 /len=981 | BG564543 | Hs.105449 | |
| 10632 | 0.010701 | UI-H-EI1-aze-g-21-0-UI.s1 NCI_CGAP_EI1 cDNA clone IMAGE:5847596 3', mRNA sequence /clone=IMAGE:5847596 /clone_end=3' /gb=BQ003542 /gi=19728442 /ug=Hs.190642 /len=1086 | BQ003542 | Hs.190642 | |
| 10660 | 0.023762 | BX111472 Soares_senescent_fibroblasts_NbHSF cDNA clone IMAGp998B18737, mRNA sequence /clone=IMAGp998B18737; IMAGE:3251 69 /gb=BX111472 /gi=27878522 /ug=Hs.56025 /len=714 | BX111472 | Hs.56025 | |
| 10697 | 0.021147 | EST(PM0-HT0913-100401-013-c08 HT0913 cDNA, MRNA sequence) | BG998053 | | |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|-------|----------|--|--------------------|-----------------------|-----------------------|
| 10771 | 0.039257 | HUM515D03B Clontech placenta polyA mRNA (#6518) cDNA clone GEN-515D03 5', mRNA sequence /clone=GEN-515D03 /clone_end=5' /gb=D58893 /gi=968527 /ug=Hs.335953 /len=365 | D58893 | Hs.335953 | |
| 10779 | 0.01471 | EST (ADB cDNA clone ADBAKA02 5') | AV704531 | | |
| 10780 | 0.037084 | hypothetical protein FLJ10300 (FLJ10300), mRNA /cds=(1710,3359) /gb=NM_018051 /gi=21361686 /ug=Hs.42233 /len=3785 | NM_018051 | Hs.42233 | NP_060521 |
| 10793 | 0.041237 | im56f03.y1 HR85 islet cDNA clone IMAGE:6039292 5', mRNA sequence /clone=IMAGE:6039292 /clone_end=5' /gb=CA773752 /gi=26011160 /ug=Hs.380642 /len=630 | CA773752 | Hs.380642 | |
| 10794 | 0.002773 | FSDH region gene 1 (FRG1), mRNA /cds=(192,968) /gb=NM_004477 /gi=4758403 /ug=Hs.203772 /len=1042 | NM_004477 | Hs.203772 | NP_004468 |
| 10798 | 0.016639 | EST (ta16g05.x1 NCI_CGAP_Lym5 IMAGE:2044280 3') | AI471814 | | |
| 10843 | 0.025168 | EST (QV0-ST0236-171299-075-c08 ST0236 cDNA) | AW816517 | | |
| 10852 | 0.011417 | EST yb28f09.s1 Stratagene fetal spleen #937205) H.sapiens cDNA clone IMAGE:72521 3' | T51639 | | |
| 10853 | 6.69E-04 | EST(z189c05.r1 Soares testis NHT clone 729512 5') | AA398038 | | NP_004632 |
| 10862 | 0.003758 | mitochondrion, complete genome | NC_001807 | | |
| 10864 | 0.016639 | EST (ab81d11.s1 Stratagene fetal retina 937202 IMAGE:853365 3') | AA663308 | | |
| 10888 | 2.60E-05 | UI-H-DH0-aui-j-10-0-UI.s1 NCI_CGAP_DH0 cDNA clone IMAGE:5871081 3', mRNA sequence /clone=IMAGE:5871081 /clone_end=3' /gb=BM994461 /gi=19719362 /ug=Hs.434057 /len=2059 | BM994461 | Hs.434057 | |
| 10897 | 0.029809 | hypothetical protein FLJ25534 (FLJ25534), mRNA /cds=(297,1145) /gb=NM_153234 /gi=23397511 /ug=Hs.23197 /len=2550 | NM_153234 | Hs.23197 | NP_694966 |
| 10912 | 0.028189 | cDNA FLJ34675 fis, clone LIVER2001608. /gb=AK091994 /gi=21750487 /ug=Hs.380100 /len=1725 | AK091994 | Hs.380100 | |
| 10950 | 0.011417 | cDNA FLJ38913 fis, clone NT2NE2008017. /gb=AK096232 /gi=21755673 /ug=Hs.50094 /len=2555 | AK096232 | Hs.50094 | NP_835224 |
| 10991 | 0.028189 | ribosomal protein L12 (RPL12), mRNA /cds=(89,586) /gb=NM_000976 /gi=15431291 /ug=Hs.405042 /len=632 | NM_000976 | Hs.405042 | NP_000967 |

| Spot | p-value | Description | Gen Accession No. | Unigene Accession No. | Protein Accession No. |
|-------|----------|---|-------------------------|-----------------------------|-----------------------------|
| 10996 | 0.028189 | BX118052 Soares breast 2NbHBst cDNA clone IMAGp998C21252, mRNA sequence /clone=IMAGp998C21252 IMAGE:158156 /gb=BX118052 /gi=27840946 /ug=Hs.32250 /len=612 | BX118052 | Hs.32250 | |
| 11003 | 0.002372 | cDNA FLJ14832 fis, clone OVARC1001169. /gb=AK027738 /gi=14042638 /ug=Hs.235860 /len=2350 | AK027738 | Hs.235860 | |
| 11011 | 0.007162 | EST(cDNA clone IMAGE:2686869 3') | AW197394 | | |
| 11016 | 0.033283 | mitochondrion, complete genome | NC_001807 | | |
| 11030 | 0.048172 | ESTs, cDNA, 3' end /clone=IMAGE:2308223 /clone_end=3' /gb=AI671885 /gi=4851616 /ug=Hs.110855 /len=593 | AI671885 | Hs.110855 | |
| 11032 | 0.017682 | nj38c05.s1 NCI_CGAP_AA1 cDNA clone IMAGE:994760 3' similar to gb:M62424 THROMBIN RECEPTOR PRECURSOR mRNA sequence /clone=IMAGE:994760 /clone_end=3' /gb=AA548630 /gi=2318912 /ug=Hs.105848 /len=555 | AA548630 | Hs.105848 | |
| 11033 | 0.021147 | FLJ30661 fis, clone DFNES2000526 /cds=UNKNOWN /gb=AK055223 /gi=16549904 /ug=Hs.265540 /len=2514 | AK055223 | Hs.265540 | NP_057178 |
| 11046 | 0.017682 | wc25f11.x1 NCI_CGAP_Kid11 cDNA clone IMAGE:2316237 3', mRNA sequence /clone=IMAGE:2316237 /clone_end=3' /gb=AI678258 /gi=4888440 /ug=Hs.174257 /len=585 | AI678258 | Hs.174257 | |
| 11085 | 0.008208 | EST(cDNA clone IMAGE:2126419 3') | AI435109 | | |
| 11136 | 0.016639 | clone IMAGE:3138608, mRNA /cds=UNKNOWN /gb=BC007266 /gi=13938277 /ug=Hs.334566 /len=1635 | BC007266 | Hs.334566 | |
| 11138 | 0.045762 | nn90a10.s1 NCI_CGAP_Br2 cDNA clone IMAGE:1098426 3', mRNA sequence /clone=IMAGE:1098426 /clone_end=3' /gb=AA614814 /gi=2467010 /ug=Hs.270700 /len=404 | AA614814 | Hs.270700 | |
| 11148 | 0.019933 | ij23g01.x1 Melton Normalized Islet 4 N4-HIS 1 cDNA clone IMAGE:6135721 3', mRNA sequence /clone=IMAGE:6135721 /clone_end=3' /gb=BQ100789 /gi=20133773 /ug=Hs.372964 /len=568 | BQ100789 | Hs.372964 | |
| 11169 | 0.018775 | nad13a08.x1 NCI_CGAP_Lu24 cDNA clone IMAGE:3365271 3', mRNA sequence /clone=IMAGE:3365271 /clone_end=3' /gb=BF439728 /gi=11452245 /ug=Hs.257883 /len=202 | BF439728 | Hs.257883 | |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Prot in Acc ssion No. |
|-------|----------|---|--------------------|-----------------------|-----------------------|
| 11218 | 0.007162 | chromosome 3q clone CTD-2650N22, WORKING DRAFT SEQUENCE, 5 unordered pieces | AC108668 | | |
| 11243 | 0.029809 | apoA polymorphism Kringle IV gene, exons 1 and 2 | L14005 | | |
| 11256 | 0.045762 | cDNA FLJ31919 fis, clone NT2RP7004964. /gb=AK056481 /gi=16551895 /ug=Hs.400872 /len=4013 | AK056481 | Hs.400872 | |
| 11266 | 9.20E-05 | B-cell translocation gene 1, anti-proliferative (BTG1), mRNA /cds=(309,824) /gb=NM_001731 /gi=4502472 /ug=Hs.77054 /len=1783 | NM_001731 | Hs.77054 | NP_001722 |
| 11275 | 0.031506 | glucose phosphate isomerase (GPI), mRNA /cds=(104,1780) /gb=NM_000175 /gi=18201904 /ug=Hs.406458 /len=2075 | NM_000175 | Hs.406458 | NP_000166 |
| 11299 | 0.039115 | ATX1 antioxidant protein 1 (yeast) (ATOX1), mRNA /cds=(114,320) /gb=NM_004045 /gi=4757803 /ug=Hs.279910 /len=502 | NM_004045 | Hs.279910 | NP_004036 |
| 11305 | 0.010023 | tousled-like kinase 2 (TLK2), mRNA /cds=(147,2396) /gb=NM_006852 /gi=11140818 /ug=Hs.57553 /len=3327 | NM_006852 | Hs.57553 | NP_006843 |
| 11321 | 0.039115 | transient receptor potential cation channel, subfamily C, member 1 (TRPC1), mRNA /cds=(138,2417) /gb=NM_003304 /gi=27545448 /ug=Hs.250687 /len=4085 | NM_003304 | Hs.250687 | NP_003295 |
| 11331 | 0.017682 | cell cycle progression 8 protein (CPR8), mRNA /cds=(13,1140) /gb=NM_004748 /gi=4758047 /ug=Hs.82506 /len=1856 | NM_004748 | Hs.82506 | NP_004739 |
| 11335 | 0.023762 | COX11 cytochrome c oxidase assembly protein (yeast) (COX11), nuclear gene encoding mitochondrial protein, mRNA /cds=(48,878) /gb=NM_004375 /gi=17921983 /ug=Hs.241515 /len=2717 | NM_004375 | Hs.241515 | NP_004366 |
| 11353 | 0.005412 | mRNA; cDNA DKFZp434E2321 (from clone DKFZp434E2321); partial cds /cds=(1,1051) /gb=AL133619 /gi=6599234 /ug=Hs.29383 /len=3447 | AL133619 | Hs.29383 | |
| 11365 | 6.45E-05 | Rho-specific guanine-nucleotide exchange factor 164 kDa (P164RHOGEF), mRNA /cds=(16,6207) /gb=NM_014786 /gi=21361457 /ug=Hs.45180 /len=7540 | NM_014786 | Hs.45180 | NP_055601 |
| 11402 | 0.033283 | cytochrome c, somatic (CYCS), mRNA /cds=(61,378) /gb=NM_018947 /gi=21361707 /ug=Hs.169248 /len=3990 | NM_018947 | Hs.169248 | NP_061820 |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|-------|----------|---|--------------------|-----------------------|-----------------------|
| 11422 | 0.048172 | CGI-45 protein (CGI-45), mRNA /cds=(194,1321) /gb=NM_015999 /gi=21361518 /ug=Hs.5298 /len=2108 | NM_015999 | Hs.5298 | NP_057083 |
| 11446 | 0.021147 | ornithine decarboxylase antizyme 1 (OAZ1), mRNA /gb=NM_004152 /gi=9845504 /ug=Hs.281960 /len=986 | NM_004152 | Hs.281960 | NP_004143 |
| 11479 | 0.033283 | B lymphocyte activation-related protein BC-2048 | AAL26788 | | |
| 11482 | 0.013819 | clone IMAGE:5271722, mRNA /gb=BC038786 /gi=24270905 /ug=Hs.190456 /len=1535 | BC038786 | Hs.190456 | |
| 11498 | 0.048653 | clone MGC:16614 IMAGE:4111344, mRNA, complete cds /cds=(258,998) /gb=BC009313 /gi=14424569 /ug=Hs.373515 /len=2052 | BC009313 | Hs.193700 | |
| 11503 | 0.045762 | hypothetical protein DKFZp564K0822 (DKFZP564K0822), mRNA /cds=(10,528) /gb=NM_030796 /gi=13540577 /ug=Hs.4750 /len=2789 | NM_030796 | Hs.4750 | NP_110423 |
| 11519 | 0.008208 | mRNA; cDNA DKFZp761O0611 (from clone DKFZp761O0611) /gb=AL834155 /gi=21739631 /ug=Hs.22969 /len=4502 | AL834155 | Hs.22969 | |
| 11539 | 0.041237 | mRNA for KIAA1327 protein, partial cds. /cds=(1,5417) /gb=AB037748 /gi=20521883 /ug=Hs.106204 /len=6687 | AB037748 | Hs.106204 | |
| 11608 | 0.029809 | EST(MR0-HT0407-140300-013-h01 HT0407) | BE159552 | | NP_003751 |
| 11615 | 0.048172 | mRNA for KIAA0261 gene, partial cds. /cds=(1,3866) /gb=D87450 /gi=1665788 /ug=Hs.154978 /len=6155 | D87450 | Hs.154978 | |
| 11616 | 0.030757 | EST qz49d11.x1 NCI_CGAP_Kid11 IMAGE:2030229 3' | AI493076 | | |
| 11634 | 0.003233 | hypothetical protein FLJ12118 (FLJ12118), mRNA /cds=(24,1718) /gb=NM_024537 /gi=13375694 /ug=Hs.381043 /len=1843 | NM_024537 | Hs.381043 | NP_078813 |
| 11691 | 0.023762 | cDNA sequence cDNA sequence DKFZp434D0935 (from clone cDNA sequence DKFZp434D0935) | AL117502 | | NP_149107 |
| 11700 | 0.031506 | EST(qh83b09.x1 Soares_NFL_T_GBC_S1 cDNA clone IMAGE:1853561 3') | AI243681 | | NP_004727 |
| 11702 | 0.023762 | eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA /cds=(63,1451) /gb=NM_001402 /gi=25453469 /ug=Hs.422118 /len=1837 | NM_001402 | Hs.422118 | NP_001393 |
| 11720 | 0.035141 | mRNA for KIAA1509 protein, partial cds. /cds=(1,3983) /gb=AB040942 /gi=7959278 /ug=Hs.201500 /len=5283 | AB040942 | Hs.201500 | |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|-------|----------|--|--------------------|-----------------------|-----------------------|
| 11783 | 0.015649 | cDNA FLJ20709 fis, clone KAIA1124, highly similar to D86324 mRNA for CMP-N-acetylneuraminic acid. /gb=AK000716 /gi=7020978 /ug=Hs.24697 /len=3488 | AK000716 | Hs.24697 | |
| 11784 | 0.004687 | sperm associated antigen 9 (SPAG9), transcript variant 1, mRNA /cds=(79,4002) /gb=NM_003971 /gi=27436919 /ug=Hs.129872 /len=4663 | NM_003971 | Hs.129872 | NP_758853 |
| 11788 | 0.019933 | Bardet-Biedl syndrome 2 (BBS2), mRNA /cds=(422,2587) /gb=NM_031885 /gi=22208996 /ug=Hs.332633 /len=2978 | NM_031885 | Hs.332633 | NP_114091 |
| 11797 | 0.013819 | UI-E-C10-aae-d-12-0-UI.s1 UI-E-C10 cDNA clone UI-E-C10-aae-d-12-0-UI 3', mRNA sequence /clone=UI-E-C10-aae-d-12-0-UI /clone_end=3' /gb=BM663444 /gi=18968780 /ug=Hs.395779 /len=1260 | BM663444 | Hs.395779 | |
| 11811 | 0.039115 | FLJ11481 fis, clone HEMBA1001803 /cds=UNKNOWN /gb=AK021543 /gi=10432744 /ug=Hs.135159 /len=1539 | AK021543 | Hs.135159 | |
| 11816 | 0.019933 | likely ortholog of rat V-1 protein (V-1), mRNA /cds=(229,585) /gb=NM_145808 /gi=21956644 /ug=Hs.21321 /len=3770 | NM_145808 | Hs.21321 | NP_665807 |
| 11822 | 0.006234 | protein phosphatase 2, regulatory subunit B (B56), gamma isoform (PPP2R5C), mRNA /cds=(89,1633) /gb=NM_002719 /gi=4506022 /ug=Hs.171734 /len=4064 | NM_002719 | Hs.171734 | NP_848703 |
| 11830 | 0.035141 | DKFZp564P2064_s1 564 (synonym: hfbr2) cDNA clone DKFZp564P2064 3', mRNA sequence /clone=DKFZp564P2064 /clone_end=3' /gb=AL037172 /gi=5406623 /ug=Hs.328612 /len=682 | AL037172 | Hs.328612 | |
| 11839 | 0.015649 | proteasome (prosome, macropain) 26S subunit, ATPase, 2 (PSMC2), mRNA /cds=(71,1372) /gb=NM_002803 /gi=24430152 /ug=Hs.61153 /len=1545 | NM_002803 | Hs.61153 | NP_002794 |
| 11851 | 0.041237 | mitochondrion, complete genome | NC_001807 | | |
| 11860 | 0.009383 | FOXJ2 forkhead factor (FHX), mRNA /cds=(490,2214) /gb=NM_018416 /gi=8923841 /ug=Hs.120844 /len=4873 | NM_018416 | Hs.120844 | NP_060886 |
| 11865 | 0.039115 | protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha) (PPP3CA), mRNA /cds=(407,1972) /gb=NM_000944 /gi=19923130 /ug=Hs.272458 /len=4425 | NM_000944 | Hs.272458 | NP_000935 |

| Spot | p-value | D scription | Gene Accession No. | Unigen Accession No. | Protein Accession No. |
|-------|----------|--|--------------------|----------------------|-----------------------|
| 11875 | 0.045762 | general transcription factor IIIC, polypeptide 3, 102kDa (GTF3C3), mRNA /cds=(94,2754) /gb=NM_012086 /gi=6912397 /ug=Hs.90847 /len=2961 | NM_012086 | Hs.90847 | NP_036218 |
| 11876 | 0.047799 | immediate early response 3 (IER3), transcript variant long, mRNA /cds=(30,611) /gb=NM_052815 /gi=16554596 /ug=Hs.76095 /len=1345 | NM_052815 | Hs.76095 | NP_434702 |
| 11897 | 0.037084 | hypothetical protein FLJ20701 (FLJ20701), mRNA /cds=(39,938) /gb=NM_017933 /gi=8923631 /ug=Hs.424598 /len=2284 | NM_017933 | Hs.424598 | NP_060403 |
| 11921 | 0.028189 | hypothetical protein DKFZp762O076 (DKFZp762O076), mRNA /cds=(77,850) /gb=NM_018710 /gi=24308164 /ug=Hs.21621 /len=2266 | NM_018710 | Hs.21621 | NP_061180 |
| 11927 | 0.005038 | CCR4-NOT transcription complex, subunit 8 (CNOT8), mRNA /cds=(245,1123) /gb=NM_004779 /gi=24496777 /ug=Hs.26703 /len=2489 | NM_004779 | Hs.26703 | NP_004770 |
| 11938 | 0.022422 | BTAf1 RNA polymerase II, B-TFIID transcription factor-associated, 170kDa (Mot1 S. cerevisiae) (BTAf1), mRNA /cds=(118,5667) /gb=NM_003972 /gi=27477069 /ug=Hs.180930 /len=6345 | NM_003972 | Hs.180930 | NP_003963 |
| 11939 | 0.043451 | tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide (YWHAG), mRNA /cds=(192,935) /gb=NM_012479 /gi=21464100 /ug=Hs.25001 /len=3747 | NM_012479 | Hs.25001 | NP_036611 |
| 11963 | 0.022422 | proline rich 2 (PROL2), mRNA /cds=(114,1097) /gb=NM_006813 /gi=5802981 /ug=Hs.75969 /len=2061 | NM_006813 | Hs.75969 | NP_006804 |
| 11979 | 0.003594 | chromosome 20 open reading frame 6 (C20orf6), mRNA /cds=(109,2664) /gb=NM_016649 /gi=22507381 /ug=Hs.88820 /len=3216 | NM_016649 | Hs.88820 | NP_057733 |
| 12079 | 0.023762 | EST nj89e12.s1 NCI_CGAP_Pr11 cDNA clone IMAGE:999694 | AA552262 | | |
| 12085 | 0.033283 | retinoic acid induced 14 (RAI14), mRNA /cds=(112,3054) /gb=NM_015577 /gi=13470085 /ug=Hs.15165 /len=4925 | NM_015577 | Hs.15165 | NP_056392 |
| 12123 | 0.031506 | UI-H-BI0-aaa-f-10-0-UI.s1 NCI_CGAP_Sub1 cDNA clone IMAGE:2708874 3', mRNA sequence /clone=IMAGE:2708874 /clone_end=3' /gb=AW014102 /gi=5862859 /ug=Hs.304671 /len=654 | AW014102 | Hs.304671 | |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|-------|----------|--|--------------------|-----------------------|-----------------------|
| 12231 | 0.01471 | EST (UI-H-BI3-akf-b-05-0-UI.s1 NCI_CGAP_Sub5 clone IMAGE:2734017 3') | AW449060 | | NP_061174 |
| 12257 | 0.033283 | EST390958 MAGE resequences, MAGP cDNA, mRNA sequence /gb=AW978849 /gi=8170126 /ug=Hs.124977 /len=678 | AW978849 | Hs.124977 | |
| 12259 | 0.048172 | EST (Similar to pleckstrin homology, Sec7 and coiled/coil domains 3, clone MGC:5340 IMAGE:2984886, complete cds /cds=(3,542) /gb=BC008191 /gi=14198262 /ug=Hs.7984 /len=3720) | BC008191 | Hs.7984 | NP_004218 |
| 12297 | 0.026643 | hypothetical protein MGC10744 (MGC10744), mRNA /cds=(77,184) /gb=NM_032354 /gi=14150156 /ug=Hs.25092 /len=1212 | NM_032354 | Hs.25092 | NP_115730 |
| 12320 | 0.037084 | EST(EST178403 Colon carcinoma (HCC) cell line cDNA 5' end similar to similar to ribosomal protein L30) | AA307521 | | NP_000980 |
| 12346 | 0.048172 | selenoprotein H (SELH), mRNA /cds=(243,611) /gb=NM_170746 /gi=25014108 /ug=Hs.290874 /len=834 | NM_170746 | Hs.290874 | NP_734467 |
| 12352 | 0.021147 | UI-H-BI2-ahm-d-05-0-UI.s1 NCI_CGAP_Sub4 cDNA clone IMAGE:2727224 3', mRNA sequence /clone=IMAGE:2727224 /clone_end=3' /gb=AW293452 /gi=6700088 /ug=Hs.16228 /len=634 | AW293452 | Hs.16228 | |
| 12355 | 0.021147 | cDNA FLJ36238 fis, clone THYMJ2001422. /gb=AK093557 /gi=21752458 /ug=Hs.345588 /len=2269 | AK093557 | Hs.345588 | |
| 12371 | 0.041237 | ESTs, cDNA, 5' end /clone=BMFBFE06 /clone_end=5' /gb=AV756341 /gi=10914189 /ug=Hs.244273 /len=766 | AV756341 | Hs.244273 | |
| 12375 | 0.037157 | UI-H-DT0-avk-p-22-0-UI.s1 NCI_CGAP_DT0 cDNA clone IMAGE:5880837 3', mRNA sequence /clone=IMAGE:5880837 /clone_end=3' /gb=BM996358 /gi=19721259 /ug=Hs.433458 /len=838 | BM996358 | Hs.433458 | |
| 12395 | 0.007162 | SH3-domain binding protein 4 (SH3BP4), mRNA /cds=(336,3227) /gb=NM_014521 /gi=7657561 /ug=Hs.17667 /len=5145 | NM_014521 | Hs.17667 | NP_055336 |
| 12399 | 0.001721 | UI-E-CK1-afh-b-14-0-UI.r1 UI-E-CK1 cDNA clone UI-E-CK1-afh-b-14-0-UI 5', mRNA sequence /clone=UI-E-CK1-afh-b-14-0-UI /clone_end=5' /gb=BM702699 /gi=19015957 /ug=Hs.446508 /len=1088 | BM702699 | Hs.446508 | |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|-------|----------|--|--------------------|-----------------------|-----------------------|
| 12412 | 0.001133 | cDNA / IL3-NT0294-060401-533-D04 NT0294 | BI041924 | | |
| 12430 | 0.004687 | mRNA; cDNA DKFZp686J19116 (from clone DKFZp686J19116) /gb=AL833458 /gi=21734100 /ug=Hs.428760 /len=3297 | AL833458 | Hs.428760 | |
| 12431 | 0.043451 | ESTs, cDNA /gb=AW993259 /gi=8253410 /ug=Hs.113105 /len=678 | AW993259 | Hs.113105 | |
| 12432 | 0.037084 | BX102166 Soares_fetal_liver_spleen_1NFLS_S1 cDNA clone IMAGp998H154200, mRNA sequence /clone=IMAGp998H154200; IMAGE:1655102 /gb=BX102166 /gi=27845155 /ug=Hs.131494 /len=724 | BX102166 | Hs.131494 | |
| 12435 | 0.045762 | clone IMAGE:5263531, mRNA /gb=BC037740 /gi=22902216 /ug=Hs.18016 /len=5036 | BC037740 | Hs.18016 | |
| 12439 | 0.048653 | cDNA FLJ12048 fis, clone HEMBB1001990. /gb=AK022110 /gi=10433433 /ug=Hs.289044 /len=1805 | AK022110 | Hs.289044 | |
| 12465 | 0.022422 | ESTs, cDNA, 5' end /clone=IMAGE:3922401 /clone_end=5' /gb=BE894201 /gi=10356330 /ug=Hs.176376 /len=916 | BE894201 | Hs.176376 | |
| 12484 | 0.04068 | qa50a08.x1 Soares_NhHMPu_S1 cDNA clone IMAGE:1690166 3', mRNA sequence /clone=IMAGE:1690166 /clone_end=3' /gb=AI123569 /gi=3539335 /ug=Hs.117060 /len=773 | AI123569 | Hs.117060 | |
| 12501 | 0.015649 | EST(cDNA clone IMAGE:4693130 5') | BG539987 | | NP_005397 |
| 12513 | 0.00767 | AGENCOURT_8841454 Lupski_sciatic_nerve cDNA clone IMAGE:6199422 5', mRNA sequence /clone=IMAGE:6199422 /clone_end=5' /gb=BQ924341 /gi=22339372 /ug=Hs.442591 /len=930 | BQ924341 | Hs.442591 | |
| 12514 | 0.041237 | DCBCQH10 DCB cDNA, mRNA sequence /gb=BU198777 /gi=22717083 /ug=Hs.50273 /len=867 | BU198777 | Hs.50273 | |
| 12574 | 1.92E-04 | UI-H-ED0-awx-b-15-0-UI.s1 NCI_CGAP_ED0 cDNA clone IMAGE:5824814 3', mRNA sequence /clone=IMAGE:5824814 /clone_end=3' /gb=BQ020068 /gi=19755345 /ug=Hs.396278 /len=1351 | BQ020068 | Hs.396278 | |
| 12580 | 0.035141 | No significant match | SEQ.ID.No.34 | | |
| 12609 | 0.010265 | Similar to hypothetical protein FLJ31322, clone IMAGE:5296647, mRNA /gb=BC045189 /gi=28277118 /ug=Hs.350001 /len=2971 | BC045189 | Hs.350001 | NP_787112 |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|-------|----------|---|--------------------------|-----------------------------|-----------------------------|
| 12656 | 0.035141 | hypothetical protein DKFZp564B1162 (DKFZP564B1162), mRNA /cds=(661,2628) /gb=NM_031305 /gi=13775229 /ug=Hs.93589 /len=4593 | NM_031305 | Hs.93589 | NP_112595 |
| 12664 | 0.010023 | hypothetical protein FLJ12888 (FLJ12888), mRNA /cds=(333,2210) /gb=NM_024945 /gi=13376426 /ug=Hs.284137 /len=3413 | NM_024945 | Hs.284137 | NP_079221 |
| 12695 | 0.025168 | mitochondrion, complete genome | NC_001807 | | |
| 12720 | 0.012975 | mRNA; cDNA DKFZp667O1616 (from clone DKFZp667O1616) /gb=AL713722 /gi=19584452 /ug=Hs.365655 /len=1773 | AL713722 | Hs.365655 | |
| 12725 | 2.60E-04 | EST(CM3-BN0151-130400-146-f01_1 BN0151) | BE008220 | | |
| 12734 | 0.023762 | mRNA for FLJ00201 protein. /cds=(1,2119) /gb=AK074129 /gi=18676605 /ug=Hs.353001 /len=4443 | AK074129 | Hs.353001 | |
| 12739 | 0.022422 | xn86b03.x1 Soares_NFL_T_GBC_S1 cDNA clone IMAGE:2701325 3', mRNA sequence /clone=IMAGE:2701325 /clone_end=3' /gb=AW195867 /gi=6475097 /ug=Hs.370978 /len=571 | AW195867 | Hs.370978 | |
| 12743 | 0.041237 | EST (RC3-BN0036-090200-011-h11 BN0036 cDNA) | AW994082 | | |
| 12750 | 0.019933 | mRNA; cDNA DKFZp667H216 (from clone DKFZp667H216) /gb=AL833204 /gi=21733834 /ug=Hs.356145 /len=3782 | AL833204 | Hs.356145 | |
| 12794 | 0.039115 | ribosomal protein L12 (RPL12), mRNA /cds=(89,586) /gb=NM_000976 /gi=15431291 /ug=Hs.405042 /len=632 | NM_000976 | Hs.405042 | NP_000967 |
| 12797 | 0.026643 | EST(xu17f02.x1 NCI_CGAP_Co14 cDNA clone IMAGE:2800443 3') | AW272306 | | NP_002201 |
| 12798 | 0.015649 | UI-H-DF0-bem-a-10-0-UI.s1: NCI_CGAP_DF0 cDNA clone UI-H-DF0-bem-a-10-0-UI 3', mRNA sequence /clone=UI-H-DF0-bem-a-10-0-UI /clone_end=3' /gb=CA425521 /gi=24788247 /ug=Hs.411829 /len=1131 | CA425521 | Hs.411829 | |
| 12835 | 0.013819 | AGENCOURT_8856629 Lupski_sciatic_nerve cDNA clone IMAGE:6200636 5', mRNA sequence /clone=IMAGE:6200636 /clone_end=5' /gb=BQ947179 /gi=22362657 /ug=Hs.356605 /len=1277 | BQ947179 | Hs.356605 | |
| 12843 | 0.008208 | cDNA clone IMAGE:123789 3' similar to contains Alu repetitive element; contains THR repetitive element ; Soares fetal liver spleen 1NFLS | R01434 | | |
| 12847 | 0.041237 | EST(cDNA clone IMAGE:4472298 5') | BG251774 | | NP_598001 |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|-------|----------|---|--------------------|-----------------------|-----------------------|
| 12848 | 0.006762 | cDNA: FLJ23165 fis, clone LNG09846. /gb=AK026818 /gi=10439763 /ug=Hs.279898 /len=2117 | AK026818 | Hs.279898 | |
| 12871 | 0.048172 | wg97c03.x1 NCI_CGAP_Kid11 cDNA clone IMAGE:2379172 3' similar to contains L1.b1 L1 repetitive element ;, mRNA sequence /clone=IMAGE:2379172 /clone_end=3' /gb=AI762342 /gi=5178009 /ug=Hs.304298 /len=531 | AI762342 | Hs.304298 | |
| 12882 | 0.026643 | DKFZp564A2463 (from clone DKFZp564A2463) /cds=UNKNOWN /gb=AL137573 /gi=6808283 /ug=Hs.43143 /len=1320 | AL137573 | Hs.43143 | |
| 12891 | 0.045762 | cDNA FLJ38472 fis, clone FEBRA2022148. /gb=AK095791 /gi=21755125 /ug=Hs.50150 /len=2454 | AK095791 | Hs.50150 | |
| 12892 | 0.004048 | ESTs, cDNA, 5' end /clone=IMAGE:1554245 /clone_end=5' /gb=AI792925 /gi=5340641 /ug=Hs.137097 /len=585 | AI792925 | Hs.137097 | |
| 12898 | 0.025168 | 603395193F1 NIH_MGC_90 cDNA clone IMAGE:5405278 5', mRNA sequence /clone=IMAGE:5405278 /clone_end=5' /gb=BI871283 /gi=16044958 /ug=Hs.443147 /len=845 | BI871283 | Hs.443147 | |
| 12907 | 0.045762 | UI-E-EO0-ahy-j-09-0-UI.r1 UI-E-EO0 cDNA clone UI-E-EO0-ahy-j-09-0-UI 5', mRNA sequence /clone=UI-E-EO0-ahy-j-09-0-UI /clone_end=5' /gb=BM722772 /gi=19043589 /ug=Hs.433569 /len=1166 | BM722772 | Hs.433569 | |
| 12961 | 0.028189 | yp92f09.r1 Soares fetal liver spleen 1NFLS cDNA clone IMAGE:194921 5', mRNA sequence /clone=IMAGE:194921 /clone_end=5' /gb=R91059 /gi=958599 /ug=Hs.330761 /len=430 | R91059 | Hs.330761 | |
| 13007 | 0.023762 | EST(cDNA clone GKCAHD03 5') | AV696986 | | NP_072179 |
| 13042 | 0.033283 | EST(cDNA clone IMAGE:4717063 5') | BG569807 | | |
| 13065 | 0.003487 | control | | | |
| 13109 | 0.025168 | cDNA FLJ13752 fis, clone PLACE3000352. /gb=AK023814 /gi=10435863 /ug=Hs.144871 /len=3904 | AK023814 | Hs.144871 | |
| 13110 | 5.57E-04 | hypothetical protein P1 p373c6 (P1P373C6), mRNA /cds=(254,1891) /gb=NM_019110 /gi=17738284 /ug=Hs.44720 /len=2316 | NM_019110 | Hs.44720 | NP_061983 |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|-------|----------|---|--------------------|-----------------------|-----------------------|
| 13127 | 0.035141 | brain abundant, membrane attached signal protein 1 (BASP1), mRNA /cds=(53,736) /gb=NM_006317 /gi=5453749 /ug=Hs.79516 /len=1486 | NM_006317 | Hs.79516 | NP_006308 |
| 13139 | 0.035141 | chromosome 1 open reading frame 8 (C1orf8), mRNA /cds=(251,1222) /gb=NM_004872 /gi=27545320 /ug=Hs.416495 /len=1709 | NM_004872 | Hs.416495 | NP_004863 |
| 13151 | 0.039115 | cell division cycle associated 4 (CDCA4), transcript variant 1, mRNA /cds=(164,889) /gb=NM_017955 /gi=22027508 /ug=Hs.34045 /len=2171 | NM_017955 | Hs.34045 | NP_663747 |
| 13160 | 0.011417 | retinoid X receptor, beta (RXRB), mRNA /cds=(180,1781) /gb=NM_021976 /gi=27436942 /ug=Hs.79372 /len=2892 | NM_021976 | Hs.79372 | NP_068811 |
| 13161 | 0.00767 | hypothetical protein FLJ10035 (FLJ10035), mRNA /cds=(251,1132) /gb=NM_030803 /gi=24475809 /ug=Hs.16390 /len=2404 | NM_030803 | Hs.16390 | NP_110430 |
| 13188 | 0.001867 | hypothetical protein PRO2013 (PRO2013), mRNA /cds=(136,381) /gb=NM_021243 /gi=24308272 /ug=Hs.238205 /len=876 | NM_021243 | Hs.238205 | |
| 13193 | 0.048172 | protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform (PPP2CA), mRNA /cds=(210,1139) /gb=NM_002715 /gi=4506016 /ug=Hs.91773 /len=2181 | NM_002715 | Hs.91773 | NP_002706 |
| 13206 | 0.005412 | spinal cord-derived growth factor-B (SCDGF-B), transcript variant 1, mRNA /cds=(176,1288) /gb=NM_025208 /gi=15451919 /ug=Hs.112885 /len=3808 | NM_025208 | Hs.112885 | NP_149126 |
| 13207 | 0.002024 | ARP8 actin-related protein 8 (yeast) (ACTR8), mRNA /cds=(5,1129) /gb=NM_022899 /gi=12597636 /ug=Hs.124219 /len=2797 | NM_022899 | Hs.124219 | NP_075050 |
| 13225 | 0.017682 | hypothetical protein MGC4276 similar to CG8198 (MGC4276), mRNA /cds=(70,462) /gb=NM_030940 /gi=24475709 /ug=Hs.177776 /len=1978 | NM_030940 | Hs.177776 | NP_112202 |
| 13227 | 0.033283 | cysteine dioxygenase, type I (CDO1), mRNA /cds=(255,857) /gb=NM_001801 /gi=4502754 /ug=Hs.3229 /len=1556 | NM_001801 | Hs.3229 | NP_001792 |
| 13302 | 0.025168 | nuclear pore complex protein (NUP107), mRNA /cds=(116,2893) /gb=NM_020401 /gi=9966880 /ug=Hs.236204 /len=3131 | NM_020401 | Hs.236204 | NP_065134 |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|-------|----------|---|--------------------|-----------------------|-----------------------|
| 13304 | 0.029809 | wl27d01.x1 NCI_CGAP_Ut1 cDNA clone IMAGE:2426113 3', mRNA sequence /clone=IMAGE:2426113 /clone_end=3' /gb=AI866216 /gi=5530323 /ug=Hs.413738 /len=133 | AI866216 | Hs.413738 | |
| 13309 | 0.01471 | nuclear receptor subfamily 3, group C, member 2 (NR3C2), mRNA /cds=(217,3171) /gb=NM_000901 /gi=4505198 /ug=Hs.1790 /len=5749 | NM_000901 | Hs.1790 | NP_000892 |
| 13319 | 0.004357 | cDNA FLJ33540 fis, clone BRAMY2007613. /gb=AK090859 /gi=21749098 /ug=Hs.21213 /len=2030 | AK090859 | Hs.21213 | |
| 13357 | 0.005811 | mRNA; cDNA DKFZp451B1418 (from clone DKFZp451B1418) /gb=AL832622 /gi=21733197 /ug=Hs.446489 /len=5612 | AL832622 | Hs.446489 | |
| 13425 | 0.025168 | EST(wk79e07.x1 NCI_CGAP_Pan1 clone IMAGE:2421636 3') | AI813780 | | |
| 13453 | 0.035141 | mesoderm induction early response 1 (MIE-1), mRNA /cds=(234,1844) /gb=NM_020948 /gi=24308260 /ug=Hs.222746 /len=4972 | NM_020948 | Hs.222746 | NP_065999 |
| 13457 | 0.045762 | translin (TSN), mRNA /cds=(236,922) /gb=NM_004622 /gi=20302160 /ug=Hs.75066 /len=3408 | NM_004622 | Hs.75066 | NP_004613 |
| 13459 | 0.039115 | N-ethylmaleimide-sensitive factor (NSF), mRNA /cds=(61,2295) /gb=NM_006178 /gi=11079227 /ug=Hs.108802 /len=3960 | NM_006178 | Hs.108802 | NP_006169 |
| 13467 | 0.010701 | EST(zt04d06.r1 NCI_CGAP_GCB1 clone IMAGE:712139 5') | AA280235 | | NP_005728 |
| 13469 | 0.029809 | clone IMAGE:5299642, mRNA /gb=BC041913 /gi=27469540 /ug=Hs.17132 /len=2227 | BC041913 | Hs.17132 | |
| 13501 | 0.007162 | likely ortholog of mouse WD-40-repeat-containing protein with a SOCS box 2 (WSB2), mRNA /cds=(66,1280) /gb=NM_018639 /gi=20149658 /ug=Hs.136644 /len=2610 | NM_018639 | Hs.136644 | NP_061109 |
| 13513 | 0.015649 | EST(PM3-SN0020-270300-001-h08 SN0020) | AW865025 | | NP_115668 |
| 13520 | 0.031506 | EST(tz32c11.x1 NCI_CGAP_Ut2 clone IMAGE:2290292 3') | AI631079 | | NP_079436 |
| 13522 | 0.021147 | mRNA; cDNA DKFZp451O1818 (from clone DKFZp451O1818) /gb=AL832650 /gi=21733226 /ug=Hs.12396 /len=4870 | AL832650 | Hs.12396 | |
| 13530 | 7.32E-04 | synaptic nuclei expressed gene 1 (SYNE-1), transcript variant beta, mRNA /cds=(121,10086) /gb=NM_015293 /gi=19526752 /ug=Hs.192102 /len=10742 | NM_015293 | Hs.192102 | NP_598411 |

| Spot | p-value | D description | Gene Accession No. | Unigen Accession No. | Protein Accession No. |
|-------|----------|---|--------------------|----------------------|-----------------------|
| 13562 | 0.041237 | AGENCOURT_6653840 NIH_MGC_116 cDNA clone IMAGE:5761286 5', mRNA sequence /clone=IMAGE:5761286 /clone_end=5' /gb=BM924828 /gi=19375207 /ug=Hs.181174 /len=1422 | BM924828 | Hs.181174 | |
| 13599 | 0.00767 | mRNA; cDNA DKFZp313E1012 (from clone DKFZp313E1012) /gb=AL832661 /gi=21733237 /ug=Hs.94694 /len=3233 | AL832661 | Hs.94694 | |
| 13601 | 0.001234 | similar to rat myomegalin (LOC64182), mRNA /cds=(336,1268) /gb=NM_022359 /gi=21314705 /ug=Hs.333512 /len=1717 | NM_022359 | Hs.333512 | NP_071754 |
| 13602 | 0.003758 | UI-1-BC1p-asi-a-02-0-UI.s1 NCI_CGAP_PI3 cDNA clone UI-1-BC1p-asi-a-02-0-UI 3', mRNA sequence /clone=UI-1-BC1p-asi-a-02-0-UI /clone_end=3' /gb=BQ011545 /gi=19736446 /ug=Hs.361171 /len=1143 | BQ011545 | Hs.361171 | |
| 13615 | 0.018779 | mRNA full length insert cDNA clone EUROIMAGE 1476475 /gb=AJ420560 /gi=17066424 /ug=Hs.93231 /len=1346 | AJ420560 | Hs.93231 | |
| 13619 | 0.014281 | FLJ30633 fis, clone CTONG2002418, weakly similar to Homo sapiens scaffold attachment factor B (SAF-B) mRNA (AK055195.1) | AK055195 | Hs.331328 | NP_079031 |
| 13642 | 0.031506 | calpastatin (CAST), transcript variant 2, mRNA /cds=(155,2215) /gb=NM_173060 /gi=27765084 /ug=Hs.359682 /len=4296 | NM_173060 | Hs.359682 | NP_775085 |
| 13665 | 0.003758 | ubiquitin-conjugating enzyme E2 variant 2 (UBE2V2), mRNA /cds=(22,459) /gb=NM_003350 /gi=12025664 /ug=Hs.79300 /len=1535 | NM_003350 | Hs.79300 | NP_003341 |
| 13670 | 0.048172 | hypothetical protein FLJ11506 (FLJ11506), mRNA /cds=(16,963) /gb=NM_024666 /gi=20070334 /ug=Hs.77703 /len=2774 | NM_024666 | Hs.77703 | NP_078942 |
| 13729 | 0.023762 | EH-domain containing 1 (EHD1), mRNA /cds=(247,1851) /gb=NM_006795 /gi=5803008 /ug=Hs.155119 /len=3508 | NM_006795 | Hs.155119 | NP_006786 |
| 13731 | 0.022422 | diacylglycerol O-acyltransferase homolog 2 (mouse) (DGAT2), mRNA /cds=(777,1670) /gb=NM_032564 /gi=14211870 /ug=Hs.334305 /len=2713 | NM_032564 | Hs.334305 | NP_115953 |
| 13768 | 0.021586 | likely ortholog of mouse hypoxia induced gene 1 (HIG1), mRNA /cds=(93,374) /gb=NM_014056 /gi=7661619 /ug=Hs.7917 /len=1362 | NM_014056 | Hs.7917 | NP_054775 |
| 13786 | 0.011417 | mitochondrion, complete genome | NC_001807 | | |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|-------|----------|---|--------------------|-----------------------|-----------------------|
| 13795 | 0.045762 | hypothetical protein FLJ21302 (FLJ21302), mRNA /cds=(91,1203) /gb=NM_022901 /gi=12597640 /ug=Hs.128071 /len=3160 | NM_022901 | Hs.128071 | NP_075052 |
| 13797 | 0.037084 | 603041572T1 NIH_MGC_116 cDNA clone IMAGE:5163112 3', mRNA sequence /clone=IMAGE:5163112 /clone_end=3' /gb=BI517954 /gi=15342746 /ug=Hs.398211 /len=964 | BI517954 | Hs.398211 | |
| 13835 | 0.013819 | mRNA for KIAA1078 protein, partial cds. /cds=(1,4098) /gb=AB029001 /gi=20521755 /ug=Hs.23585 /len=6740 | AB029001 | Hs.23585 | |
| 13945 | 0.018779 | EST(tx88e11.x1 NCI_CGAP_Ut4 clone IMAGE:2276684 3' contains Alu repeat) | AI690725 | | |
| 13961 | 0.021147 | Novel | SEQ.ID.No.90 | | |
| 13986 | 0.019933 | phosphodiesterase 6D, cGMP-specific, rod, delta (PDE6D), mRNA /cds=(151,603) /gb=NM_002601 /gi=4505670 /ug=Hs.48291 /len=1131 | NM_002601 | Hs.48291 | NP_002592 |
| 14059 | 0.045762 | EST (cDNA clone IMAGE:2490676 3') | AI972954 | | NP_000996 |
| 14076 | 0.023762 | hypothetical protein FLJ22611 (FLJ22611), mRNA /cds=(295,1923) /gb=NM_032226 /gi=24308321 /ug=Hs.27774 /len=2821 | NM_032226 | Hs.27774 | NP_115602 |
| 14111 | 0.039115 | hypothetical protein MGC3121 (MGC3121), mRNA /cds=(179,1936) /gb=NM_024031 /gi=13128979 /ug=Hs.293629 /len=2063 | NM_024031 | Hs.293629 | NP_076936 |
| 14122 | 0.033283 | 602152950F1 NIH_MGC_81 cDNA clone IMAGE:4293853 5', mRNA sequence /clone=IMAGE:4293853 /clone_end=5' /gb=BF673050 /gi=11946945 /ug=Hs.208558 /len=830 | BF673050 | Hs.208558 | |
| 14129 | 0.035141 | zu07g05.s1 Soares_testis_NHT cDNA clone IMAGE:731192 3' similar to P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR. ;, mRNA sequence /clone=IMAGE:731192 /clone_end=3' /gb=AA417352 /gi=2077434 /ug=Hs.445851 /len=519 | AA417352 | Hs.445851 | |
| 14132 | 0.00767 | EST (ie64h03.x1 Homo sapiens cDNA, 3' end/clone_end=3' /gb=BI963813 /gi=16338218 /ug=Hs.349015/len=555) | BI963813 | Hs.349015 | NP_116159 |
| 14163 | 0.016639 | EST(AV657608 GLC cDNA clone GLCFDF10 3') | AV657608 | | |
| 14219 | 0.041237 | cDNA FLJ37978 fis, clone CTONG2010348. /gb=AK095297 /gi=21754529 /ug=Hs.381207 /len=3284 | AK095297 | Hs.381207 | |
| 14249 | 0.043451 | mitochondrion, complete genome | NC_001807 | | |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|-------|----------|--|--------------------|-----------------------|-----------------------|
| 14266 | 0.028189 | EST, cDNA /clone=IMAGE:1266535 /gb=AA729300 /gi=2750659 /ug=Hs.325555 /len=173 | AA729300 | Hs.325555 | |
| 14268 | 0.037084 | calcium/calmodulin-dependent protein kinase (CaM kinase) II delta (CAMK2D), transcript variant 1, mRNA /cds=(505,1941) /gb=NM_172127 /gi=26667185 /ug=Hs.111460 /len=4098 | NM_172127 | Hs.111460 | NP_742126 |
| 14294 | 0.035141 | decorin (DCN), transcript variant A1, mRNA /cds=(200,1279) /gb=NM_001920 /gi=19743844 /ug=Hs.433989 /len=1751 | NM_001920 | Hs.433989 | NP_598014 |
| 14295 | 0.011417 | cDNA: FLJ22765 fis, clone KAIA1180. /gb=AK026418 /gi=10439279 /ug=Hs.163986 /len=1994 | AK026418 | Hs.163986 | |
| 14375 | 8.74E-04 | ESTs, cDNA, 3' end /clone=IMAGE:2402646 /clone_end=3' /gb=AI768858 /gi=5235367 /ug=Hs.157149 /len=562 | AI768858 | Hs.157149 | NP_066012 |
| 14386 | 0.004357 | UI-E-EJ0-aik-i-20-0-UI.r1 UI-E-EJ0 cDNA clone UI-E-EJ0-aik-i-20-0-UI 5', mRNA sequence /clone=UI-E-EJ0-aik-i-20-0-UI /clone_end=5' /gb=BM727413 /gi=19048746 /ug=Hs.112619 /len=1667 | BM727413 | Hs.112619 | |
| 14387 | 0.016639 | likely ortholog of rat V-1 protein (V-1), mRNA /cds=(229,585) /gb=NM_145808 /gi=21956644 /ug=Hs.21321 /len=3770 | NM_145808 | Hs.21321 | NP_665807 |
| 14417 | 0.019933 | proteasome (prosome, macropain) subunit, alpha type, 4 (PSMA4), mRNA /cds=(137,922) /gb=NM_002789 /gi=23110940 /ug=Hs.251531 /len=1189 | NM_002789 | Hs.251531 | NP_002780 |
| 14453 | 0.023762 | NO significant match, ORF+1(16~273) | SEQ.ID.No.41 | | |
| 14455 | 0.004357 | No significant match, ORF+3(135~404) | SEQ.ID.No.50 | | |
| 14504 | 0.021586 | No significant match (ORF:none) | SEQ.ID.No.22 | | |
| 14521 | 0.036435 | HSC15D092 normalized infant brain cDNA cDNA clone c-15d09 3', mRNA sequence /clone=c-15d09 /clone_end=3' /gb=Z39248 /gi=562440 /ug=Hs.27328 /len=352 | Z39248 | Hs.27328 | |
| 14524 | 0.001721 | EST (wa75f06.x1 Soares_NFL_T_GBC_S1 | AI685268 | | |
| 14546 | 4.21E-04 | EST (601819273F1 NIH_MGC_58 cDNA clone IMAGE:4051098 5') | BF130672 | | NP_003655 |
| 14549 | 0.036435 | UI-H-BI3-alq-c-04-0-UI.s1 NCI_CGAP_Sub5 cDNA clone IMAGE:3068166 3', mRNA sequence /clone=IMAGE:3068166 /clone_end=3' /gb=BF512182 /gi=11597361 /ug=Hs.196953 /len=864 | BF512182 | Hs.196953 | |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|-------|----------|---|--------------------|-----------------------|-----------------------|
| 14560 | 0.017682 | TRAM-like protein (KIAA0057), mRNA /cds=(76,1188) /gb=NM_012288 /gi=6912449 /ug=Hs.153954 /len=6974 | NM_012288 | Hs.153954 | NP_036420 |
| 14614 | 0.019094 | EST(yq95a02.r1 Soares fetal liver spleen 1NFLS cDNA clone IMAGE:203498 5' similar to contains Alu repetitive element) | H56096 | | |
| 14637 | 0.01471 | hypothetical protein PRO1331 (PRO1331), mRNA /cds=(423,617) /gb=NM_030778 /gi=13562115 /ug=Hs.301824 /len=1634 | NM_030778 | Hs.301824 | NP_110405 |
| 14704 | 0.043451 | qz33c01.x1 NCI_CGAP_Kid11 cDNA clone IMAGE:2028672 3', mRNA sequence /clone=IMAGE:2028672 /clone_end=3' /gb=AI262059 /gi=3870262 /ug=Hs.386784 /len=229 | AI262059 | Hs.386784 | |
| 14833 | 0.013819 | EST380251 MAGE resequences, MAGJ cDNA, mRNA sequence /gb=AW968281 /gi=8158016 /ug=Hs.319460 /len=689 | AW968281 | Hs.319460 | |
| 14837 | 0.026643 | EST(RC4-CT0322-261299-011-h03 CT0322 Homo sapiens cDNA, mRNA sequence) | AW857814 | | |
| 14842 | 0.008208 | mitochondrion, complete genome | NC_001807 | | |
| 14864 | 0.018779 | cDNA FLJ31594 fis, clone NT2RI2002507 | AK056156 | | NP_006818 |
| 14934 | 0.007918 | No significant match (ORF:+1:1~102[102]) | SEQ.ID.No.59 | | |
| 14942 | 0.005811 | EST, cDNA /gb=AW360966 /gi=6865616 /ug=Hs.6653 /len=661 | AW360966 | Hs.6653 | NP_055942 |
| 14948 | 0.048172 | EST(Fetal Cochlea Homo sapiens cDNA clone IMAGE:2537435 5') | BI497119 | | NP_006826 |

| TABLE 3C | | | | | |
|--|----------|---|--------------------|-----------------------|-----------------------|
| Genes Corresponding To Differentially Expressed Genes in Figure 10-Allergies | | | | | |
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 167 | 0.041383 | corticotropin releasing hormone binding protein (CRHBP), mRNA /cds=(94,1062) /gb=NM_001882 /gi=5921997 /ug=Hs.115617 /len=1295 | NM_001882 | Hs.115617 | NP_001873 |
| 169 | 0.041383 | nuclear protein double minute 1 (MDM1), mRNA /cds=(93,2237) /gb=NM_017440 /gi=24586654 /ug=Hs.12871 /len=2942 | NM_017440 | Hs.12871 | NP_064513 |
| 170 | 0.04789 | Duffy blood group (FY), mRNA /cds=(495,1511) /gb=NM_002036 /gi=4503818 /ug=Hs.183 /len=1559 | NM_002036 | Hs.183 | NP_002027 |
| 178 | 0.025981 | zinc finger protein 161 (ZNF161), mRNA /cds=(42,1592) /gb=NM_007146 /gi=6005967 /ug=Hs.223754 /len=2306 | NM_007146 | Hs.223754 | NP_009077 |
| 179 | 0.04789 | ubiquitin specific protease 9, X chromosome (fat facets-like Drosophila) (USP9X), transcript variant 1, mRNA /cds=(60,7751) /gb=NM_004652 /gi=11641424 /ug=Hs.77578 /len=8171 | NM_004652 | Hs.77578 | NP_068706 |
| 205 | 0.01859 | mRNA for KIAA0268 gene, partial cds. /cds=(1,3582) /gb=D87742 /gi=1665824 /ug=Hs.241552 /len=5976 | D87742 | Hs.241552 | |
| 248 | 0.04789 | hemoglobin, beta (HBB), mRNA /cds=(51,494) /gb=NM_000518 /gi=28302128 /ug=Hs.155376 /len=626 | NM_000518 | Hs.155376 | NP_000509 |
| 252 | 0.01859 | hypothetical protein HSPC177 (HSPC177), mRNA /cds=(80,739) /gb=NM_016410 /gi=20127557 /ug=Hs.36237 /len=1434 | NM_016410 | Hs.36237 | NP_057494 |
| 278 | 0.041383 | coatamer protein complex, subunit gamma (COPG), mRNA /cds=(76,2700) /gb=NM_016128 /gi=21359909 /ug=Hs.266914 /len=3075 | NM_016128 | Hs.266914 | NP_663768 |
| 313 | 0.020961 | FLI-LRR associated protein-1 | AF045573 | | NP_032541 |
| 324 | 0.030485 | phosphoprotein enriched in astrocytes 15 (PEA15), mRNA /cds=(194,586) /gb=NM_003768 /gi=21359835 /ug=Hs.194673 /len=2486 | NM_003768 | Hs.194673 | NP_003759 |
| 355 | 0.025981 | double-stranded RNA-binding nuclear protein NFAR-1 | AF167569 | | NP_703194 |
| 394 | 0.04789 | FLJ11874 fis, clone HEMBA1007073 /cds=UNKNOWN /gb=AK021936 /gi=10433239 /ug=Hs.367819 /len=2737 | AK021936 | Hs.367819 | |
| 419 | 0.035601 | SYNCRIP | AB035725 | | NP_062770 |
| 429 | 0.025981 | NPD009 protein (NPD009), mRNA /cds=(1327,1677) /gb=NM_020686 /gi=24476005 /ug=Hs.283675 /len=2514 | NM_020686 | Hs.283675 | NP_065737 |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|------|----------|--|--------------------|-----------------------|-----------------------|
| 458 | 0.025981 | zinc finger protein 354B (ZNF354B), mRNA /cds=(180,2018) /gb=NM_058230 /gi=17530790 /ug=Hs.325804 /len=2140 | NM_058230 | Hs.325804 | NP_478137 |
| 460 | 0.035601 | sorting nexin 3 (SNX3), transcript variant 3, mRNA /cds=(326,667) /gb=NM_152828 /gi=23111042 /ug=Hs.12102 /len=1559 | NM_152828 | Hs.12102 | NP_690041 |
| 549 | 0.011794 | guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1 (GNB2L1), mRNA /cds=(96,1049) /gb=NM_006098 /gi=24475893 /ug=Hs.5662 /len=1093 | NM_006098 | Hs.5662 | NP_006089 |
| 589 | 0.025981 | AGENCOURT_6640990 NIH_MGC_68 cDNA clone IMAGE:5735856 5', mRNA sequence /clone=IMAGE:5735856 /clone_end=5' /gb=BM907553 /gi=19357932 /ug=Hs.424427 /len=645 | BM907553 | Hs.424427 | |
| 625 | 0.030485 | fragile X mental retardation 1 (FMR1), mRNA /cds=(220,2118) /gb=NM_002024 /gi=4503764 /ug=Hs.89764 /len=4362 | NM_002024 | Hs.89764 | NP_002015 |
| 633 | 0.044987 | A kinase (PRKA) anchor protein 13 (AKAP13), transcript variant 2, mRNA /cds=(214,8655) /gb=NM_007200 /gi=21493028 /ug=Hs.301946 /len=10156 | NM_007200 | Hs.301946 | NP_658913 |
| 648 | 0.044987 | HLA class-I (HLA-A26) heavy chain, complete cds (clone cMIY-1) | D32129 | | NP_002107 |
| 658 | 0.001504 | KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3 (KDEL3), transcript variant 1, mRNA /cds=(157,801) /gb=NM_006855 /gi=8051612 /ug=Hs.250696 /len=1705 | NM_006855 | Hs.250696 | NP_057839 |
| 662 | 0.022033 | insulin-like growth factor binding protein 5 (IGFBP5), mRNA /cds=(752,1570) /gb=NM_000599 /gi=10834981 /ug=Hs.380833 /len=1722 | NM_000599 | Hs.380833 | NP_000590 |
| 693 | 0.04789 | ubiquitin-conjugating enzyme E2L 3 (UBE2L3), mRNA /cds=(16,480) /gb=NM_003347 /gi=4507788 /ug=Hs.108104 /len=2845 | NM_003347 | Hs.108104 | NP_003338 |
| 700 | 0.022033 | major histocompatibility complex, class II, DR alpha (HLA-DRA), mRNA /cds=(65,829) /gb=NM_019111 /gi=18641378 /ug=Hs.409805 /len=1237 | NM_019111 | Hs.409805 | NP_061984 |
| 709 | 0.019692 | ATP synthase, H transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein) (ATP5O), mRNA /cds=(37,678) /gb=NM_001697 /gi=4502302 /ug=Hs.433960 /len=772 | NM_001697 | Hs.433960 | NP_001688 |
| 721 | 0.025981 | mitochondrion, complete genome | NC_001807 | | |

| Spot | p-value | Description | Gen Accession No. | Unigene Accession No. | Protein Accession No. |
|------|----------|--|-------------------------|-----------------------------|-----------------------------|
| 726 | 0.01081 | tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide (YWHAG), mRNA /cds=(192,935) /gb=NM_012479 /gi=21464100 /ug=Hs.25001 /len=3747 | NM_012479 | Hs.25001 | NP_036611 |
| 765 | 0.041383 | peripheral myelin protein 22 (PMP22), transcript variant 1, mRNA /cds=(209,691) /gb=NM_000304 /gi=24430161 /ug=Hs.103724 /len=1828 | NM_000304 | Hs.103724 | NP_696997 |
| 771 | 0.04789 | zinc finger protein (ZFD25) (62% aa) | AB027251 | | NP_057304 |
| 772 | 0.04789 | acid sphingomyelinase (ASM) gene, exons a, and alternative a (3' end), b and c (5' end). | M59917 | | |
| 806 | 0.035601 | ring finger protein 19 (RNF19), mRNA /cds=(318,2834) /gb=NM_015435 /gi=19923421 /ug=Hs.48320 /len=4357 | NM_015435 | Hs.48320 | NP_056250 |
| 807 | 0.025981 | KIAA0102 gene product (KIAA0102), mRNA /cds=(308,679) /gb=NM_014752 /gi=7661907 /ug=Hs.77665 /len=1370 | NM_014752 | Hs.77665 | NP_055567 |
| 808 | 0.035601 | PIX1 mRNA (ORF) | AF037219 | | NP_570854 |
| 809 | 0.01859 | methylcrotonoyl-Coenzyme A carboxylase 1 (alpha) (MCCC1), mRNA /cds=(133,2310) /gb=NM_020166 /gi=13518227 /ug=Hs.47649 /len=2528 | NM_020166 | Hs.47649 | NP_064551 |
| 815 | 0.022033 | SnRNP assembly defective 1 (SAD1), mRNA /cds=(493,1467) /gb=NM_006590 /gi=5730024 /ug=Hs.12820 /len=2166 | NM_006590 | Hs.12820 | NP_006581 |
| 829 | 0.022033 | zinc finger protein 103 (mouse) (ZFP103), mRNA /cds=(923,2980) /gb=NM_005667 /gi=5031824 /ug=Hs.155968 /len=3423 | NM_005667 | Hs.155968 | NP_005658 |
| 844 | 0.013024 | sorting nexin 2 (SNX2), mRNA /cds=(50,1609) /gb=NM_003100 /gi=23111037 /ug=Hs.11183 /len=2091 | NM_003100 | Hs.11183 | NP_003091 |
| 846 | 0.04789 | LAG1 longevity assurance 2 (S. cerevisiae) (LASS2), mRNA /cds=(50,742) /gb=NM_013384 /gi=9937997 /ug=Hs.285976 /len=1646 | NM_013384 | Hs.285976 | NP_071358 |
| 847 | 0.01859 | peroxisomal biogenesis factor 3 (PEX3), mRNA /cds=(64,1185) /gb=NM_003630 /gi=4505726 /ug=Hs.7277 /len=1979 | NM_003630 | Hs.7277 | NP_003621 |
| 865 | 0.025981 | mitochondrion, complete genome | NC_001807 | | |
| 869 | 0.008919 | receptor associated protein 80 (RAP80), mRNA /cds=(110,2269) /gb=NM_016290 /gi=21361592 /ug=Hs.7889 /len=2516 | NM_016290 | Hs.7889 | NP_057374 |
| 873 | 0.04789 | dynactin 4 (p62) (DCTN4), mRNA /cds=(22,1404) /gb=NM_016221 /gi=19923450 /ug=Hs.328865 /len=3837 | NM_016221 | Hs.328865 | NP_057305 |
| 874 | 0.025981 | proline rich 2 (PROL2), mRNA /cds=(114,1097) /gb=NM_006813 /gi=5802981 /ug=Hs.75969 /len=2061 | NM_006813 | Hs.75969 | NP_006804 |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|------|----------|---|--------------------|-----------------------|-----------------------|
| 877 | 0.035601 | ring finger protein 11 (RNF11), mRNA /cds=(128,592) /gb=NM_014372 /gi=7657519 /ug=Hs.96334 /len=2529 | NM_014372 | Hs.96334 | NP_055187 |
| 878 | 0.04789 | protein tyrosine phosphatase, non-receptor type 12 (PTPN12), mRNA /cds=(30,2372) /gb=NM_002835 /gi=18375651 /ug=Hs.62 /len=3161 | NM_002835 | Hs.62 | NP_002826 |
| 894 | 0.04789 | splicing factor, arginine/serine-rich 11 (SFRS11), mRNA /cds=(125,1579) /gb=NM_004768 /gi=23111060 /ug=Hs.433581 /len=2775 | NM_004768 | Hs.433581 | NP_004759 |
| 896 | 0.022033 | hypothetical protein FLJ32949 (FLJ32949), mRNA /cds=(1,2277) /gb=NM_173812 /gi=27883873 /ug=Hs.125472 /len=2277 | NM_173812 | Hs.125472 | NP_776173 |
| 901 | 0.04789 | signal transducing adaptor molecule (SH3 domain and ITAM motif) 2 (STAM2), mRNA /cds=(351,1928) /gb=NM_005843 /gi=21265030 /ug=Hs.17200 /len=3928 | NM_005843 | Hs.17200 | NP_005834 |
| 904 | 0.041383 | tumor susceptibility gene 101 (TSG101), mRNA /cds=(127,1299) /gb=NM_006292 /gi=18765712 /ug=Hs.118910 /len=1550 | NM_006292 | Hs.118910 | NP_006283 |
| 906 | 0.041383 | transaldolase 1 (TALDO1), mRNA /cds=(51,1064) /gb=NM_006755 /gi=5803186 /ug=Hs.77290 /len=1319 | NM_006755 | Hs.77290 | NP_006746 |
| 909 | 0.00388 | integral membrane protein Tmp21-I (p23) | AJ004913 | | NP_006818 |
| 910 | 0.041383 | CD9 antigen (p24) (CD9), mRNA /cds=(112,798) /gb=NM_001769 /gi=21237762 /ug=Hs.1244 /len=1246 | NM_001769 | Hs.1244 | NP_001760 |
| 923 | 0.003097 | eukaryotic translation initiation factor 3, subunit 3 gamma, 40kDa (EIF3S3), mRNA /cds=(6,1064) /gb=NM_003756 /gi=4503514 /ug=Hs.58189 /len=1280 | NM_003756 | Hs.58189 | NP_003747 |
| 947 | 0.041383 | inhibitor of DNA binding 4, dominant negative helix-loop-helix protein (ID4), mRNA /cds=(370,855) /gb=NM_001546 /gi=19923138 /ug=Hs.34853 /len=2389 | NM_001546 | Hs.34853 | NP_001537 |
| 968 | 0.04789 | translin (TSN), mRNA /cds=(236,922) /gb=NM_004622 /gi=20302160 /ug=Hs.75066 /len=3408 | NM_004622 | Hs.75066 | NP_004613 |
| 1030 | 0.030485 | px19-like protein (PX19), mRNA /cds=(177,836) /gb=NM_013237 /gi=7019508 /ug=Hs.279529 /len=1217 | NM_013237 | Hs.279529 | NP_037369 |
| 1034 | 0.041383 | N-myristoyltransferase 2 (NMT2), mRNA /cds=(47,1543) /gb=NM_004808 /gi=4758815 /ug=Hs.122647 /len=2838 | NM_004808 | Hs.122647 | NP_004799 |
| 1058 | 0.025981 | Williams-Beuren syndrome chromosome region 1 (WBSCR1), transcript variant 1, mRNA /cds=(9,755) /gb=NM_022170 /gi=11559922 /ug=Hs.180900 /len=2546 | NM_022170 | Hs.180900 | NP_114381 |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Prot in Accession No. |
|------|----------|--|--------------------|-----------------------|-----------------------|
| 1209 | 0.04789 | membrane protein, palmitoylated 6 (MAGUK p55 subfamily member 6) (MPP6), mRNA /cds=(300,1922) /gb=NM_016447 /gi=21361597 /ug=Hs.108931 /len=2201 | NM_016447 | Hs.108931 | NP_057531 |
| 1318 | 0.038534 | SH3-domain binding protein 5 (BTK-associated) (SH3BP5), mRNA /cds=(64,1341) /gb=NM_004844 /gi=4759057 /ug=Hs.109150 /len=2570 | NM_004844 | Hs.109150 | NP_004835 |
| 1385 | 0.032841 | hypothetical protein FLJ11267 (FLJ11267), mRNA /cds=(292,771) /gb=NM_019607 /gi=9624987 /ug=Hs.165741 /len=1817 | NM_019607 | Hs.165741 | NP_062553 |
| 1409 | 0.035601 | KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2 (KDEL2), mRNA /cds=(13,651) /gb=NM_006854 /gi=8051609 /ug=Hs.372755 /len=1153 | NM_006854 | Hs.372755 | NP_006845 |
| 1437 | 0.01859 | SRY (sex determining region Y)-box 9 (campomelic dysplasia, autosomal sex-reversal) (SOX9), mRNA /cds=(373,1902) /gb=NM_000346 /gi=4557852 /ug=Hs.2316 /len=3936 | NM_000346 | Hs.2316 | NP_000337 |
| 1441 | 0.041383 | RE1-silencing transCRiption factor (REST) | NM_005612 | | NP_005603 |
| 1445 | 0.008919 | nuclear receptor coactivator 6 (NCOA6), mRNA /cds=(2755,8760) /gb=NM_014071 /gi=7661975 /ug=Hs.159613 /len=9301 | NM_014071 | Hs.159613 | NP_054790 |
| 1448 | 0.035601 | retinoic acid repressible protein (RARG-1), mRNA /cds=(33,806) /gb=NM_016167 /gi=15743546 /ug=Hs.106346 /len=896 | NM_016167 | Hs.106346 | NP_057251 |
| 1482 | 0.007315 | ATP synthase, H transporting, mitochondrial F1 complex, epsilon subunit (ATP5E), nuclear gene encoding mitochondrial protein, mRNA /cds=(95,250) /gb=NM_006886 /gi=21327678 /ug=Hs.177530 /len=417 | NM_006886 | Hs.177530 | NP_008817 |
| 1505 | 0.04789 | TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 32kDa (TAF9), transcript variant 1, mRNA /cds=(159,953) /gb=NM_003187 /gi=21166375 /ug=Hs.60679 /len=1153 | NM_003187 | Hs.60679 | NP_057367 |
| 1557 | 0.04789 | MR2-CI0186-291100-010-a06 CI0186 cDNA, mRNA sequence /gb=BF814502 /gi=12147047 /ug=Hs.446594 /len=530 | BF814502 | Hs.446594 | |
| 1574 | 0.030485 | similar to triple functional domain (PTPRF interacting) (LOC115557), mRNA /cds=(331,1755) /gb=NM_133483 /gi=19311007 /ug=Hs.61581 /len=2166 | NM_133483 | Hs.61581 | NP_597840 |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|------|----------|---|--------------------|-----------------------|-----------------------|
| 1579 | 0.030485 | chromosome 14 open reading frame 108 (C14orf108), mRNA /cds=(407,1879) /gb=NM_018229 /gi=21361775 /ug=Hs.106210 /len=3088 | NM_018229 | Hs.106210 | NP_060699 |
| 1598 | 0.007315 | troponin I, skeletal, slow (TNNI1), mRNA /cds=(74,637) /gb=NM_003281 /gi=21361554 /ug=Hs.84673 /len=1108 | NM_003281 | Hs.84673 | NP_003272 |
| 1599 | 0.015602 | protein XP_037672 (aa, 58%) | XP_037672 | | |
| 1618 | 0.04789 | mRNA for KIAA0570 protein, partial cds. /cds=(480,10718) /gb=AB011142 /gi=20521084 /ug=Hs.180948 /len=11269 | AB011142 | Hs.180948 | |
| 1646 | 0.041383 | testis derived transcript (3 LIM domains) (TES), transcript variant 1, mRNA /cds=(182,1447) /gb=NM_015641 /gi=23238186 /ug=Hs.165986 /len=2766 | NM_015641 | Hs.165986 | NP_690042 |
| 1647 | 0.041383 | asporin (LRR class 1) (ASP), mRNA /cds=(228,1373) /gb=NM_017680 /gi=16596677 /ug=Hs.10760 /len=2466 | NM_017680 | Hs.10760 | NP_060150 |
| 1683 | 0.01859 | mitochondrion, complete genome | NC_001807 | | |
| 1687 | 0.004826 | diazepam binding inhibitor (GABA receptor modulator, acyl-Coenzyme A binding protein) (DBI), mRNA /cds=(20,334) /gb=NM_020548 /gi=24475624 /ug=Hs.78888 /len=556 | NM_020548 | Hs.78888 | NP_065438 |
| 1723 | 0.035601 | CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5, EJ16, EJ30, EL32 and G344) (CD59), mRNA /cds=(50,436) /gb=NM_000611 /gi=20127410 /ug=Hs.278573 /len=1946 | NM_000611 | Hs.278573 | NP_000602 |
| 1793 | 0.01081 | nuclear receptor subfamily 4, group A, member 1 (NR4A1), transcript variant 1, mRNA /cds=(315,2111) /gb=NM_002135 /gi=27894342 /ug=Hs.1119 /len=2699 | NM_002135 | Hs.1119 | NP_775181 |
| 1836 | 0.00388 | hypothetical protein FLJ23445 (FLJ23445), mRNA /cds=(44,658) /gb=NM_025075 /gi=13376622 /ug=Hs.288151 /len=963 | NM_025075 | Hs.288151 | NP_079351 |
| 1883 | 0.030485 | cytochrome c oxidase subunit VIIb (COX7B), nuclear gene encoding mitochondrial protein, mRNA /cds=(91,333) /gb=NM_001866 /gi=18105038 /ug=Hs.432170 /len=456 | NM_001866 | Hs.432170 | NP_001857 |
| 1999 | 0.041383 | chromosome 20 open reading frame 40 (C20orf40), mRNA /cds=(208,396) /gb=NM_014054 /gi=7661709 /ug=Hs.105379 /len=417 | NM_014054 | Hs.105379 | NP_054773 |
| 2070 | 0.041383 | myotubular myopathy 1 (MTM1), mRNA /cds=(55,1866) /gb=NM_000252 /gi=4557895 /ug=Hs.75302 /len=3411 | NM_000252 | Hs.75302 | NP_000243 |

| Spot | p-value | D description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|------|----------|---|--------------------|-----------------------|-----------------------|
| 2088 | 0.013024 | hypothetical protein LOC51257 (LOC51257), mRNA /cds=(352,1092) /gb=NM_016496 /gi=24475980 /ug=Hs.132744 /len=1614 | NM_016496 | Hs.132744 | NP_057580 |
| 2141 | 0.025981 | transcription factor 12 (HTF4, helix-loop-helix transcription factors 4) (TCF12), mRNA /cds=(214,2262) /gb=NM_003205 /gi=4585865 /ug=Hs.21704 /len=4202 | NM_003205 | Hs.21704 | NP_003196 |
| 2175 | 0.035601 | clone IMAGE:4799018, mRNA /gb=BC045722 /gi=28277129 /ug=Hs.153527 /len=2587 | BC045722 | Hs.153527 | |
| 2210 | 0.04789 | CGI-09 protein (CGI-09), mRNA /cds=(73,1566) /gb=NM_015939 /gi=19923474 /ug=Hs.128791 /len=2272 | NM_015939 | Hs.128791 | NP_057023 |
| 2212 | 0.01081 | chromosome 21 open reading frame 4 (C21orf4), mRNA /cds=(159,635) /gb=NM_006134 /gi=8659558 /ug=Hs.284142 /len=750 | NM_006134 | Hs.284142 | NP_006125 |
| 2230 | 0.022033 | PMS1 postmeiotic segregation increased 1 (S. cerevisiae) (PMS1), mRNA /cds=(81,2879) /gb=NM_000534 /gi=11496979 /ug=Hs.111749 /len=3121 | NM_000534 | Hs.111749 | NP_000525 |
| 2273 | 0.030485 | Pirin (PIR), mRNA /cds=(231,1103) /gb=NM_003662 /gi=4505822 /ug=Hs.424966 /len=1318 | NM_003662 | Hs.424966 | NP_003653 |
| 2278 | 0.022033 | latent transforming growth factor beta binding protein 1 (LTBP1), mRNA /cds=(91,4275) /gb=NM_000627 /gi=4557730 /ug=Hs.241257 /len=5075 | NM_000627 | Hs.241257 | NP_000618 |
| 2339 | 0.035601 | chemokine (C-C motif) receptor 5 (CCR5), mRNA /cds=(358,1416) /gb=NM_000579 /gi=4502638 /ug=Hs.54443 /len=3655 | NM_000579 | Hs.54443 | NP_000570 |
| 2399 | 0.04789 | mitochondrion, complete genome | NC_001807 | | |
| 2473 | 0.030485 | Pseudoautosomal GTP-binding protein-like (PGPL), mRNA /cds=(330,1541) /gb=NM_012227 /gi=6912587 /ug=Hs.372587 /len=1867 | NM_012227 | Hs.372587 | NP_036359 |
| 2499 | 0.04789 | dynein, cytoplasmic, light intermediate polypeptide 1 (DNCL1), mRNA /cds=(81,1652) /gb=NM_016141 /gi=7705852 /ug=Hs.266483 /len=2487 | NM_016141 | Hs.266483 | NP_057225 |
| 2507 | 0.025981 | cDNA FLJ13552 fis, clone PLACE1007218. /gb=AK023614 /gi=10435594 /ug=Hs.204945 /len=1850 | AK023614 | Hs.204945 | |
| 2550 | 0.004826 | uncharacterized bone marrow protein BM042 (BM042) (=cDNA sequence DKFZp761A1124) | NM_018458 | | |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|------|----------|---|--------------------|-----------------------|-----------------------|
| 2557 | 0.01859 | leucine-rich PPR-motif containing (LRPPRC), mRNA /cds=(46,3867) /gb=NM_133259 /gi=18959201 /ug=Hs.182490 /len=4782 | NM_133259 | Hs.182490 | NP_573566 |
| 2617 | 0.035601 | collagen, type I, alpha 1 (COL1A1), mRNA /cds=(120,4514) /gb=NM_000088 /gi=14719826 /ug=Hs.172928 /len=5921 | NM_000088 | Hs.172928 | NP_000079 |
| 2680 | 0.04789 | SEC63, endoplasmic reticulum translocon component (S. cerevisiae (SEC63L), mRNA /cds=(133,2415) /gb=NM_007214 /gi=14591934 /ug=Hs.31575 /len=3368 | NM_007214 | Hs.31575 | NP_009145 |
| 2698 | 0.005961 | topoisomerase (DNA) II alpha 170kDa (TOP2A), mRNA /cds=(127,4722) /gb=NM_001067 /gi=19913405 /ug=Hs.156346 /len=5698 | NM_001067 | Hs.156346 | NP_001058 |
| 2799 | 0.015602 | glia maturation factor, beta (GMFB), mRNA /cds=(98,526) /gb=NM_004124 /gi=4758441 /ug=Hs.151413 /len=4131 | NM_004124 | Hs.151413 | NP_004115 |
| 2829 | 0.022033 | mitochondrion, complete genome | NC_001807 | | |
| 2865 | 0.030485 | nudix (nucleoside diphosphate linked moiety X)-type motif 4 (NUDT4), mRNA /cds=(191,736) /gb=NM_019094 /gi=24432097 /ug=Hs.355399 /len=3652 | NM_019094 | Hs.355399 | NP_061967 |
| 2866 | 0.00388 | translation initiation factor IF2 (IF2), mRNA /cds=(142,3804) /gb=NM_015904 /gi=15451891 /ug=Hs.158688 /len=4170 | NM_015904 | Hs.158688 | NP_056988 |
| 2940 | 0.01859 | hypothetical protein FLJ20421 (FLJ20421), mRNA /cds=(284,1363) /gb=NM_017813 /gi=8923391 /ug=Hs.378857 /len=1668 | NM_017813 | Hs.378857 | NP_060283 |
| 3005 | 0.013024 | likely ortholog of mouse Paneth cell enhanced expression (HCLA-ISO), mRNA /cds=(1152,2198) /gb=NM_030937 /gi=24475708 /ug=Hs.143601 /len=2943 | NM_030937 | Hs.143601 | NP_112199 |
| 3015 | 0.022033 | mitochondrion, complete genome | NC_001807 | | |
| 3050 | 0.035601 | DnaJ (Hsp40) subfamily B, member 9 (DNAJB9), mRNA /cds=(203,874) /gb=NM_012328 /gi=9558754 /ug=Hs.6790 /len=2371 | NM_012328 | Hs.6790 | NP_036460 |
| 3051 | 0.030485 | clone MGC:45564 IMAGE:4384472, mRNA, complete cds /cds=(188,1123) /gb=BC036746 /gi=22477830 /ug=Hs.132230 /len=3767 | BC036746 | Hs.132230 | |
| 3056 | 0.041383 | biglycan (BGN), mRNA /cds=(145,1251) /gb=NM_001711 /gi=19718760 /ug=Hs.821 /len=2367 | NM_001711 | Hs.821 | NP_001702 |
| 3088 | 0.01859 | sulfotransferase family, cytosolic, 1C, member 2 (SULT1C2), mRNA /cds=(330,1238) /gb=NM_006588 /gi=5730070 /ug=Hs.312644 /len=2143 | NM_006588 | Hs.312644 | NP_006579 |

| Spot | p-value | D scription | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|------|----------|---|--------------------|-----------------------|-----------------------|
| 3143 | 0.01081 | hypothetical protein FLJ20671 (FLJ20671), mRNA /cds=(43,465) /gb=NM_017924 /gi=19923511 /ug=Hs.180201 /len=2855 | NM_017924 | Hs.180201 | NP_060394 |
| 3173 | 0.035601 | hypothetical protein FLJ11730 (FLJ11730), mRNA /cds=(33,608) /gb=NM_022756 /gi=20149668 /ug=Hs.17118 /len=1558 | NM_022756 | Hs.17118 | NP_073593 |
| 3181 | 0.022033 | protein phosphatase 2A, regulatory subunit B' (PR 53) (PPP2R4), mRNA /cds=(190,1161) /gb=NM_021131 /gi=10880986 /ug=Hs.400740 /len=2661 | NM_021131 | Hs.400740 | NP_821070 |
| 3187 | 0.04789 | clone IMAGE:5229459, mRNA /gb=BC044229 /gi=28277403 /ug=Hs.266263 /len=2044 | BC044229 | Hs.266263 | |
| 3208 | 0.041383 | Sry-related HMG-box protein (SOX18) mRNA, complete cds | AF270652 | | NP_060889 |
| 3243 | 0.022033 | FK506 binding protein 11, 19 kDa (FKBP11), mRNA /cds=(73,678) /gb=NM_016594 /gi=7706130 /ug=Hs.24048 /len=727 | NM_016594 | Hs.24048 | NP_057678 |
| 3247 | 0.04789 | 602410168F1 NIH_MGC_92 cDNA clone IMAGE:4538560 5', mRNA sequence /clone=IMAGE:4538560 /clone_end=5' /gb=BG394022 /gi=13287470 /ug=Hs.421597 /len=1059 | BG394022 | Hs.421597 | |
| 3264 | 0.025981 | TEA domain family member 4 (TEAD4), mRNA /cds=(164,1468) /gb=NM_003213 /gi=4507426 /ug=Hs.94865 /len=1670 | NM_003213 | Hs.94865 | NP_003204 |
| 3265 | 0.04789 | hypothetical protein similar to actin related protein 2/3 complex, subunit 5 (MGC3038), mRNA /cds=(87,548) /gb=NM_030978 /gi=13569955 /ug=Hs.315164 /len=1041 | NM_030978 | Hs.315164 | NP_112240 |
| 3273 | 0.013024 | golgi reassembly stacking protein 2, 55kDa (GORASP2), mRNA /cds=(52,1524) /gb=NM_015530 /gi=20127538 /ug=Hs.6880 /len=2424 | NM_015530 | Hs.6880 | NP_056345 |
| 3288 | 0.041383 | cyclin G2 (CCNG2), mRNA /cds=(136,1170) /gb=NM_004354 /gi=4757935 /ug=Hs.79069 /len=2044 | NM_004354 | Hs.79069 | NP_004345 |
| 3335 | 0.041383 | signal sequence receptor, gamma (translocon-associated protein gamma) (SSR3), mRNA /cds=(57,614) /gb=NM_007107 /gi=6005883 /ug=Hs.28707 /len=3061 | NM_007107 | Hs.28707 | NP_009038 |
| 3361 | 0.025981 | integrin, beta 8 (ITGB8), mRNA /cds=(681,2990) /gb=NM_002214 /gi=4504778 /ug=Hs.355722 /len=3789 | NM_002214 | Hs.355722 | NP_002205 |
| 3371 | 0.022033 | KIAA0372 gene product (KIAA0372), mRNA /cds=(298,4992) /gb=NM_014639 /gi=7662077 /ug=Hs.170098 /len=5704 | NM_014639 | Hs.170098 | NP_055454 |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|------|----------|--|--------------------------|-----------------------------|-----------------------------|
| 3456 | 0.041383 | ionized calcium binding adapter molecule 2 (IBA2), mRNA /cds=(89,541) /gb=NM_031426 /gi=13899240 /ug=Hs.4944 /len=3381 | NM_031426 | Hs.4944 | NP_113614 |
| 3492 | 0.013024 | UI-H-BI2-ags-a-03-0-UI.s1 NCI_CGAP_Sub4 cDNA clone IMAGE:2725156 3', mRNA sequence /clone=IMAGE:2725156 /clone_end=3' /gb=AW292521 /gi=6699157 /ug=Hs.227074 /len=685 | AW292521 | Hs.227074 | |
| 3518 | 0.04789 | hypothetical protein FLJ23548 (FLJ23548), mRNA /cds=(204,713) /gb=NM_024590 /gi=13375780 /ug=Hs.22895 /len=1871 | NM_024590 | Hs.22895 | NP_078866 |
| 3555 | 0.04789 | cartilage oligomeric matrix protein (pseudoachondroplasia, epiphyseal dysplasia 1, multiple) (COMP), mRNA /cds=(26,2299) /gb=NM_000095 /gi=4557482 /ug=Hs.1584 /len=2439 | NM_000095 | Hs.1584 | NP_000086 |
| 3592 | 0.041383 | solute carrier family 30 (zinc transporter), member 5 (SLC30A5), mRNA /cds=(202,2499) /gb=NM_022902 /gi=20070322 /ug=Hs.129445 /len=2952 | NM_022902 | Hs.129445 | NP_076960 |
| 3644 | 0.025981 | hypothetical protein FLJ20343 (FLJ20343), mRNA /cds=(19,1524) /gb=NM_017775 /gi=22547158 /ug=Hs.252692 /len=2784 | NM_017775 | Hs.252692 | NP_060245 |
| 3657 | 0.005961 | oxysterol binding protein-like 5 (OSBPL5), transcript variant 1, mRNA /cds=(117,2756) /gb=NM_020896 /gi=22035607 /ug=Hs.112034 /len=3873 | NM_020896 | Hs.112034 | NP_663613 |
| 3702 | 0.035601 | ferritin, heavy polypeptide 1 (FTH1), mRNA /cds=(92,664) /gb=NM_002032 /gi=4503794 /ug=Hs.418650 /len=801 | NM_002032 | Hs.418650 | NP_002023 |
| 3719 | 0.015602 | putative ribonuclease III (RNASE3L), mRNA /cds=(246,4370) /gb=NM_013235 /gi=21359821 /ug=Hs.49163 /len=4764 | NM_013235 | Hs.49163 | NP_037367 |
| 3804 | 0.041383 | thymidine kinase 1, soluble (TK1), mRNA /cds=(58,762) /gb=NM_003258 /gi=4507518 /ug=Hs.105097 /len=1421 | NM_003258 | Hs.105097 | NP_003249 |
| 3861 | 0.00388 | basigin (BSG), mRNA /cds=(58,867) /gb=NM_001728 /gi=4502458 /ug=Hs.74631 /len=1638 | NM_001728 | Hs.74631 | NP_001719 |
| 3911 | 0.015602 | mitochondrion, complete genome | NC_001807 | | |
| 3979 | 0.001929 | TGFB inducible early growth response (TIEG), mRNA /cds=(124,1566) /gb=NM_005655 /gi=5032176 /ug=Hs.82173 /len=2899 | NM_005655 | Hs.82173 | NP_005646 |
| 4004 | 0.022033 | bromodomain containing 2 (BRD2), mRNA /cds=(1702,4107) /gb=NM_005104 /gi=12408641 /ug=Hs.75243 /len=4693 | NM_005104 | Hs.75243 | NP_005095 |

| Spot | p-value | Description | Gene Accession No. | Unigene Acc ssion No. | Protein Accession No. |
|------|----------|---|--------------------|-----------------------|-----------------------|
| 4020 | 0.022033 | CASP8 associated protein 2 (CASP8AP2), mRNA /cds=(197,6145) /gb=NM_012115 /gi=16306505 /ug=Hs.122843 /len=6782 | NM_012115 | Hs.122843 | NP_036247 |
| 4054 | 0.022033 | histamine N-methyltransferase (HNMT), mRNA /cds=(253,1131) /gb=NM_006895 /gi=5901969 /ug=Hs.81182 /len=1667 | NM_006895 | Hs.81182 | NP_008826 |
| 4064 | 0.035601 | ubiquitin-like 5 (UBL5), mRNA /cds=(66,287) /gb=NM_024292 /gi=13236509 /ug=Hs.13836 /len=413 | NM_024292 | Hs.13836 | NP_077268 |
| 4100 | 0.04789 | splicing factor 30, survival of motor neuron-related (SPF30), mRNA /cds=(193,909) /gb=NM_005871 /gi=21361283 /ug=Hs.79968 /len=2033 | NM_005871 | Hs.79968 | NP_005862 |
| 4114 | 0.04789 | cullin 2 (CUL2) | AF126404 | | NP_003582 |
| 4119 | 0.041383 | reverse transcriptase homolog - human retrotransposon L1 | I38588 | | |
| 4121 | 0.022033 | natural killer cell enhancing factor (NKEFA) | L19184 | | NP_002565 |
| 4125 | 0.008919 | for protein disulfide isomerase-related (PDIR), mRNA /cds=(57,1616) /gb=NM_006810 /gi=5803120 /ug=Hs.76901 /len=1693 | NM_006810 | Hs.76901 | NP_006801 |
| 4138 | 0.008919 | mRNA; cDNA DKFZp451M092 (from clone DKFZp451M092) /gb=AL713650 /gi=19584326 /ug=Hs.336425 /len=3645 | AL713650 | Hs.336425 | |
| 4219 | 0.030485 | ATP citrate lyase (ACLY), mRNA /cds=(85,3402) /gb=NM_001096 /gi=4501864 /ug=Hs.174140 /len=4297 | NM_001096 | Hs.174140 | NP_001087 |
| 4225 | 0.007315 | Parkinson disease (autosomal recessive, early onset) 7 (PARK7), mRNA /cds=(21,590) /gb=NM_007262 /gi=6005748 /ug=Hs.10958 /len=842 | NM_007262 | Hs.10958 | NP_009193 |
| 4238 | 0.04789 | cytokine SDF-1-beta (=L36033) | U16752 | | NP_000600 |
| 4271 | 0.01859 | ras gene family, member E (ARHE), mRNA /cds=(141,875) /gb=NM_005168 /gi=21361257 /ug=Hs.6838 /len=2685 | NM_005168 | Hs.6838 | NP_005159 |
| 4340 | 0.04789 | heat shock 90kDa protein 1, beta (HSPCB), mRNA /cds=(85,2259) /gb=NM_007355 /gi=20149593 /ug=Hs.74335 /len=2567 | NM_007355 | Hs.74335 | NP_031381 |
| 4390 | 0.013024 | ataxia telangiectasia and Rad3 related (ATR), mRNA /cds=(106,8040) /gb=NM_001184 /gi=20143978 /ug=Hs.77613 /len=8265 | NM_001184 | Hs.77613 | NP_001175 |
| 4402 | 0.01081 | putative homeodomain transcription factor 1 (PHTF1), mRNA /cds=(32,2320) /gb=NM_006608 /gi=5729975 /ug=Hs.123637 /len=2806 | NM_006608 | Hs.123637 | NP_006599 |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|------|----------|--|--------------------|-----------------------|-----------------------|
| 4421 | 0.041383 | sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), mRNA /cds=(46,2430) /gb=NM_005065 /gi=19923668 /ug=Hs.181300 /len=7885 | NM_005065 | Hs.181300 | NP_005056 |
| 4432 | 0.01081 | dentin matrix acidic | NM_004407 | | NP_004398 |
| 4438 | 0.022033 | trypsin-like serine protease (TLSP) gene | AF164623 | | |
| 4506 | 0.041383 | chronic myelogenous leukemia tumor antigen 66 (CML66), mRNA /cds=(233,1984) /gb=NM_032869 /gi=23618845 /ug=Hs.195870 /len=2288 | NM_032869 | Hs.195870 | NP_116258 |
| 4518 | 0.00388 | leptin receptor (ORF) | U66496 | | NP_002294 |
| 4520 | 0.01859 | centrosome-associated protein 350 (CAP350), mRNA /cds=(168,9521) /gb=NM_014810 /gi=18378734 /ug=Hs.92200 /len=11740 | NM_014810 | Hs.92200 | NP_055625 |
| 4531 | 0.04789 | erythrocyte membrane protein band 4.1-like 2 (EPB41L2), mRNA /cds=(45,3062) /gb=NM_001431 /gi=4503578 /ug=Hs.7857 /len=4336 | NM_001431 | Hs.7857 | NP_001422 |
| 4608 | 0.030485 | MacGAP protein (MacGAP), mRNA /cds=(23,1879) /gb=NM_033515 /gi=15723375 /ug=Hs.178705 /len=3305 | NM_033515 | Hs.178705 | NP_277050 |
| 4614 | 0.01859 | sperm antigen-36 | AF187554 | | |
| 4619 | 0.04789 | IMP (inosine monophosphate) dehydrogenase 2 (IMPDH2), mRNA /cds=(48,1592) /gb=NM_000884 /gi=4504688 /ug=Hs.75432 /len=1654 | NM_000884 | Hs.75432 | NP_000875 |
| 4641 | 0.015602 | major histocompatibility complex, class II, DR beta 1 (HLA-DRB1), mRNA /cds=(63,863) /gb=NM_002124 /gi=4504410 /ug=Hs.375570 /len=1182 | NM_002124 | Hs.375570 | NP_002115 |
| 4678 | 0.041383 | hydroxysteroid (17-beta) dehydrogenase 4 (HSD17B4), mRNA /cds=(49,2259) /gb=NM_000414 /gi=4504504 /ug=Hs.75441 /len=2593 | NM_000414 | Hs.75441 | NP_000405 |
| 4710 | 0.008919 | vinculin (VCL), transcript variant meta-VCL, mRNA /cds=(86,3490) /gb=NM_014000 /gi=7669549 /ug=Hs.75350 /len=5341 | NM_014000 | Hs.75350 | NP_054706 |
| 4738 | 0.015602 | hypothetical protein (KIAA1439) | AB037860 | | NP_005586 |
| 4746 | 0.035601 | snail 2 (Drosophila) (SNAI2), mRNA /cds=(165,971) /gb=NM_003068 /gi=24497625 /ug=Hs.93005 /len=2101 | NM_003068 | Hs.93005 | NP_003059 |
| 4823 | 0.01859 | SH3-domain GRB2-like endophilin B2 (SH3GLB2), mRNA /cds=(147,1334) /gb=NM_020145 /gi=24431995 /ug=Hs.30002 /len=2039 | NM_020145 | Hs.30002 | NP_064530 |
| 4834 | 0.022033 | mitochondrion, complete genome | NC_001807 | | |

| Spot | p-value | D scription | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|------|----------|--|--------------------|-----------------------|-----------------------|
| 4848 | 0.041383 | aggrecan 1 (chondroitin sulfate proteoglycan 1, large aggregating proteoglycan, antigen identified by monoclonal antibody A0122) (AGC1), transcript variant 2, mRNA /cds=(61,7308) /gb=NM_013227 /gi=6995993 /ug=Hs.2159 /len=7434 | NM_013227 | Hs.2159 | NP_037359 |
| 4853 | 0.025981 | clone 24571 mRNA sequence /gb=AF070564 /gi=3387932 /ug=Hs.421200 /len=1487 | AF070564 | Hs.421200 | |
| 4885 | 0.004826 | clone alpha_est218/52C1 mRNA sequence /gb=AF001542 /gi=2529714 /ug=Hs.356442 /len=2992 | AF001542 | Hs.356442 | |
| 4887 | 0.035601 | mRNA; cDNA DKFZp434N079 (from clone DKFZp434N079) /gb=AL133591 /gi=6599179 /ug=Hs.141480 /len=1965 | AL133591 | Hs.141480 | |
| 4916 | 0.025981 | collagen, type X, alpha 1(Schmid metaphyseal chondrodysplasia) (COL10A1), mRNA /cds=(97,2139) /gb=NM_000493 /gi=18105031 /ug=Hs.179729 /len=3285 | NM_000493 | Hs.179729 | NP_000484 |
| 4922 | 0.015602 | topoisomerase (DNA) II beta 180kDa (TOP2B), mRNA /cds=(1,4866) /gb=NM_001068 /gi=19913407 /ug=Hs.75248 /len=5189 | NM_001068 | Hs.75248 | NP_001059 |
| 4928 | 0.01859 | mitochondrion, complete genome | NC_001807 | | |
| 4963 | 0.01081 | cytochrome c oxidase subunit VIIa polypeptide 2 (liver) (COX7A2), nuclear gene encoding mitochondrial protein, mRNA /cds=(76,327) /gb=NM_001865 /gi=18105035 /ug=Hs.70312 /len=470 | NM_001865 | Hs.70312 | NP_001856 |
| 5001 | 0.041383 | mRNA; cDNA DKFZp564F053 (from clone DKFZp564F053) /gb=AL049265 /gi=4500013 /ug=Hs.71968 /len=2864 | AL049265 | Hs.71968 | |
| 5071 | 0.003097 | cDNA FLJ10004 fis, clone HEMBA1000076. /gb=AK000866 /gi=7021190 /ug=Hs.411490 /len=1974 | AK000866 | Hs.411490 | |
| 5079 | 1.45E-04 | APR-1 protein (MAGEH1), mRNA /cds=(271,930) /gb=NM_014061 /gi=18105051 /ug=Hs.279819 /len=1475 | NM_014061 | Hs.279819 | NP_054780 |
| 5138 | 0.035601 | exostoses (multiple) 2 (EXT2), mRNA /cds=(488,2644) /gb=NM_000401 /gi=4557572 /ug=Hs.75334 /len=3781 | NM_000401 | Hs.75334 | NP_000392 |
| 5150 | 0.013024 | HSPC039 protein mRNA, complete cds /cds=(81,329) /gb=AF125100 /gi=5106995 /ug=Hs.406542 /len=1583 | AF125100 | Hs.406542 | NP_057181 |
| 5222 | 0.041383 | Saccharomyces cerevisiae chromosome XII, complete chromosome sequence | NC_001144 | | |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|------|----------|--|--------------------|-----------------------|-----------------------|
| 5225 | 0.04789 | platelet-derived growth factor receptor, beta polypeptide (PDGFRB), mRNA /cds=(357,3677) /gb=NM_002609 /gi=15451788 /ug=Hs.76144 /len=5598 | NM_002609 | Hs.76144 | NP_002600 |
| 5235 | 0.030485 | major histocompatibility complex, class II, DR beta 1 (HLA-DRB1), mRNA /cds=(63,863) /gb=NM_002124 /gi=4504410 /ug=Hs.375570 /len=1182 | NM_002124 | Hs.375570 | NP_002115 |
| 5258 | 0.004826 | testis derived transcript (3 LIM domains) (TES), transcript variant 1, mRNA /cds=(182,1447) /gb=NM_015641 /gi=23238186 /ug=Hs.165986 /len=2766 | NM_015641 | Hs.165986 | NP_690042 |
| 5290 | 0.04789 | hypothetical protein FLJ20719 (FLJ20719), mRNA /cds=(402,2213) /gb=NM_017940 /gi=24308174 /ug=Hs.446473 /len=3745 | NM_017940 | Hs.446473 | NP_060410 |
| 5294 | 0.035601 | KIAA0063 gene product (KIAA0063), mRNA /cds=(280,888) /gb=NM_014876 /gi=7661887 /ug=Hs.3094 /len=3168 | NM_014876 | Hs.3094 | NP_055691 |
| 5301 | 0.035601 | X-box binding protein 1 (XBP1), mRNA /cds=(49,834) /gb=NM_005080 /gi=14110394 /ug=Hs.149923 /len=1836 | NM_005080 | Hs.149923 | NP_005071 |
| 5332 | 0.041383 | clone IMAGE:5262128, mRNA, partial cds /cds=(1,1409) /gb=BC035036 /gi=23271542 /ug=Hs.356247 /len=4728 | BC035036 | Hs.356247 | |
| 5363 | 0.030485 | MAD, mothers against decapentaplegic (Drosophila) interacting protein, receptor activation anchor (MADHIP), transcript variant 3, mRNA /cds=(439,4410) /gb=NM_004799 /gi=4759059 /ug=Hs.194716 /len=4839 | NM_004799 | Hs.194716 | NP_015563 |
| 5402 | 0.025981 | brain cDNA, clone:QnpA-21421 | AB050422 | | |
| 5431 | 0.013024 | thymine-DNA glycosylase (TDG), mRNA /cds=(400,1632) /gb=NM_003211 /gi=4507422 /ug=Hs.173824 /len=3410 | NM_003211 | Hs.173824 | NP_003202 |
| 5432 | 0.022033 | zinc finger protein 202 (ZNF202), mRNA /cds=(11,1957) /gb=NM_003455 /gi=10835040 /ug=Hs.9443 /len=4053 | NM_003455 | Hs.9443 | NP_003446 |
| 5434 | 0.015602 | ATP synthase, H transporting, mitochondrial F0 complex, subunit b, isoform 1 (ATP5F1), mRNA /cds=(98,868) /gb=NM_001688 /gi=21361564 /ug=Hs.81634 /len=1230 | NM_001688 | Hs.81634 | NP_001679 |
| 5438 | 0.035601 | mitochondrion, complete genome | NC_001807 | | |
| 5439 | 0.030485 | hypothetical protein MGC4276 similar to CG8198 (MGC4276), mRNA /cds=(70,462) /gb=NM_030940 /gi=24475709 /ug=Hs.177776 /len=1978 | NM_030940 | Hs.177776 | NP_112202 |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|------|----------|--|--------------------|-----------------------|-----------------------|
| 5468 | 0.030485 | Deleted in split-hand/split-foot 1 region (DSS1), mRNA /cds=(129,341) /gb=NM_006304 /gi=5453639 /ug=Hs.333495 /len=509 | NM_006304 | Hs.333495 | NP_006295 |
| 5628 | 0.030485 | v-fos FBJ murine osteosarcoma viral oncogene (FOS), mRNA /cds=(156,1298) /gb=NM_005252 /gi=6552332 /ug=Hs.25647 /len=2084 | NM_005252 | Hs.25647 | NP_005243 |
| 5639 | 0.022033 | mitogen-activated protein kinase 7 (MAPK7), transcript variant 1, mRNA /cds=(355,2805) /gb=NM_139033 /gi=20986500 /ug=Hs.3080 /len=3113 | NM_139033 | Hs.3080 | NP_620603 |
| 5676 | 0.035601 | discs, large 7 (Drosophila) (DLG7), mRNA /cds=(218,2758) /gb=NM_014750 /gi=21361644 /ug=Hs.77695 /len=2979 | NM_014750 | Hs.77695 | NP_055565 |
| 5701 | 0.041383 | mitochondrion, complete genome | NC_001807 | | |
| 5743 | 0.022033 | heme-regulated initiation factor 2-alpha kinase (HRI), mRNA /cds=(63,1955) /gb=NM_014413 /gi=11125767 /ug=Hs.258730 /len=2813 | NM_014413 | Hs.258730 | NP_055228 |
| 5745 | 0.035601 | clone IMAGE:5299888, mRNA /gb=BC039397 /gi=24659826 /ug=Hs.112237 /len=1338 | BC039397 | Hs.112237 | |
| 5749 | 0.030485 | up-regulated gene 4 (URG4), mRNA /cds=(14,2782) /gb=NM_017920 /gi=19923541 /ug=Hs.5131 /len=3606 | NM_017920 | Hs.5131 | NP_060390 |
| 5769 | 0.025981 | cDNA: FLJ21561 fis, clone COL06415. /gb=AK025214 /gi=10437681 /ug=Hs.96918 /len=1641 | AK025214 | Hs.96918 | |
| 5783 | 0.04789 | ATPase inhibitory factor 1 (ATPIF1), mRNA /cds=(52,372) /gb=NM_016311 /gi=20149627 /ug=Hs.241336 /len=515 | NM_016311 | Hs.241336 | NP_835498 |
| 5889 | 0.041383 | mRNA for KIAA0640 protein, partial cds. /cds=(1,1813) /gb=AB014540 /gi=3327093 /ug=Hs.153026 /len=4824 | AB014540 | Hs.153026 | NP_055870 |
| 5903 | 0.025981 | dinucleotide miCRosatellite HUJII77 | M96348 | | |
| 5920 | 0.025981 | mitochondrion, complete genome | NC_001807 | | |
| 5928 | 0.035601 | ubiquitin-conjugating enzyme E2B (RAD6 (UBE2B), mRNA /cds=(422,880) /gb=NM_003337 /gi=4507770 /ug=Hs.811 /len=2591 | NM_003337 | Hs.811 | NP_003328 |
| 5935 | 0.004826 | MR2-CI0186-291100-010-a06 CI0186 cDNA, mRNA sequence /gb=BF814502 /gi=12147047 /ug=Hs.446594 /len=530 | BF814502 | Hs.446594 | |
| 5939 | 0.035601 | BTAF1 RNA polymerase II, B-TFIID transcription factor-associated, 170kDa (Mot1 S. cerevisiae) (BTAF1), mRNA /cds=(118,5667) /gb=NM_003972 /gi=27477069 /ug=Hs.180930 /len=6345 | NM_003972 | Hs.180930 | NP_003963 |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|------|----------|---|--------------------|-----------------------|-----------------------|
| 5975 | 0.01859 | cell-line RPMI 8226 chloride ion current inducer protein I(Cln) gene, | AF232225 | | |
| 6035 | 0.013024 | BCL2 gene, exon 3 and breakpoint region | AF217803 | | |
| 6063 | 0.022033 | eukaryotic translation initiation factor 4A, isoform 2 (EIF4A2), mRNA /cds=(16,1239) /gb=NM_001967 /gi=9945313 /ug=Hs.173912 /len=1864 | NM_001967 | Hs.173912 | NP_001958 |
| 6065 | 0.022033 | NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2, 14.5kDa (NDUFC2), mRNA /cds=(151,510) /gb=NM_004549 /gi=19923255 /ug=Hs.193313 /len=2168 | NM_004549 | Hs.193313 | NP_004540 |
| 6068 | 0.035601 | mitochondrial ribosomal protein L27 (MRPL27), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA /cds=(32,316) /gb=NM_148571 /gi=22547130 /ug=Hs.7736 /len=2472 | NM_148571 | Hs.7736 | NP_683412 |
| 6091 | 0.041383 | cDNA FLJ35150 fis, clone PLACE6010568, moderately similar to mRNA for TU12B1-TY. /gb=AK092469 /gi=21751073 /ug=Hs.425567 /len=1714 | AK092469 | Hs.425567 | |
| 6097 | 0.004826 | tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide (YWHAG), mRNA /cds=(192,935) /gb=NM_012479 /gi=21464100 /ug=Hs.25001 /len=3747 | NM_012479 | Hs.25001 | NP_036611 |
| 6148 | 0.00388 | zinc finger RNA binding protein (ZFR), mRNA /cds=(44,1300) /gb=NM_016107 /gi=7706372 /ug=Hs.173518 /len=2734 | NM_016107 | Hs.173518 | NP_057191 |
| 6238 | 0.022033 | tb97a11.x1 NCI_CGAP_Co16 cDNA clone IMAGE:2062268 3' similar to contains Alu repetitive element; mRNA sequence /clone=IMAGE:2062268 /clone_end=3' /gb=AI343476 /gi=4080682 /ug=Hs.183850 /len=515 | AI343476 | Hs.183850 | |
| 6239 | 0.008919 | Similar to RD RNA-binding protein, clone MGC:2263 IMAGE:3050953, mRNA, complete cds /cds=(34,1035) /gb=BC011600 /gi=15079543 /ug=Hs.356818 /len=2478 | BC011600 | Hs.356818 | |
| 6251 | 0.035601 | interferon-related developmental regulator 1 (IFRD1), mRNA /cds=(220,1581) /gb=NM_001550 /gi=4504606 /ug=Hs.7879 /len=1791 | NM_001550 | Hs.7879 | NP_001541 |
| 6266 | 0.038534 | cosmid LL12NCO1-67C6, ETV6 gene, intron 1A, partial sequence | U81831 | | |

| Spot | p-value | Description | Gen Accession No. | Unigene Accession No. | Protein Accession No. |
|------|----------|--|-------------------------|-----------------------------|-----------------------------|
| 6302 | 0.044987 | diphtheria toxin receptor (heparin-binding epidermal growth factor-like growth factor) (DTR), mRNA /cds=(262,888) /gb=NM_001945 /gi=4503412 /ug=Hs.799 /len=2360 | NM_001945 | Hs.799 | NP_001936 |
| 6347 | 0.007315 | mitochondrion, complete genome | NC_001807 | | |
| 6348 | 0.041383 | major histocompatibility complex, class I, F (HLA-F), mRNA /cds=(1,1089) /gb=NM_018950 /gi=9665231 /ug=Hs.110309 /len=1188 | NM_018950 | Hs.110309 | NP_061823 |
| 6407 | 0.013024 | hypothetical protein LOC51244 (LOC51244), mRNA /cds=(340,1233) /gb=NM_016474 /gi=24475969 /ug=Hs.158006 /len=1614 | NM_016474 | Hs.158006 | NP_057558 |
| 6451 | 0.035601 | mRNA; cDNA DKFZp586C1723 (from clone DKFZp586C1723) /gb=AL050192 /gi=4884408 /ug=Hs.80285 /len=1797 | AL050192 | Hs.80285 | |
| 6487 | 0.035601 | tumor protein D52 (TPD52), mRNA /cds=(92,646) /gb=NM_005079 /gi=4827037 /ug=Hs.2384 /len=3247 | NM_005079 | Hs.2384 | NP_005070 |
| 6522 | 0.035601 | Rattus norvegicus mitochondrial genome | NC_001665 | | |
| 6590 | 0.035601 | mRNA for KIAA0981 protein, partial cds. /cds=(1,1738) /gb=AB023198 /gi=4589605 /ug=Hs.158135 /len=5182 | AB023198 | Hs.158135 | |
| 6595 | 0.04789 | H factor 1 (complement) (HF1), mRNA /cds=(74,3769) /gb=NM_000186 /gi=4504374 /ug=Hs.250651 /len=3926 | NM_000186 | Hs.250651 | NP_000177 |
| 6598 | 0.030485 | phosphomannomutase 2 (PMM2) gene (5e-10 match) | AF157794 | | |
| 6616 | 0.025981 | LPS-induced TNF-alpha factor (PIG7), mRNA /cds=(234,920) /gb=NM_004862 /gi=4758913 /ug=Hs.76507 /len=1773 | NM_004862 | Hs.76507 | NP_004853 |
| 6619 | 0.025981 | phosphodiesterase 1A, calmodulin-dependent (PDE1A) mRNA | NM_005019 | | NP_005010 |
| 6657 | 0.035601 | serine hydroxymethyltransferase 2 (mitochondrial) (SHMT2), mRNA /cds=(20,1534) /gb=NM_005412 /gi=24942125 /ug=Hs.75069 /len=2122 | NM_005412 | Hs.75069 | NP_005403 |
| 6738 | 0.035601 | ankyrin repeat and SOCS box-containing 3 (ASB3), transcript variant 1, mRNA /cds=(136,1692) /gb=NM_016115 /gi=22208952 /ug=Hs.9893 /len=2214 | NM_016115 | Hs.9893 | NP_665862 |
| 6758 | 0.041383 | proteasome (prosome, macropain) 26S subunit, ATPase, 2 (PSMC2), mRNA /cds=(71,1372) /gb=NM_002803 /gi=24430152 /ug=Hs.61153 /len=1545 | NM_002803 | Hs.61153 | NP_002794 |
| 6837 | 0.022033 | cDNA FLJ39699 fis, clone SMINT2011567, weakly similar to mRNA for ALEX1. /gb=AK097018 /gi=21756651 /ug=Hs.83530 /len=2257 | AK097018 | Hs.83530 | NP_061880 |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|------|----------|---|--------------------|-----------------------|-----------------------|
| 6860 | 0.041383 | cDNA: FLJ21440 fis, clone COL04389. /gb=AK025093 /gi=10437540 /ug=Hs.218008 /len=1810 | AK025093 | Hs.218008 | |
| 6865 | 0.007315 | NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa (NDUFA4), mRNA /cds=(91,336) /gb=NM_002489 /gi=4505356 /ug=Hs.50098 /len=518 | NM_002489 | Hs.50098 | NP_002480 |
| 6866 | 0.035601 | E1A binding protein p300 (EP300), mRNA /cds=(1200,8444) /gb=NM_001429 /gi=4557556 /ug=Hs.25272 /len=9046 | NM_001429 | Hs.25272 | NP_001420 |
| 6970 | 0.030485 | neuroblastoma apoptosis-related RNA-binding protein (CUGBP2) gene, exons 10, 11a, 11b, 12, 13a, 13b, 14, and complete cds, alternatively spliced | AF295068 | | |
| 6989 | 0.030485 | transmembrane 9 superfamily member 1 (TM9SF1), mRNA /cds=(35,1855) /gb=NM_006405 /gi=21361314 /ug=Hs.91586 /len=2138 | NM_006405 | Hs.91586 | NP_006396 |
| 6990 | 0.04789 | mRNA for KIAA1866 protein, partial cds. /cds=(1,2299) /gb=AB058769 /gi=14017948 /ug=Hs.334838 /len=4811 | AB058769 | Hs.334838 | |
| 7052 | 0.022033 | SUMO-1-specific protease (SUSP1), mRNA /cds=(1,3339) /gb=NM_015571 /gi=7662311 /ug=Hs.27197 /len=4210 | NM_015571 | Hs.27197 | NP_056386 |
| 7077 | 0.04789 | mitochondrion, complete genome | NC_001807 | | |
| 7087 | 0.01859 | mitochondrion, complete genome | NC_001807 | | |
| 7152 | 0.022033 | cellular retinoic acid binding protein 1 (CRABP1), mRNA /cds=(75,488) /gb=NM_004378 /gi=4758051 /ug=Hs.346950 /len=735 | NM_004378 | Hs.346950 | NP_004369 |
| 7162 | 0.041383 | protein-O-mannosyltransferase 1 (POMT1), mRNA /cds=(180,2423) /gb=NM_007171 /gi=21361381 /ug=Hs.99654 /len=3150 | NM_007171 | Hs.99654 | NP_009102 |
| 7204 | 0.041383 | chromosome 20 open reading frame 98 (C20orf98), mRNA /cds=(134,748) /gb=NM_024958 /gi=13376446 /ug=Hs.286128 /len=2042 | NM_024958 | Hs.286128 | NP_079234 |
| 7227 | 0.015602 | cytidine monophosphate kinase CMP mRNA, (=UMP-CMP kinase (LOC51727)) | AF259961 | | NP_057392 |
| 7234 | 0.04789 | chemokine-like factor 1 (CKLF1), mRNA /cds=(148,606) /gb=NM_016951 /gi=10092593 /ug=Hs.15159 /len=689 | NM_016951 | Hs.15159 | NP_058647 |
| 7235 | 0.022033 | SOCS box-containing WD protein SWiP-1 (WSB1), transcript variant 3, mRNA /cds=(317,1051) /gb=NM_134264 /gi=20143909 /ug=Hs.187991 /len=4243 | NM_134264 | Hs.187991 | NP_599027 |
| 7330 | 0.04789 | mitochondrion, complete genome | NC_001807 | | |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|------|----------|---|--------------------|-----------------------|-----------------------|
| 7331 | 0.01859 | AGENCOURT_8856629 Lupski_sciatic_nerve cDNA clone IMAGE:6200636 5', mRNA sequence /clone=IMAGE:6200636 /clone_end=5' /gb=BQ947179 /gi=22362657 /ug=Hs.356605 /len=1277 | BQ947179 | Hs.356605 | |
| 7381 | 0.025981 | NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1, 8kDa (NDUFAB1), mRNA /cds=(25,495) /gb=NM_005003 /gi=4826851 /ug=Hs.5556 /len=663 | NM_005003 | Hs.5556 | NP_004994 |
| 7406 | 0.01081 | hypothetical protein FLJ14511 (FLJ14511), mRNA /cds=(23,1273) /gb=NM_033087 /gi=14861835 /ug=Hs.40919 /len=1835 | NM_033087 | Hs.40919 | NP_149078 |
| 7433 | 0.035601 | KIAA1579 protein, partial cds /cds=UNKNOWN /gb=AB046799 /gi=10047232 /ug=Hs.49933 /len=4352 (=FLJ25300) | AB046799 | Hs.49933 | NP_060681 |
| 7462 | 0.04789 | TRAF family member-associated NFKB activator (TANK), transcript variant 1, mRNA /cds=(159,1436) /gb=NM_004180 /gi=19743568 /ug=Hs.146847 /len=2089 | NM_004180 | Hs.146847 | NP_597841 |
| 7532 | 0.035601 | a disintegrin and metalloproteinase domain 33 (ADAM33), transcript variant 1, mRNA /cds=(88,2529) /gb=NM_025220 /gi=24041037 /ug=Hs.173716 /len=3594 | NM_025220 | Hs.173716 | NP_694882 |
| 7564 | 0.035601 | paired basic amino acid cleaving system 4 (PACE4), transcript variant 1, mRNA /cds=(315,3224) /gb=NM_002570 /gi=20336178 /ug=Hs.170414 /len=4553 | NM_002570 | Hs.170414 | NP_612198 |
| 7578 | 0.035601 | hypothetical protein DKFZp586G0123 (DKFZp586G0123), mRNA /cds=(25,315) /gb=NM_013386 /gi=9558726 /ug=Hs.24713 /len=1294 | NM_013386 | Hs.24713 | NP_037518 |
| 7583 | 0.030485 | AGENCOURT_8929105 NIH_MGC_40 cDNA clone IMAGE:6484442 5', mRNA sequence /clone=IMAGE:6484442 /clone_end=5' /gb=BQ939558 /gi=22355036 /ug=Hs.405871 /len=1129 | BQ939558 | Hs.405871 | |
| 7611 | 0.041383 | RAB14, member RAS oncogene family (RAB14), mRNA /cds=(184,831) /gb=NM_016322 /gi=19923482 /ug=Hs.5807 /len=4106 | NM_016322 | Hs.5807 | NP_057406 |
| 7656 | 0.01081 | cDNA FLJ35517 fis, clone SPLEN2000698. /gb=AK092836 /gi=21751529 /ug=Hs.291804 /len=2536 | AK092836 | Hs.291804 | |

| Spot | p-value | Description | Gene Accession No. | Unigen Accession No. | Prot in Accession No. |
|------|----------|---|--------------------|----------------------|-----------------------|
| 7762 | 0.015602 | Similar to ubiquitin protein ligase E3A papilloma virus E6-associated protein, Angelman syndrome), clone IMAGE:4811444, mRNA /gb=BC040187 /gi=25455694 /ug=Hs.25320 /len=4823 | BC040187 | Hs.25320 | |
| 7763 | 0.015602 | chromosome 21 open reading frame 6 (C21orf6), mRNA /cds=(92,1051) /gb=NM_016940 /gi=8393017 /ug=Hs.34136 /len=1729 | NM_016940 | Hs.34136 | NP_058636 |
| 7877 | 0.030485 | myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax Drosophila) (MLL5), mRNA /cds=(202,5778) /gb=NM_018682 /gi=23503326 /ug=Hs.333300 /len=6543 | NM_018682 | Hs.333300 | NP_061152 |
| 7910 | 0.004826 | hypothetical protein MGC33365 (MGC33365), mRNA /cds=(268,1560) /gb=NM_173552 /gi=27734894 /ug=Hs.288954 /len=4096 | NM_173552 | Hs.288954 | NP_775823 |
| 7927 | 0.008919 | UI-H-EZ1-bca-n-05-0-UI.s1 NCI_CGAP_Ch2 cDNA clone UI-H-EZ1-bca-n-05-0-UI 3', mRNA sequence /clone=UI-H-EZ1-bca-n-05-0-UI /clone_end=3' /gb=BQ774356 /gi=21982825 /ug=Hs.43227 /len=1083 | BQ774356 | Hs.43227 | |
| 7953 | 0.04789 | UI-H-DP0-avb-i-09-0-UI.s1 NCI_CGAP_Fs1 cDNA clone IMAGE:5877200 3', mRNA sequence /clone=IMAGE:5877200 /clone_end=3' /gb=BQ020506 /gi=19755784 /ug=Hs.43546 /len=1168 | BQ020506 | Hs.43546 | |
| 8104 | 0.01859 | mRNA; cDNA DKFZp761C169 (from clone DKFZp761C169); partial cds /cds=(997,2475) /gb=AL161991 /gi=7328122 /ug=Hs.71252 /len=3324 | AL161991 | Hs.71252 | NP_075064 |
| 8136 | 0.035601 | 601661342R1 NIH_MGC_72 cDNA clone IMAGE:3915994 3', mRNA sequence /clone=IMAGE:3915994 /clone_end=3' /gb=BE966653 /gi=11772295 /ug=Hs.330958 /len=703 | BE966653 | Hs.330958 | |
| 8151 | 0.013024 | cDNA: FLJ23115 fis, clone LNG07933. /gb=AK026768 /gi=10439696 /ug=Hs.98728 /len=1917 | AK026768 | Hs.98728 | |
| 8269 | 0.035601 | clone IMAGE:5243705, mRNA /gb=BC043383 /gi=27695948 /ug=Hs.439631 /len=2177 | BC043383 | Hs.439631 | |
| 8278 | 0.030485 | EST(wf82e10.x1 Soares_NFL_T_GBC_S1 clone IMAGE:2362122 3') | AI873423 | | |
| 8308 | 0.035601 | EST(ty24e09.x1 NCI_CGAP_Ut3 clone IMAGE:2280040 3' contains Alu repeat) | AI758800 | | |

| Spot | p-value | Description | Gene Accession No. | Unigen Accession No. | Protein Accession No. |
|------|----------|---|--------------------|----------------------|-----------------------|
| 8310 | 0.002454 | phosphatidylinositol-3 phosphate 3-phosphatase adaptor subunit (3PAP), mRNA /cds=(132,2375) /gb=NM_019061 /gi=27477131 /ug=Hs.93872 /len=5064 | NM_019061 | Hs.93872 | NP_061934 |
| 8326 | 0.015602 | BX118128 Soares fetal liver spleen 1NFLS cDNA clone IMAGp998L20388, mRNA sequence /clone=IMAGp998L20388;_IMAGE:201763 /gb=BX118128 /gi=27840987 /ug=Hs.15328 /len=783 | BX118128 | Hs.15328 | |
| 8381 | 0.041383 | Tho2 mRNA, complete cds /cds=(1,4437) /gb=AF441770 /gi=20799317 /ug=Hs.16411 /len=4452 | AF441770 | Hs.16411 | |
| 8422 | 0.008919 | cDNA FLJ13792 fis, clone THYRO1000072, weakly similar to MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC 2.7.1.117). /cds=(9,1337) /gb=AK023854 /gi=10435918 /ug=Hs.154751 /len=2184 | AK023854 | Hs.154751 | |
| 8423 | 0.025981 | ot96g10.s1 Soares_total_fetus_Nb2HF8_9w cDNA clone IMAGE:1624674 3', mRNA sequence /clone=IMAGE:1624674 /clone_end=3' /gb=AA993566 /gi=3180111 /ug=Hs.369984 /len=498 | AA993566 | Hs.369984 | |
| 8431 | 0.041383 | df57g01.y1 Morton Fetal Cochlea cDNA clone IMAGE:2487720 5', mRNA sequence /clone=IMAGE:2487720 /clone_end=5' /gb=AW023610 /gi=5877140 /ug=Hs.370582 /len=458 | AW023610 | Hs.370582 | |
| 8504 | 0.01081 | zinc finger-like protein 9 (ZPR9), mRNA /cds=(130,1563) /gb=NM_033414 /gi=15529977 /ug=Hs.60300 /len=1719 | NM_033414 | Hs.60300 | NP_219482 |
| 8505 | 6.76E-04 | EST (hv67h07.x1 NCI_CGAP_Lu24 IMAGE:3178525 3') | BE220163 | | |
| 8518 | 0.011207 | clone IMAGE:5311197, mRNA /gb=BC042002 /gi=27469533 /ug=Hs.260395 /len=1498 | BC042002 | Hs.260395 | |
| 8519 | 0.035601 | AGENCOURT_6423660 NIH_MGC_67 cDNA clone IMAGE:5580917 5', mRNA sequence /clone=IMAGE:5580917 /clone_end=5' /gb=BM465996 /gi=18515038 /ug=Hs.32990 /len=1594 | BM465996 | Hs.32990 | |
| 8520 | 0.035601 | chromosome 20 open reading frame 52 (C20orf52), mRNA /cds=(164,403) /gb=NM_080748 /gi=18152784 /ug=Hs.401703 /len=602 | NM_080748 | Hs.401703 | NP_542786 |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|------|----------|--|--------------------|-----------------------|-----------------------|
| 8545 | 0.04789 | as32a11.x1 Barstead aorta HPLRB6 cDNA clone IMAGE:2318876 3', mRNA sequence /clone=IMAGE:2318876 /clone_end=3' /gb=AI707688 /gi=4997464 /ug=Hs.369595 /len=518 | AI707688 | Hs.369595 | |
| 8553 | 0.008919 | EST (we35d08.x1 NCI_CGAP_Lu24 cDNA clone IMAGE:2343087 3' similar to contains L1.t1 L1 repetitive element) | AI701473 | | |
| 8557 | 0.041383 | UI-H-ED0-awy-a-01-0-UI.s1 NCI_CGAP_ED0 cDNA clone IMAGE:5825160 3', mRNA sequence /clone=IMAGE:5825160 /clone_end=3' /gb=BQ017647 /gi=19752924 /ug=Hs.124747 /len=1445 | BQ017647 | Hs.124747 | |
| 8572 | 0.04789 | UI-H-EU0-azo-d-01-0-UI.s1 NCI_CGAP_Car1 cDNA clone IMAGE:5851344 3', mRNA sequence /clone=IMAGE:5851344 /clone_end=3' /gb=BQ180851 /gi=20356343 /ug=Hs.436432 /len=1067 | BQ180851 | Hs.436432 | |
| 8577 | 0.005961 | RC5-FT0194-271100-022-B06 FT0194 cDNA, mRNA sequence /gb=BF858635 /gi=12246379 /ug=Hs.270272 /len=590 | BF858635 | Hs.270272 | |
| 8619 | 0.041383 | FLJ11481 fis, clone HEMBA1001803 /cds=UNKNOWN /gb=AK021543 /gi=10432744 /ug=Hs.135159 /len=1539 | AK021543 | Hs.135159 | |
| 8623 | 0.04789 | cDNA FLJ31753 fis, clone NT2RI2007468 /gb=AK056315 /gi=16551681 /ug=Hs.349283 /len=2361 | AK056315 | Hs.349283 | |
| 8647 | 0.004826 | tm62d04.x1 NCI_CGAP_Brn25 cDNA clone IMAGE:2162695 3', mRNA sequence /clone=IMAGE:2162695 /clone_end=3' /gb=AI475033 /gi=4328078 /ug=Hs.36915 /len=453 | AI475033 | Hs.36915 | |
| 8649 | 0.030485 | nah90b12.x1 NCI_CGAP_HN19 cDNA clone IMAGE:4257766 similar to P39194 ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING ENTRY. [1] contains Alu repetitive element, mRNA sequence /clone=IMAGE:4257766 /gb=BG272785 /gi=12982288 /ug=Hs.440690 /len=360 | BG272785 | Hs.440690 | |
| 8662 | 0.030485 | ts93d11.x1 NCI_CGAP_GC6 cDNA clone IMAGE:2238837 3', mRNA sequence /clone=IMAGE:2238837 /clone_end=3' /gb=AI631165 /gi=4682495 /ug=Hs.196952 /len=537 | AI631165 | Hs.196952 | |
| 8686 | 0.01859 | mRNA; cDNA DKFZp564P016 (from clone DKFZp564P016) /gb=AL049337 /gi=4500118 /ug=Hs.132571 /len=1938 | AL049337 | Hs.132571 | |

| Spot | p-value | Description | Gen Accession No. | Unigene Accession No. | Prot. in Accession No. |
|------|----------|---|-------------------|-----------------------|------------------------|
| 8709 | 0.002454 | clone alpha_est218/52C1 mRNA sequence /gb=AF001542 /gi=2529714 /ug=Hs.356442 /len=2992 | AF001542 | Hs.356442 | |
| 8710 | 0.01859 | EST(cDNA clone IMAGE:6617359 5') | BU569767 | | NP_005339 |
| 8719 | 0.041383 | clone UWGC:y17c090 from 6p21, complete sequence | AC004188 | | |
| 8723 | 0.022033 | mRNA; cDNA DKFZp586F071 (from clone DKFZp586F071) /gb=AL050125 /gi=4884333 /ug=Hs.22907 /len=3537 | AL050125 | Hs.22907 | |
| 8749 | 0.030485 | ferritin, heavy polypeptide-1 (FTH1), mRNA /cds=(92,664) /gb=NM_002032 /gi=4503794 /ug=Hs.418650 /len=801 | NM_002032 | Hs.418650 | NP_002023 |
| 8758 | 0.013024 | ESTs, cDNA, 3' end /clone_end=3' /gb=BM314871 /gi=18049216 /ug=Hs.352487 /len=451 | BM314871 | Hs.352487 | |
| 8780 | 0.015602 | MR2-CI0186-291100-010-a06 CI0186 cDNA, mRNA sequence /gb=BF814502 /gi=12147047 /ug=Hs.446594 /len=530 | BF814502 | Hs.446594 | |
| 8791 | 0.005961 | tg51b06.x1 Soares_NFL_T_GBC_S1 cDNA clone IMAGE:2112275 3', mRNA sequence /clone=IMAGE:2112275 /clone_end=3' /gb=AI419722 /gi=4265653 /ug=Hs.161220 /len=484 | AI419722 | Hs.161220 | |
| 8803 | 8.90E-04 | clone alpha_est218/52C1 mRNA sequence /gb=AF001542 /gi=2529714 /ug=Hs.356442 /len=2992 | AF001542 | Hs.356442 | |
| 8809 | 0.01081 | cDNA: FLJ23013 fis, clone LNG00740. /gb=AK026666 /gi=10439567 /ug=Hs.372737 /len=1909 | AK026666 | Hs.372737 | |
| 8818 | 0.04789 | Similar to KIAA1753 protein, clone IMAGE:5210724, mRNA /gb=BC033751 /gi=21707446 /ug=Hs.44976 /len=1275 | BC033751 | Hs.44976 | |
| 8859 | 0.013024 | clone IMAGE:5263177, mRNA /gb=BC035116 /gi=23272470 /ug=Hs.19339 /len=4267 | BC035116 | Hs.19339 | |
| 8860 | 0.022033 | clone 23612 mRNA sequence /gb=U90902 /gi=1913880 /ug=Hs.82141 /len=1548 | U90902 | Hs.82141 | |
| 8865 | 0.030485 | cDNA, FLJ12091 fis, clone HEMBB1002582 | AK022153 | | |
| 8901 | 0.030485 | sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), mRNA /cds=(46,2430) /gb=NM_005065 /gi=19923668 /ug=Hs.181300 /len=7885 | NM_005065 | Hs.181300 | NP_005056 |
| 8924 | 0.022033 | BX112599 Soares fetal liver spleen 1NFLS cDNA clone IMAGp998N15537, mRNA sequence /clone=IMAGp998N15537 IMAGE:248654 /gb=BX112599 /gi=27837735 /ug=Hs.424205 /len=606 | BX112599 | Hs.424205 | |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|------|----------|---|--------------------|-----------------------|-----------------------|
| 8926 | 0.01859 | clone IMAGE:5001859, mRNA /gb=BC040072 /gi=25303948 /ug=Hs.194051 /len=3016 | BC040072 | Hs.194051 | |
| 8940 | 0.04789 | EST(qp46g11.x1 NCI_CGAP_Co8 clone IMAGE:1926116 3') | AI346632 | | NP_004646 |
| 8972 | 0.005961 | EST (ym20a08.r1 Soares infant brain 1NIB IMAGE:48353 5') | H15948 | | |
| 9088 | 0.030485 | clone IMAGE:3875308, mRNA, partial cds /cds=UNKNOWN /gb=BC013784 /gi=15489380 /ug=Hs.351379 /len=2872 | BC013784 | Hs.351379 | |
| 9123 | 0.04789 | ESTs, cDNA, 3' end /clone=IMAGE:2730647 /clone_end=3' /gb=AW296700 /gi=6703336 /ug=Hs.335620 /len=451 | AW296700 | Hs.335620 | |
| 9129 | 0.015602 | EST(cDNA. | AW896077 | | |
| 9141 | 0.025981 | EST384025 MAGE resequences, MAGL cDNA, mRNA sequence /gb=AW972041 /gi=8161782 /ug=Hs.190176 /len=617 | AW972041 | Hs.190176 | |
| 9265 | 0.022033 | clone IMAGE:4052238, mRNA, partial cds /cds=(1,73) /gb=BC014384 /gi=15680102 /ug=Hs.348514 /len=1449 | BC014384 | Hs.348514 | |
| 9270 | 0.002454 | 602122561F1 NIH_MGC_56 cDNA clone IMAGE:4279766 5', mRNA sequence /clone=IMAGE:4279766 /clone_end=5' /gb=BF668349 /gi=11942244 /ug=Hs.44731 /len=906 | BF668349 | Hs.44731 | |
| 9302 | 0.041383 | No significant match, ORF-1(1~102,214~317) | SEQ.ID.No.11 | | |
| 9353 | 0.04789 | No significant match, ORF-2(1~153,226~333) | SEQ.ID.No.97 | | |
| 9384 | 0.030485 | mitochondrial ribosomal protein L45 (MRPL45), nuclear gene encoding mitochondrial protein, mRNA /cds=(22,942) /gb=NM_032351 /gi=21735611 /ug=Hs.19347 /len=1582 | NM_032351 | Hs.19347 | NP_115727 |
| 9454 | 0.00388 | praja 1 (PJA1), mRNA /cds=(295,1662) /gb=NM_022368 /gi=21539662 /ug=Hs.21122 /len=2122 | NM_022368 | Hs.21122 | NP_071763 |
| 9489 | 0.013024 | similar to putative (H. sapiens) (LOC129641), mRNA | XM_059369 | | |
| 9492 | 0.041383 | 601846634F1 NIH_MGC_55 cDNA clone IMAGE:4077632 5', mRNA sequence /clone=IMAGE:4077632 /clone_end=5' /gb=BF214729 /gi=11108315 /ug=Hs.446581 /len=835 | BF214729 | Hs.446581 | |
| 9581 | 3.77E-04 | partial steerin-1 gene | AJ251973 | | |
| 9623 | 0.030485 | KIAA0854 protein (KIAA0854), mRNA /cds=(305,2818) /gb=NM_014943 /gi=7662341 /ug=Hs.30209 /len=4089 | NM_014943 | Hs.30209 | NP_055758 |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Prot in Accession No. |
|-------|----------|--|--------------------|-----------------------|-----------------------|
| 9641 | 0.041383 | translocase of inner mitochondrial membrane 17 A (yeast) (TIMM17A), mRNA /cds=(8,523) /gb=NM_006335 /gi=5454119 /ug=Hs.20716 /len=1645 | NM_006335 | Hs.20716 | NP_006326 |
| 9674 | 0.01081 | EST(DKFZp564I112 (from clone DKFZp564I112)) | AL110136 | | |
| 9717 | 0.04789 | EST(yu74g03.s1 clone 239572 3' contains Alu repeat) | H81306 | | |
| 9733 | 0.01859 | hypothetical protein LOC92597 (LOC92597), mRNA /cds=(151,801) /gb=NM_173468 /gi=27735028 /ug=Hs.31422 /len=6956 | NM_173468 | Hs.31422 | NP_775739 |
| 9763 | 0.04789 | EST(ze13e01.r1 Soares_fetal_heart_NbHH19WcDNA clone IMAGE:358872 5') | W94505 | | |
| 9806 | 0.01081 | 7k03e02.x1 NCI_CGAP_GC6 cDNA clone IMAGE:3443402 3', mRNA sequence /clone=IMAGE:3443402 /clone_end=3' /gb=BF056273 /gi=10810169 /ug=Hs.188920 /len=572 | BF056273 | Hs.188920 | |
| 9918 | 0.04789 | chromosome 20 open reading frame 108 (C20orf108), mRNA /cds=(41,619) /gb=NM_080821 /gi=18201877 /ug=Hs.352413 /len=3026 | NM_080821 | Hs.352413 | NP_543011 |
| 9920 | 0.015602 | hypothetical protein FLJ22419 (FLJ22419), mRNA /cds=(409,1596) /gb=NM_024697 /gi=13375980 /ug=Hs.99256 /len=1674 | NM_024697 | Hs.99256 | NP_078973 |
| 9921 | 0.04789 | hypothetical protein FLJ10477 (FLJ10477), mRNA /cds=(232,873) /gb=NM_018105 /gi=8922445 /ug=Hs.7432 /len=2167 | NM_018105 | Hs.7432 | NP_060575 |
| 9928 | 0.008919 | LIM domain containing preferred translocation partner in lipoma (LPP), mRNA /cds=(247,2085) /gb=NM_005578 /gi=5031886 /ug=Hs.180398 /len=5656 | NM_005578 | Hs.180398 | NP_005569 |
| 9953 | 0.030485 | Fatty acid binding protein 1, liver (Fabp1), mRNA | NM_012556 | | |
| 10026 | 0.001162 | dishevelled associated activator of morphogenesis 1 (DAAM1), mRNA /cds=(126,3362) /gb=NM_014992 /gi=21071076 /ug=Hs.197751 /len=4256 | NM_014992 | Hs.197751 | NP_055807 |
| 10085 | 0.041383 | mRNA for KIAA0931 protein, partial cds. /cds=(1,2205) /gb=AB023148 /gi=4589505 /ug=Hs.173373 /len=6167 | AB023148 | Hs.173373 | |
| 10145 | 0.025981 | EST(fi21a05.x1 Sugano Kawakami zebrafish DRA clone 2601776 3') | AW116880 | | |
| 10178 | 0.030485 | EST382135 MAGE resequences, MAGK cDNA, mRNA sequence /gb=AW970055 /gi=8159900 /ug=Hs.324815 /len=764 | AW970055 | Hs.324815 | |
| 10238 | 0.01859 | EST(yr06d08.r1 Soares fetal liver spleen 1NFLS cDNA clone IMAGE:204495 5') | H58577 | | |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|-------|----------|---|--------------------|-----------------------|-----------------------|
| 10270 | 0.04789 | yh25h10.s1 Soares placenta Nb2HP cDNA clone IMAGE:130819 3', mRNA sequence /clone=IMAGE:130819 /clone_end=3' /gb=R22183 /gi=776964 /ug=Hs.307975 /len=433 | R22183 | Hs.307975 | |
| 10275 | 0.04789 | EST tn11d09.x1 NCI_CGAP_Brn25 cDNA clone IMAGE:2167313 3' | AI560484 | | NP_852556 |
| 10323 | 0.003097 | mRNA; cDNA DKFZp434K1115 (from clone DKFZp434K1115); complete cds /cds=(97,2877) /gb=AL136764 /gi=12053044 /ug=Hs.42676 /len=4868 | AL136764 | Hs.42676 | |
| 10346 | 0.04789 | UI-E-EO1-aiv-e-19-0-UI.s1 UI-E-EO1 cDNA clone UI-E-EO1-aiv-e-19-0-UI 3', mRNA sequence /clone=UI-E-EO1-aiv-e-19-0-UI /clone_end=3' /gb=BU742864 /gi=23689787 /ug=Hs.356716 /len=1044 | BU742864 | Hs.356716 | |
| 10363 | 0.005961 | Similar to RIKEN cDNA 2310026P19 gene, clone MGC:49935 IMAGE:6175382, mRNA, complete cds /cds=(288,3329) /gb=BC043352 /gi=27694113 /ug=Hs.35096 /len=5900 | BC043352 | Hs.35096 | |
| 10407 | 0.004826 | clone IMAGE:125405, mRNA sequence /gb=AF339770 /gi=13507308 /ug=Hs.221635 /len=790 | AF339770 | Hs.221635 | |
| 10451 | 0.015602 | oj03b12.s1 NCI_CGAP_Mel3 cDNA clone IMAGE:1491071 3', mRNA sequence /clone=IMAGE:1491071 /clone_end=3' /gb=AA937379 /gi=3095490 /ug=Hs.137120 /len=403 | AA937379 | Hs.137120 | |
| 10474 | 0.041383 | EST(cDNA clone IMAGE:2505486 3') | AW004819 | | NP_612487 |
| 10530 | 0.04789 | EST383317 MAGE resequences, MAGL cDNA, mRNA sequence /gb=AW971229 /gi=8161074 /ug=Hs.293372 /len=642 | AW971229 | Hs.293372 | |
| 10534 | 0.013024 | hypothetical protein DKFZp762A217 (DKFZp762A217), mRNA /cds=(433,2943) /gb=NM_152588 /gi=22749210 /ug=Hs.396456 /len=4855 | NM_152588 | Hs.396456 | NP_689801 |
| 10558 | 0.025981 | ESTs, cDNA /clone=IMAGE:1372579 /gb=AA833868 /gi=2908636 /ug=Hs.156300 /len=495 | AA833868 | Hs.156300 | |
| 10564 | 0.01081 | UI-1-BB1p-akj-h-02-0-UI.s1 NCI_CGAP_PI6 cDNA clone UI-1-BB1p-akj-h-02-0-UI 3', mRNA sequence /clone=UI-1-BB1p-akj-h-02-0-UI /clone_end=3' /gb=BQ021906 /gi=19757184 /ug=Hs.317762 /len=1296 | BQ021906 | Hs.317762 | |
| 10571 | 0.022033 | EST(qv09f01.x1 cDNA, 3' end/clone=IMAGE:1981081 /clone_end=3' /gb=AI274446 /gi=3896714 /ug=Hs.327194 /len=230 | AI274446 | Hs.327194 | |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|-------|----------|--|--------------------------|-----------------------------|-----------------------------|
| 10592 | 0.030485 | EST(cDNA clone IMAGE:3054307 3') | AW575133 | | NP_005162 |
| 10594 | 0.008919 | UI-H-EZ1-bbh-j-15-0-UI.s1 NCI_CGAP_Ch2 cDNA clone UI-H-EZ1-bbh-j-15-0-UI 3', mRNA sequence /clone=UI-H-EZ1-bbh-j-15- 0-UI /clone_end=3' /gb=BQ575990 /gi=21479307 /ug=Hs.445509 /len=1032 | BQ575990 | Hs.445509 | |
| 10596 | 0.013024 | 602584296F1 NIH_MGC_76 cDNA clone IMAGE:4712302 5', mRNA sequence /clone=IMAGE:4712302 /clone_end=5' /gb=BG564611 /gi=13572263 /ug=Hs.136470 /len=896 | BG564611 | Hs.136470 | |
| 10597 | 0.01859 | BX106681 Soares_parathyroid_tumor_NbHPA cDNA clone IMAGp998F054235, mRNA sequence /clone=IMAGp998F054235; IMAGE:16684 84 /gb=BX106681 /gi=27847079 /ug=Hs.293334 /len=605 | BX106681 | Hs.293334 | |
| 10624 | 0.030485 | AGENCOURT_6417307 NIH_MGC_67 cDNA clone IMAGE:5492062 5', mRNA sequence /clone=IMAGE:5492062 /clone_end=5' /gb=BM799896 /gi=19116719 /ug=Hs.304926 /len=913 | BM799896 | Hs.304926 | |
| 10629 | 0.04789 | ac74b05.x5 Stratagene lung (#937210) cDNA clone IMAGE:868305 3' similar to contains Alu repetitive element; mRNA sequence /clone=IMAGE:868305 /clone_end=3' /gb=AI791153 /gi=5338869 /ug=Hs.444952 /len=498 | AI791153 | Hs.444952 | |
| 10633 | 0.035601 | UI-E-CL1-afa-n-02-0-UI.r1 UI-E-CL1 cDNA clone UI-E-CL1-afa-n-02-0-UI 5', mRNA sequence /clone=UI-E-CL1-afa-n-02-0-UI /clone_end=5' /gb=BM696235 /gi=19009493 /ug=Hs.446332 /len=1366 | BM696235 | Hs.446332 | |
| 10637 | 0.002454 | EST(NIH_MGC_71 cDNA clone IMAGE:3909162 5') | BE885396 | | NP_060114 |
| 10642 | 0.022033 | HSC3IC021 normalized infant brain cDNA cDNA clone c-3ic02 | F13068 | | |
| 10669 | 0.025981 | EST(Hippocampus SN pool 1 cDNA clone IMAGE:1948863 similar to contains L1.t2 L1 repetitive element ;) | AI217038 | | |
| 10675 | 0.002454 | cDNA FLJ11309 fis, clone PLACE1010076. /gb=AK002171 /gi=7023887 /ug=Hs.28005 /len=3232 | AK002171 | Hs.28005 | |
| 10698 | 0.025981 | cDNA FLJ37672 fis, clone BRHIP2012059. /gb=AK094991 /gi=21754166 /ug=Hs.125419 /len=2342 | AK094991 | Hs.125419 | |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|-------|----------|---|--------------------|-----------------------|-----------------------|
| 10733 | 0.025981 | DKFZp434O0813_s1 434 (synonym: htes3) cDNA clone DKFZp434O0813 3', mRNA sequence /clone=DKFZp434O0813 /clone_end=3' /gb=AL040360 /gi=5409314 /ug=Hs.162203 /len=772 | AL040360 | Hs.162203 | |
| 10782 | 0.025981 | EST (cDNA clone IMAGE:120476 3' similar to | T95469 | | |
| 10788 | 0.022033 | yg45f12.s1 Soares' infant brain 1NIB cDNA clone IMAGE:35625 3', mRNA sequence /clone=IMAGE:35625 /clone_end=3' /gb=R45691 /gi=822137 /ug=Hs.268774 /len=574 | R45691 | Hs.268774 | |
| 10798 | 0.035601 | EST (ta16g05.x1 NCI_CGAP_Lym5 IMAGE:2044280 3') | AI471814 | | |
| 10821 | 0.035601 | 601584240F1 NIH_MGC_7 cDNA clone IMAGE:3938912 5', mRNA sequence /clone=IMAGE:3938912 /clone_end=5' /gb=BE798289 /gi=10219487 /ug=Hs.446578 /len=793 | BE798289 | Hs.446578 | |
| 10834 | 0.025981 | EST(EST370510 MAGE resequences, MAGE) | AW958440 | | NP_061323 |
| 10855 | 0.008919 | EST 7h93e02.x1 NCI_CGAP_Co16 cDNA clone IMAGE:3323546 3' | BF064070 | | |
| 10856 | 0.01859 | clone IMAGE:4138742, mRNA /gb=BC006326 /gi=13937734 /ug=Hs.334571 /len=1666 | BC006326 | Hs.334571 | |
| 10860 | 0.030485 | mitochondrion, complete genome | NC_001807 | | |
| 10937 | 0.01859 | hypothetical protein MGC16384 (MGC16384), mRNA /cds=(450,602) /gb=NM_053048 /gi=16596689 /ug=Hs.274268 /len=1599 | NM_053048 | Hs.274268 | NP_444276 |
| 10954 | 0.01081 | desmin (DES), mRNA /cds=(81,1490) /gb=NM_001927 /gi=18105049 /ug=Hs.279604 /len=2236 | NM_001927 | Hs.279604 | NP_001918 |
| 10976 | 0.04789 | in56e04.x1 HR85 islet cDNA clone IMAGE:6126055 3', mRNA sequence /clone=IMAGE:6126055 /clone_end=3' /gb=BU784825 /gi=23830229 /ug=Hs.442971 /len=548 | BU784825 | Hs.442971 | |
| 10999 | 0.015602 | ax37a08.x1 Proliferating Erythroid Cells (LCB:ax library) cDNA clone ax37a08 random, mRNA sequence /clone=ax37a08 /gb=BG943384 /gi=14342756 /ug=Hs.339555 /len=555 | BG943384 | Hs.339555 | |
| 11002 | 0.013024 | AU119153 HEMBA1 cDNA clone HEMBA1005152 5', mRNA sequence /clone=HEMBA1005152 /clone_end=5' /gb=AU119153 /gi=10934388 /ug=Hs.288615 /len=820 | AU119153 | Hs.288615 | |

| Spot | p-value | D scription | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|-------|----------|---|--------------------|-----------------------|-----------------------|
| 11013 | 0.035601 | UI-H-FH0-bcl-g-09-0-UI.s1 NCI_CGAP_FH0 cDNA clone UI-H-FH0-bcl-g-09-0-UI 3', mRNA sequence /clone=UI-H-FH0-bcl-g-09-0-UI /clone_end=3' /gb=CA419491 /gi=24782146 /ug=Hs.293327 /len=693 | CA419491 | Hs.293327 | |
| 11014 | 0.030485 | cDNA FLJ14135 fis, clone MAMMA1002728. /gb=AK024197 /gi=10436518 /ug=Hs.289037 /len=1784 | AK024197 | Hs.289037 | |
| 11024 | 0.04789 | hypothetical protein MGC33607 (MGC33607), mRNA /cds=(42,2543) /gb=NM_152775 /gi=22749514 /ug=Hs.41101 /len=2866 | NM_152775 | Hs.41101 | NP_689988 |
| 11025 | 0.01859 | EST(cDNA 3' | BM264491 | | |
| 11031 | 0.013024 | cDNA: FLJ21228 fis, clone COL00739. /gb=AK024881 /gi=10437293 /ug=Hs.306716 /len=1869 | AK024881 | Hs.306716 | |
| 11032 | 0.01859 | nj38c05.s1 NCI_CGAP_AA1 cDNA clone IMAGE:994760 3' similar to gb:M62424 THROMBIN RECEPTOR PRECURSOR mRNA sequence /clone=IMAGE:994760 /clone_end=3' /gb=AA548630 /gi=2318912 /ug=Hs.105848 /len=555 | AA548630 | Hs.105848 | |
| 11048 | 0.005961 | EST(placenta Nb2HP Homo sapiens cDNA clone IMAGE:138431 5' similar to contains Alu repetitive element;) | R68614 | | |
| 11059 | 0.01859 | UI-E-CQ1-aew-e-07-0-UI.s1 UI-E-CQ1 cDNA clone UI-E-CQ1-aew-e-07-0-UI 3', mRNA sequence /clone=UI-E-CQ1-aew-e-07-0-UI /clone_end=3' /gb=BU728934 /gi=23651308 /ug=Hs.436272 /len=1132 | BU728934 | Hs.436272 | |
| 11063 | 0.035601 | clone alpha_est218/52C1 mRNA sequence. /gb=AF001542 /gi=2529714 /ug=Hs.356442 /len=2992 | AF001542 | Hs.356442 | |
| 11068 | 0.030485 | mRNA; cDNA DKFZp586G1520 (from clone DKFZp586G1520) /gb=AL050148 /gi=4884359 /ug=Hs.31834 /len=3030 | AL050148 | Hs.31834 | |
| 11126 | 0.01859 | full length insert cDNA clone ZD64C04 /gb=AF088052 /gi=3523258 /ug=Hs.384557 /len=831 | AF088052 | Hs.384557 | |
| 11215 | 0.015602 | Novel, ORF+3(39~203) | SEQ.ID.No.53 | | |
| 11259 | 0.041383 | actin binding LIM protein 1 (ABLIM1), transcript variant ABLIM-I, mRNA /cds=(100,2436) /gb=NM_002313 /gi=21284382 /ug=Hs.158203 /len=7581 | NM_002313 | Hs.158203 | NP_006711 |
| 11266 | 0.035601 | B-cell translocation gene 1, anti-proliferative (BTG1), mRNA /cds=(309,824) /gb=NM_001731 /gi=4502472 /ug=Hs.77054 /len=1783 | NM_001731 | Hs.77054 | NP_001722 |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|-------|----------|--|--------------------|-----------------------|-----------------------|
| 11322 | 0.041383 | Hypothetical protein (L1H 3' region) - human (AA=69%) | B34087 | | |
| 11341 | 0.041383 | similar to rat tricarboxylate carrier-like protein (BA108L7.2), mRNA /cds=(75,1040) /gb=NM_030971 /gi=13569945 /ug=Hs.283844 /len=2735 | NM_030971 | Hs.283844 | NP_112233 |
| 11343 | 0.035601 | chromosome 1 open reading frame 33 (C1orf33), mRNA /cds=(32,751) /gb=NM_016183 /gi=18490986 /ug=Hs.274201 /len=1185 | NM_016183 | Hs.274201 | NP_057267 |
| 11351 | 0.04789 | type V procollagen alpha 2 chain (COL5A2) gene, exons 34 through 52 and partial cds; and type III procollagen alpha 1 chain (COL3A1) gene, exons 2 through 52 | AY016295 | | |
| 11454 | 0.025981 | similar to protein tyrosine phosphatase, receptor type, E; Protein tyrosine phosphatase, receptor type, epsilon; protein tyrosine phosphatase, receptor type, epsilon polypeptide (H. sapiens) (LOC119466), mRNA | XM_005781 | | |
| 11465 | 0.007315 | gonadotropin-releasing hormone receptor (GNRHR), mRNA /cds=(1749,2735) /gb=NM_000406 /gi=4504058 /ug=Hs.73064 /len=2735 | NM_000406 | Hs.73064 | NP_000397 |
| 11519 | 0.025981 | mRNA; cDNA DKFZp761O0611 (from clone DKFZp761O0611) /gb=AL834155 /gi=21739631 /ug=Hs.22969 /len=4502 | AL834155 | Hs.22969 | |
| 11546 | 0.04789 | EST(PM3-NT0011-120400-001-b03 NT0011) | AW888715 | | |
| 11551 | 0.022033 | EST(EST64315 Jurkat T-cells VI 5' ribosomal protein S21) | AA355853 | | NP_114107 |
| 11569 | 0.01859 | hypothetical protein DKFZp434K1421 (DKFZP434K1421), mRNA /cds=(29,1705) /gb=NM_032141 /gi=14149806 /ug=Hs.374609 /len=2547 | NM_032141 | Hs.374609 | NP_115517 |
| 11585 | 0.035601 | EST (yd08e03.r1 clone 24895 5') | T80443 | | |
| 11604 | 0.041383 | EST(ae50c06.s1 Stratagene lung carcinoma 937218 clone IMAGE:950314 3' contains Alu repeat) | AA600135 | | |
| 11637 | 0.041383 | EST(at70b02.x1 Barstead colon HPLRB7 clone IMAGE:2377323 3' contains L1.t3 L1 repeat) | AI832565 | | |
| 11654 | 0.025981 | clone IMAGE:5260918, mRNA /gb=BC035085 /gi=23958865 /ug=Hs.250448 /len=3052 | BC035085 | Hs.250448 | |
| 11675 | 0.022033 | cDNA FLJ34480 fis, clone HLUNG2004014. /gb=AK091799 /gi=21750255 /ug=Hs.154993 /len=1976 | AK091799 | Hs.154993 | |

| Spot | p-value | Description | Gene Accession No. | Unig n Accession No. | Protein Accession No. |
|-------|----------|--|--------------------|----------------------|-----------------------|
| 11683 | 0.007453 | EST (clone IMAGE:1218466 3' similar to contains | AA662478 | | |
| 11692 | 0.035601 | KIAA0874 protein (KIAA0874), mRNA /cds=(1,6189) /gb=NM_015208 /gi=14140237 /ug=Hs.27973 /len=6189 | NM_015208 | Hs.27973 | NP_056023 |
| 11760 | 0.041383 | arrestin, beta 2 (ARRB2), mRNA /cds=(234,1463) /gb=NM_004313 /gi=21626464 /ug=Hs.18142 /len=1941 | NM_004313 | Hs.18142 | NP_004304 |
| 11766 | 0.030485 | AV701088 ADA cDNA clone ADAAGB09 5', mRNA sequence /clone=ADAAGB09 /clone_end=5' /gb=AV701088 /gi=10717418 /ug=Hs.419141 /len=652 | AV701088 | Hs.419141 | |
| 11770 | 0.00388 | FLJ33160 fis, clone UTERU2000485 /cds=UNKNOWN /gb=AK057722 /gi=16553641 /ug=Hs.124733 /len=2328 | AK057722 | Hs.124733 | |
| 11800 | 0.022033 | RAN binding protein 2-like 1 (RANBP2L1), transcript variant 1, mRNA /cds=(78,5375) /gb=NM_005054 /gi=19718754 /ug=Hs.179825 /len=7164 | NM_005054 | Hs.179825 | NP_115636 |
| 11808 | 0.035601 | Myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 4, cDNA /gb=AW582014 /gi=7257063 /ug=Hs.169986 /len=705 | AW582014 | Hs.169986 | |
| 11823 | 0.01081 | mRNA for KIAA1614 protein, partial cds. /cds=(1,3628) /gb=AB046834 /gi=10047302 /ug=Hs.287381 /len=4143 | AB046834 | Hs.287381 | |
| 11870 | 0.022033 | clone 114 tumor rejection antigen mRNA, complete cds /cds=(3482,3544) /gb=AF445027 /gi=17386079 /ug=Hs.24723 /len=3648 | AF445027 | Hs.24723 | |
| 11876 | 0.007453 | immediate early response 3 (IER3), transcript variant long, mRNA /cds=(30,611) /gb=NM_052815 /gi=16554596 /ug=Hs.76095 /len=1345 | NM_052815 | Hs.76095 | NP_434702 |
| 11898 | 0.00388 | intersectin 2 (ITSN2), transcript variant 1, mRNA /cds=(242,5332) /gb=NM_006277 /gi=22325384 /ug=Hs.166184 /len=6092 | NM_006277 | Hs.166184 | NP_671494 |
| 11912 | 0.007315 | hypothetical protein MGC40157 (MGC40157), mRNA /cds=(106,498) /gb=NM_152350 /gi=22748758 /ug=Hs.295362 /len=1250 | NM_152350 | Hs.295362 | NP_689563 |
| 11913 | 0.005961 | mRNA; cDNA DKFZp434H2019 (from clone DKFZp434H2019) /gb=AL137535 /gi=6808211 /ug=Hs.15806 /len=1974 | AL137535 | Hs.15806 | |
| 11985 | 0.001504 | protocadherin beta 16 (PCDHB16), mRNA /cds=(1156,3486) /gb=NM_020957 /gi=14195604 /ug=Hs.147674 /len=4827 | NM_020957 | Hs.147674 | NP_066008 |
| 12004 | 0.030485 | hypothetical L1 protein (third intron of gene TS) | JU0033 | | JU0033 |

| Spot | p-value | Description | Gene Accession No. | Unigen Accession No. | Protein Accession No. |
|-------|----------|--|--------------------|----------------------|-----------------------|
| 12057 | 0.013024 | qe17g05.x1 Soares_fetal_lung_NbHL19W cDNA clone IMAGE:1739288 3', mRNA sequence /clone=IMAGE:1739288 /clone_end=3' /gb=AI183765 /gi=3734403 /ug=Hs.146975 /len=382 | AI183765 | Hs.146975 | |
| 12058 | 0.014488 | HPS12_49 testis cDNA library cDNA, mRNA sequence /gb=BM422916 /gi=28192251 /ug=Hs.294041 /len=541 | BM422916 | Hs.294041 | |
| 12061 | 0.041383 | cDNA FLJ36838 fis, clone ASTRO2011426. /gb=AK094157 /gi=21753159 /ug=Hs.407030 /len=2646 | AK094157 | Hs.407030 | |
| 12074 | 0.038534 | EST(as88c04.x1 Barstead colon HPLRB7 clone IMAGE:2335782 3' TR:Q13538 Q13538 ORF2: FUNCTION UNKNOWN; contains Alu repeat) | AI735066 | | |
| 12104 | 0.009171 | helicase-like protein (KIAA2023), mRNA /cds=(399,5378) /gb=NM_173082 /gi=27436872 /ug=Hs.231907 /len=7011 | NM_173082 | Hs.231907 | NP_775105 |
| 12109 | 0.019692 | EST(wc45g02.x1 NCI_CGAP_Pr28 clone IMAGE:2321618 3') | AI675688 | | NP_714916 |
| 12120 | 0.01859 | mRNA, cDNA DKFZp761O0611 (from clone DKFZp761O0611) /gb=AL834155 /gi=21739631 /ug=Hs.22969 /len=4502 | AL834155 | Hs.22969 | |
| 12122 | 0.041383 | high-mobility group (nonhistone chromosomal) protein 1-like 10 (HMG1L10), mRNA /cds=(51,686) /gb=NM_172363 /gi=28376645 /ug=Hs.434102 /len=994 | NM_172363 | Hs.434102 | NP_758951 |
| 12161 | 0.04789 | EST(hh76d05.y1 NCI_CGAP_GU1 cDNA clone IMAGE:2968713 5' similar to contains L1.t1 L1 repetitive element ; | AW663260 | | |
| 12182 | 0.025981 | Williams-Beuren Syndrome critical region protein 20 copy B (WBSCR20B), mRNA /cds=(984,1448) /gb=NM_145645 /gi=21717802 /ug=Hs.406306 /len=1634 | NM_145645 | Hs.406306 | NP_663620 |
| 12193 | 0.013024 | EST (yd68e02.s1 Soares fetal liver spleen 1NFLS IMAGE:113402 3') | T78464 | | NP_000436 |
| 12213 | 0.04789 | repetitive sequence (ALU SUBFAMILY J) | P39188 | | |
| 12216 | 0.025981 | exon prediction only (aa 2e-15) | CAB90410 | | |
| 12244 | 0.041383 | EST(601812732F1 NIH_MGC_54 cDNA clone IMAGE:4047222 5') | BF211120 | | NP_071942 |
| 12246 | 0.022033 | EST (yo20f05.r1 Soares adult brain N2b5HB55Y cDNA clone IMAGE:178497 5') | H46503 | | |
| 12248 | 0.002454 | EST(yd28g06.r1 Soares fetal liver spleen 1NFLS IMAGE:109594 5') | T82238 | | |
| 12264 | 0.025981 | clone IMAGE:3909104, mRNA /gb=BC015719 /gi=16041698 /ug=Hs.8852 /len=3169 | BC015719 | Hs.8852 | |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|-------|----------|---|--------------------|-----------------------|-----------------------|
| 12284 | 0.030485 | EST384170 MAGE resequences, MAGL cDNA, mRNA sequence /gb=AW971961 /gi=8161927 /ug=Hs.136340 /len=642 | AW971961 | Hs.136340 | |
| 12290 | 0.041383 | EST(yd74f02.s1 Soares fetal liver spleen 1NFLS cDNA clone IMAGE:113979 3' similar to contains Alu repetitive element) | T79796 | | |
| 12329 | 0.04789 | EST(RC2-CT0298-300100-014-d01-CT0298) | AW604547 | | NP_000981 |
| 12344 | 0.025981 | EST(cDNA clone IMAGE:5303467 5') | BI597128 | | |
| 12352 | 0.013024 | UI-H-BI2-ahm-d-05-0-UI.s1 NCI_CGAP_Sub4 cDNA clone IMAGE:2727224 3', mRNA sequence /clone=IMAGE:2727224 /clone_end=3' /gb=AW293452 /gi=6700088 /ug=Hs.16228 /len=634 | AW293452 | Hs.16228 | |
| 12369 | 0.035601 | QV3-BN0047-150400-152-h07 BN0047-cDNA, mRNA sequence /gb=AW997115 /gi=8257349 /ug=Hs.274352 /len=686 | AW997115 | Hs.274352 | |
| 12371 | 0.01081 | ESTs, cDNA, 5' end /clone=BMFBFE06 /clone_end=5' /gb=AV756341 /gi=10914189 /ug=Hs.244273 /len=766 | AV756341 | Hs.244273 | |
| 12375 | 0.01081 | UI-H-DT0-avk-p-22-0-UI.s1 NCI_CGAP_DT0 cDNA clone IMAGE:5880837 3', mRNA sequence /clone=IMAGE:5880837 /clone_end=3' /gb=BM996358 /gi=19721259 /ug=Hs.433458 /len=838 | BM996358 | Hs.433458 | |
| 12378 | 0.013024 | cDNA FLJ31274 fis, clone KIDNE2006334. /gb=AK055836 /gi=16550665 /ug=Hs.351722 /len=1817 | AK055836 | Hs.351722 | |
| 12387 | 0.025981 | EST(synonym: hlcc2) cDNA clone DKFZp313J2122 5' | AL598811 | | NP_006796 |
| 12388 | 0.013024 | EST(cDNA clone IMAGE:4398135 5') | BF984363 | | |
| 12423 | 0.015602 | clone IMAGE:4800262, mRNA /gb=BC040182 /gi=25455679 /ug=Hs.235795 /len=3858 | BC040182 | Hs.235795 | |
| 12425 | 0.004826 | FLJ32080 fis, clone OCBBF2000015 /cds=UNKNOWN /gb=AK056642 /gi=16552101 /ug=Hs.336425 /len=3615 | AK056642 | Hs.336425 | |
| 12426 | 0.013024 | 602590145F1 NIH_MGC_76 cDNA clone IMAGE:4724074 5', mRNA sequence /clone=IMAGE:4724074 /clone_end=5' /gb=BG564169 /gi=13571821 /ug=Hs.444093 /len=792 | BG564169 | Hs.444093 | |
| 12429 | 0.003097 | EST(cDNA clone IMAGE:3913767 5') | BE890088 | | |
| 12430 | 0.01081 | mRNA; cDNA DKFZp686J19116 (from clone DKFZp686J19116) /gb=AL833458 /gi=21734100 /ug=Hs.428760 /len=3297 | AL833458 | Hs.428760 | |
| 12431 | 0.01859 | ESTs, cDNA /gb=AW993259 /gi=8253410 /ug=Hs.113105 /len=678 | AW993259 | Hs.113105 | |

| Spot | p-value | Description | Gene Accession No. | Unig ne Acc ssion No. | Protein Accession No. |
|-------|----------|--|--------------------|-----------------------|-----------------------|
| 12434 | 0.015602 | EST(cDNA clone HTFABF07 5') | AV731260 | | |
| 12436 | 0.035601 | UI-H-BW0-ajn-d-08-0-UI.s1 NCI_CGAP_Sub6 cDNA clone IMAGE:2732223 3', mRNA sequence /clone=IMAGE:2732223 /clone_end=3' /gb=AW297946 /gi=6704582 /ug=Hs.444392 /len=807 | AW297946 | Hs.444392 | |
| 12452 | 0.041383 | EST(cDNA clone IMAGE:784142 5') | AA446766 | | |
| 12457 | 0.035601 | EST (376579 MAGE resequences MAGH) | AW964506 | | NP_065825 |
| 12465 | 0.015602 | ESTs, cDNA, 5' end /clone=IMAGE:3922401 /clone_end=5' /gb=BE894201 /gi=10356330 /ug=Hs.176376 /len=916 | BE894201 | Hs.176376 | |
| 12467 | 0.013024 | EST(cDNA clone IMAGE:2728993 3') | AW292959 | | |
| 12489 | 0.01081 | MR2-CI0186-291100-010-a06 CI0186 cDNA, mRNA sequence /gb=BF814502 /gi=12147047 /ug=Hs.446594 /len=530 | BF814502 | Hs.446594 | |
| 12494 | 0.025981 | cDNA FLJ39046 fis, clone NT2RP7010612. /gb=AK096365 /gi=21755841 /ug=Hs.9856 /len=2161 | AK096365 | Hs.9856 | |
| 12505 | 0.041383 | EST(cDNA clone HTBBSD03 5') | AV722328 | | |
| 12541 | 0.001504 | yb61c11.s1 Stratagene ovary (#937217) cDNA clone IMAGE:75668 3', mRNA sequence /clone=IMAGE:75668 /clone_end=3' /gb=T58438 /gi=660275 /ug=Hs.189678 /len=506 | T58438 | Hs.189678 | |
| 12542 | 0.01081 | ESTs, cDNA /gb=AW797724 /gi=7849594 /ug=Hs.130350 /len=559 | AW797724 | Hs.130350 | |
| 12543 | 0.041383 | EST(cDNA clone CS0DI015YC21 5 prime) | AL545514 | | NP_003109 |
| 12547 | 0.035601 | BX096777 Soares_pregnant_uterus_NbHPU cDNA clone IMAGp998K151202, mRNA sequence /clone=IMAGp998K151202 ; IMAGE:50394 2 /gb=BX096777 /gi=27842974 /ug=Hs.193352 /len=684 | BX096777 | Hs.193352 | |
| 12568 | 0.022033 | EST, cDNA, 3' end /clone=IMAGE:1541875 /clone_end=3' /gb=AA927945 /gi=3076689 /ug=Hs.292141 /len=354 | AA927945 | Hs.292141 | |
| 12574 | 0.013024 | UI-H-ED0-awx-b-15-0-UI.s1 NCI_CGAP_ED0 cDNA clone IMAGE:5824814 3', mRNA sequence /clone=IMAGE:5824814 /clone_end=3' /gb=BQ020068 /gi=19755345 /ug=Hs.396278 /len=1351 | BQ020068 | Hs.396278 | |
| 12624 | 3.77E-04 | No significant match, ORF+3(156~314) | SEQ.ID.No.77 | | |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|-------|----------|---|--------------------|-----------------------|-----------------------|
| 12667 | 0.022033 | tq86b01.x1 NCI_CGAP_Ov23 cDNA clone IMAGE:2215657 3' similar to contains Alu repetitive element; contains element LTR5 repetitive element ;, mRNA sequence /clone=IMAGE:2215657 /clone_end=3' /gb=AI567941 /gi=4526393 /ug=Hs.436171 /len=476 | AI567941 | Hs.436171 | |
| 12668 | 0.035601 | hypothetical protein FLJ13110 (FLJ13110), mRNA /cds=(145,750) /gb=NM_022912 /gi=12597656 /ug=Hs.7358 /len=3856 | NM_022912 | Hs.7358 | NP_075063 |
| 12669 | 0.041383 | hypothetical protein FLJ31438 (FLJ31438), mRNA /cds=(347,2107) /gb=NM_152385 /gi=22748824 /ug=Hs.24423 /len=2266 | NM_152385 | Hs.24423 | NP_689598 |
| 12672 | 0.04789 | hypothetical protein FLJ10254 | NP_060511 | | |
| 12717 | 0.04789 | EST(xx99e02.x1 NCI_CGAP_Lym12 cDNA clone IMAGE:2851802 3' similar to contains Alu repetitive element) | AW515834 | | NP_387449 |
| 12751 | 0.04789 | NISC_gj03b10.x1 NCI_CGAP_Pr28 cDNA clone IMAGE:3270498 3', mRNA sequence /clone=IMAGE:3270498 /clone_end=3' /gb=CB048158 /gi=27786445 /ug=Hs.201018 /len=384 | CB048158 | Hs.201018 | |
| 12771 | 0.035601 | cDNA FLJ37324 fis, clone BRAMY2018279. /gb=AK094643 /gi=21753744 /ug=Hs.12714 /len=2844 | AK094643 | Hs.12714 | |
| 12780 | 0.013024 | clone MGC:16233 IMAGE:3677787, mRNA, complete cds /cds=(85,957) /gb=BC012766 /gi=15215342 /ug=Hs.180428 /len=2845 | BC012766 | Hs.180428 | NP_065195 |
| 12798 | 0.01081 | UI-H-DF0-bem-a-10-0-UI.s1 NCI_CGAP_DF0 cDNA clone UI-H-DF0-bem-a-10-0-UI 3', mRNA sequence /clone=UI-H-DF0-bem-a-10-0-UI /clone_end=3' /gb=CA425521 /gi=24788247 /ug=Hs.411829 /len=1131 | CA425521 | Hs.411829 | |
| 12804 | 0.022033 | hypothetical protein FLJ38716 (FLJ38716), mRNA /cds=(266,1354) /gb=NM_152367 /gi=22748790 /ug=Hs.376194 /len=3229 | NM_152367 | Hs.376194 | NP_689580 |
| 12838 | 0.04789 | EST(mRNA from cd34 stem cells Homo sapiens cDNA clone CBFDE10) | AF150252 | | |
| 12846 | 0.035601 | EST, cDNA, 5' end. /clone=DKFZp761D0315 /clone_end=5' /gb=AL137968 /gi=6854648 /ug=Hs.256115 /len=523 | AL137968 | Hs.256115 | |
| 12851 | 0.041383 | FLJ11311 fis, clone PLACE1010102/cds=UNKNOWN /gb=AK002173 /gi=7023889 /ug=Hs.5518 /len=1839 | AK002173 | Hs.5518 | NP_689971 |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|-------|----------|--|--------------------|-----------------------|-----------------------|
| 12879 | 0.030485 | hypothetical protein FLJ22415 (FLJ22415), mRNA /cds=(342,1463) /gb=NM_024769 /gi=13376114 /ug=Hs.135121 /len=2627 | NM_024769 | Hs.135121 | NP_079045 |
| 12897 | 0.01081 | EST(cDNA clone IMAGE:6106210 5') | BQ438562 | | NP_005339 |
| 12898 | 0.022033 | 603395193F1.NIH_MGC_90 cDNA clone IMAGE:5405278 5', mRNA sequence /clone=IMAGE:5405278 /clone_end=5' /gb=BI871283 /gi=16044958 /ug=Hs.443147 /len=845 | BI871283 | Hs.443147 | |
| 12902 | 0.04789 | ESTs, FLJ25251 fis, clone STM03603 /cds=UNKNOWN /gb=AK057980 /gi=16553972 /ug=Hs.256801 /len=1727 | AK057980 | Hs.256801 | |
| 12903 | 0.025981 | cDNA FLJ33097 fis, clone TRACH2000775. /gb=AK057659 /gi=16553423 /ug=Hs.415317 /len=2977 | AK057659 | Hs.415317 | |
| 12907 | 0.005961 | UI-E-EO0-ahy-j-09-0-UI.r1 UI-E-EO0 cDNA clone UI-E-EO0-ahy-j-09-0-UI 5', mRNA sequence /clone=UI-E-EO0-ahy-j-09-0-UI /clone_end=5' /gb=BM722772 /gi=19043589 /ug=Hs.433569 /len=1166 | BM722772 | Hs.433569 | |
| 12921 | 0.035601 | BX106452 NCI_CGAP_Gas4 cDNA clone IMAGp998N095583, mRNA sequence /clone=IMAGp998N095583 IMAGE:2255816 /gb=BX106452 /gi=27834105 /ug=Hs.200841 /len=458 | BX106452 | Hs.200841 | |
| 12935 | 0.025981 | clone IMAGE:35115, mRNA sequence /gb=AF339818 /gi=13507356 /ug=Hs.326718 /len=1071 | AF339818 | Hs.326718 | |
| 12936 | 0.022033 | clone IMAGE:5263531, mRNA /gb=BC037740 /gi=22902216 /ug=Hs.18016 /len=5036 | BC037740 | Hs.18016 | |
| 12941 | 0.011207 | MR2-CI0186-291100-010-a06 CI0186 cDNA, mRNA sequence /gb=BF814502 /gi=12147047 /ug=Hs.446594 /len=530 | BF814502 | Hs.446594 | |
| 12973 | 0.04789 | ESTs, cDNA, 3' end /clone=IMAGE:2504343 /clone_end=3' /gb=AW009340 /gi=5858118 /ug=Hs.372482 /len=490 | AW009340 | Hs.372482 | |
| 12975 | 0.022033 | cDNA FLJ38271 fis, clone FCBBF3002782, moderately similar to Leptin receptor. /gb=AK095590 /gi=21754877 /ug=Hs.231895 /len=2435 | AK095590 | Hs.231895 | |
| 12996 | 0.025981 | cDNA FLJ11366 fis, clone HEMBA1000282. /gb=AK021428 /gi=10432610 /ug=Hs.189002 /len=2075 | AK021428 | Hs.189002 | |

| Spot | p-value | D scription | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|-------|----------|--|--------------------|-----------------------|-----------------------|
| 13005 | 0.035601 | zx55g04.r1 Soares_fetal_liver_spleen_1NFLS_S1 cDNA clone IMAGE:446454 5', mRNA sequence /clone=IMAGE:446454 /clone_end=5' /gb=AA203502 /gi=1799213 /ug=Hs.192991 /len=952 | AA203502 | Hs.192991 | |
| 13014 | 0.041383 | cDNA FLJ13334 fis, clone OVARC1001846 /gb=AK023396 /gi=10435315 /ug=Hs.269091 /len=2361 | AK023396 | Hs.269091 | |
| 13015 | 0.007453 | hypothetical protein FLJ31131 (FLJ31131), mRNA /cds=(20,421) /gb=NM_152535 /gi=22749108 /ug=Hs.23853 /len=1970 | NM_152535 | Hs.23853 | |
| 13041 | 0.004826 | AGENCOURT_8351558 NIH_MGC_113 cDNA clone IMAGE:6282273 5', mRNA sequence /clone=IMAGE:6282273 /clone_end=5' /gb=BQ706828 /gi=21845727 /ug=Hs.132759 /len=928. | BQ706828 | Hs.132759 | |
| 13074 | 0.007453 | EST(IL3-NT0280-050201-453-A10_1 NT0280 cDNA, MRNA sequence) | BI040412 | | |
| 13081 | 0.041383 | Novel | SEQ.ID.No.8 | | |
| 13128 | 0.030485 | chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1) (CXCL12), mRNA /cds=(81,362) /gb=NM_000609 /gi=10834987 /ug=Hs.237356 /len=3541 | NM_000609 | Hs.237356 | NP_000600 |
| 13135 | 0.00388 | (clone: SS20B/E6.0) HUMALAD10 alpha- adducin gene, exon 11 | L29298 | | |
| 13161 | 0.04789 | hypothetical protein FLJ10035 (FLJ10035), mRNA /cds=(251,1132) /gb=NM_030803 /gi=24475809 /ug=Hs.16390 /len=2404 | NM_030803 | Hs.16390 | NP_110430 |
| 13171 | 0.04789 | hypothetical gene supported by XM_064780 (LOC125750), mRNA | XM_064780 | | |
| 13194 | 0.008919 | putative serine-rich protein mRNA, partial cds (AF246705.1) | AF246705 | Hs.32922 | NP_060102 |
| 13212 | 0.004826 | hypothetical protein FLJ20060 (FLJ20060), mRNA /cds=(72,2078) /gb=NM_017645 /gi=24431978 /ug=Hs.54617 /len=2884 | NM_017645 | Hs.54617 | NP_060115 |
| 13228 | 0.041383 | membrane-spanning 4-domains, subfamily A, member 7 (MS4A7), mRNA /cds=(147,869) /gb=NM_021201 /gi=23110999 /ug=Hs.11090 /len=1257 | NM_021201 | Hs.11090 | NP_067024 |
| 13240 | 0.01859 | solute carrier family 38, member 2 (SLC38A2), mRNA /cds=(352,1872) /gb=NM_018976 /gi=21361601 /ug=Hs.298275 /len=4795 | NM_018976 | Hs.298275 | NP_061849 |
| 13255 | 0.04789 | FK506 binding protein 7 (FKBP7), mRNA /cds=(96,875) /gb=NM_016105 /gi=23618828 /ug=Hs.344379 /len=1067 | NM_016105 | Hs.344379 | NP_851939 |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|-------|----------|---|--------------------|-----------------------|-----------------------|
| 13280 | 0.022033 | cDNA FLJ13792 fis, clone THYRO1000072, weakly similar to MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC 2.7.1.117). /cds=(9,1337) /gb=AK023854 /gi=10435918 /ug=Hs.154751 /len=2184 | AK023854 | Hs.154751 | |
| 13282 | 0.022033 | LIS1-interacting protein NUDEL; endooligopeptidase A (NUDEL), mRNA /cds=(134,1171) /gb=NM_030808 /gi=13540599 /ug=Hs.3850 /len=2329 | NM_030808 | Hs.3850 | NP_110435 |
| 13308 | 0.04789 | ligand of numb-protein X (LNK), mRNA /cds=(236,2134) /gb=NM_032622 /gi=14249127 /ug=Hs.66295 /len=3737 | NM_032622 | Hs.66295 | NP_116011 |
| 13315 | 0.035601 | partial RANBP7 gene for RanBP7/importin7 and partial ZNF143 gene | AJ295844 | | |
| 13419 | 0.01081 | EST(oa56h11.r1 NCI_CGAP_GCB1 clone IMAGE:1309029 5' contains MER10.b3 MER10 MER10 repeat) | AA746385 | | |
| 13423 | 0.015602 | mRNA; cDNA DKFZp686E1027 (from clone DKFZp686E1027) /gb=AL832759 /gi=21733340 /ug=Hs.269418 /len=5327 | AL832759 | Hs.269418 | |
| 13513 | 0.013024 | EST(PM3-SN0020-270300-001-h08 SN0020) | AW865025 | | NP_115668 |
| 13515 | 0.013024 | EST(hh87d03.x1 NCI_CGAP_GU1 clone IMAGE:2969765 3' contains Alu repeat) | AW627545 | | |
| 13524 | 0.015602 | hypothetical protein DKFZp586C1924 (DKFZp586C1924), mRNA /cds=(106,693) /gb=NM_032273 /gi=14150016 /ug=Hs.108338 /len=782 | NM_032273 | Hs.108338 | NP_115649 |
| 13526 | 0.041383 | non-SMC (structural maintenance of chromosomes) element 1 protein (NSE1), mRNA /cds=(24,794) /gb=NM_145080 /gi=21489972 /ug=Hs.284295 /len=992 | NM_145080 | Hs.284295 | NP_659547 |
| 13565 | 0.01859 | EST ni39e06.s1 NCI_CGAP_Lu1 cDNA clone IMAGE:979234 3' similar to contains Alu repetitive element; contains MER10.t2 MER10 repetitive element; | AA522708 | | |
| 13569 | 0.030485 | EST (tu41c10.x1 NCI_CGAP_Pr28 cDNA clone IMAGE:2253618 3' similar to contains Alu repetitive element;) | AI686385 | | |
| 13595 | 0.035601 | zinc finger protein 274 (ZNF274), transcript variant ZNF274c, mRNA /cds=(460,2421) /gb=NM_133502 /gi=19743800 /ug=Hs.83761 /len=2839 | NM_133502 | Hs.83761 | NP_598009 |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Prot in Accession No. |
|-------|----------|--|--------------------|-----------------------|-----------------------|
| 13644 | 0.025981 | AGENCOURT_6497573 NIH_MGC_125 cDNA clone IMAGE:5588748 5', mRNA sequence /clone=IMAGE:5588748 /clone_end=5' /gb=BM544964 /gi=18776658 /ug=Hs.406354 /len=1184 | BM544964 | Hs.406354 | |
| 13677 | 0.025981 | KIAA1377 protein, partial cds /cds=UNKNOWN /gb=AB037798 /gi=7243134 /ug=Hs.188790 /len=3916 | AB037798 | Hs.188790 | |
| 13713 | 0.025981 | heterogeneous nuclear ribonucleoprotein H2 (H') (HNRPH2), mRNA /cds=(79,1428) /gb=NM_019597 /gi=14141155 /ug=Hs.278857 /len=2220 | NM_019597 | Hs.278857 | NP_062543 |
| 13748 | 0.041383 | Similar to likely ortholog of yeast ARV1, clone IMAGE:4106796, mRNA /gb=BC018945 /gi=17511970 /ug=Hs.290444 /len=3219 | BC018945 | Hs.290444 | |
| 13792 | 0.019692 | hypothetical protein MGC30052 (MGC30052), mRNA /cds=(35,703) /gb=NM_144721 /gi=21389506 /ug=Hs.143692 /len=2260 | NM_144721 | Hs.143692 | NP_653322 |
| 13811 | 0.04789 | hypothetical protein FLJ20360 (FLJ20360), mRNA /cds=(80,2305) /gb=NM_017782 /gi=8923334 /ug=Hs.26434 /len=3041 | NM_017782 | Hs.26434 | NP_060252 |
| 13828 | 0.030485 | core-binding factor, beta subunit (CBFB), transcript variant 2, mRNA /cds=(11,559) /gb=NM_001755 /gi=13124872 /ug=Hs.179881 /len=2883 | NM_001755 | Hs.179881 | NP_074036 |
| 13829 | 0.013024 | FLJ11463 fis, clone HEMBA1001608 /cds=UNKNOWN /gb=AK021525 /gi=10432722 /ug=Hs.288888 /len=1898 | AK021525 | Hs.288888 | |
| 13835 | 0.04789 | mRNA for KIAA1078 protein, partial cds. /cds=(1,4098) /gb=AB029001 /gi=20521755 /ug=Hs.23585 /len=6740 | AB029001 | Hs.23585 | |
| 13891 | 0.013024 | cDNA FLJ38641 fis, clone HHDPC2003983 /gb=AK095960 /gi=21755328 /ug=Hs.24831 /len=2685 | AK095960 | Hs.24831 | |
| 13913 | 0.008919 | EST(zx56f11.r1 Soares fetal liver spleen 1NFLS S1 cDNA clone 446541 5') | AA203529 | | |
| 13922 | 0.005961 | cDNA FLJ36579 fis, clone TRACH2012647 /gb=AK093898 /gi=21752852 /ug=Hs.48653 /len=2318 | AK093898 | Hs.48653 | |
| 13945 | 0.035601 | EST(tx88e11.x1 NCI_CGAP_Ut4 clone IMAGE:2276684 3' contains Alu repeat) | AI690725 | | |
| 13956 | 0.04789 | zh79h09.s1 Soares_fetal_liver_spleen_1NFLS_S1 cDNA clone IMAGE:418337 3', mRNA sequence /clone=IMAGE:418337 /clone_end=3' /gb=W92715 /gi=1421867 /ug=Hs.59358 /len=397 | W92715 | Hs.59358 | |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|-------|----------|--|--------------------|-----------------------|-----------------------|
| 13959 | 0.022033 | wi63d02.x1 NCI_CGAP_Kid12 cDNA clone IMAGE:2397987 3', mRNA sequence /clone=IMAGE:2397987 /clone_end=3' /gb=AI762877 /gi=5178544 /ug=Hs.369625 /len=467 | AI762877 | Hs.369625 | |
| 13969 | 0.041383 | EST(te50g08.x1 Soares_NFL_T_GBC_S1 clone IMAGE:2090174 3') | AI539295 | | |
| 13982 | 0.032841 | EST(nv54h12.r1 NCI_CGAP_Ew1 cDNA clone IMAGE:1233671) | AA721522 | | |
| 13992 | 0.003097 | EST oi10c01.s1 NCI_CGAP_GC4 IMAGE:1476096 3' | AA872487 | | NP_055862 |
| 13996 | 0.04789 | nuclear pore complex protein (NUP107), mRNA /cds=(116,2893) /gb=NM_020401 /gi=9966880 /ug=Hs.236204 /len=3131 | NM_020401 | Hs.236204 | NP_065134 |
| 14060 | 0.04789 | beta-amyloid binding protein precursor (BBP), mRNA /cds=(304,927) /gb=NM_032027 /gi=17738309 /ug=Hs.333541 /len=1250 | NM_032027 | Hs.333541 | NP_114416 |
| 14069 | 0.035601 | EST np77c06.s1 NCI_CGAP_Pr2 cDNA clone IMAGE:1132330 similar to contains Alu repetitive element; | AA622809 | | |
| 14074 | 0.030485 | EST tf62g05.x1 NCI_CGAP_Brn23 cDNA clone IMAGE:2103896 3' similar to gb:L21934 STEROL O-ACYLTRANSFERASE (HUMAN);contains L1.t1 L1 repetitive element ; | AI423779 | | |
| 14080 | 0.04789 | EST(af08g07.s1 Soares_testis_NHT cDNA clone IMAGE:1031100 3') | AA610081 | | |
| 14085 | 0.015602 | EST (np87f03.s1 NCI_CGAP_Thy1 IMAGE:1133309) | AA632677 | | |
| 14094 | 0.022033 | EST (wh67d04.x1 NCI_CGAP_Kid11 IMAGE:2385799 3') | AI766049 | | |
| 14105 | 0.030485 | Kruppel-like factor 12 (KLF12), transcript variant 1, mRNA /cds=(199,1407) /gb=NM_007249 /gi=21071073 /ug=Hs.23510 /len=10891 | NM_007249 | Hs.23510 | NP_057369 |
| 14163 | 0.013024 | EST(AV657608 GLC cDNA clone GLCFDF10 3') | AV657608 | | |
| 14169 | 0.025981 | UI-H-EI0-ayg-o-16-0-UI.s1 NCI_CGAP_EI0 cDNA clone UI-H-EI0-ayg-o-16-0-UI 3', mRNA sequence /clone=UI-H-EI0-ayg-o-16-0-UI /clone_end=3' /gb=CA449027 /gi=24813447 /ug=Hs.44888 /len=573 | CA449027 | Hs.44888 | |
| 14199 | 0.01859 | EST(HS-1029-A1-B05-MF.abi CIT Genomic Sperm Library C genomic clone) | B35426 | | |
| 14208 | 0.004826 | EST (qh03a05.x1 Soares_NFL_T_GBC_S1 IMAGE:1843568 3') | AI222189 | | NP_002547 |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|-------|----------|---|--------------------|-----------------------|-----------------------|
| 14247 | 0.04789 | clone IMAGE:4836898, mRNA /gb=BC042527 /gi=27502923 /ug=Hs.434231 /len=2935 | BC042527 | Hs.434231 | |
| 14250 | 0.025981 | ferritin, light polypeptide (FTL), mRNA /cds=(189,716) /gb=NM_000146 /gi=20149497 /ug=Hs.430150 /len=878 | NM_000146 | Hs.430150 | NP_000137 |
| 14295 | 0.013024 | cDNA: FLJ22765 fis, clone KAIA1180. /gb=AK026418 /gi=10439279 /ug=Hs.163986 /len=1994 | AK026418 | Hs.163986 | |
| 14300 | 0.041383 | twisted gastrulation 1 (Drosophila) (TWSG1), mRNA /cds=(106,777) /gb=NM_020648 /gi=21314788 /ug=Hs.247302 /len=3693 | NM_020648 | Hs.247302 | NP_065699 |
| 14307 | 0.00388 | EST(cDNA clone IMAGE:6104513 5') | BQ429184 | | |
| 14322 | 0.041383 | clone IMAGE:4297077, mRNA /gb=BC017920 /gi=17389820 /ug=Hs.375771 /len=1247 | BC017920 | Hs.375771 | |
| 14324 | 0.001162 | EST, cDNA, 3' end /clone=IMAGE:1692758 /clone_end=3' /gb=AI092853 /gi=3431829 /ug=Hs.134911 /len=486 | AI092853 | Hs.134911 | |
| 14339 | 0.030485 | 7a19b02.x1 NCI_CGAP_GC6 cDNA clone IMAGE:3219147 3' similar to contains element MER36 repetitive element ;, mRNA sequence /clone=IMAGE:3219147 /clone_end=3' /gb=BE503478 /gi=9705875 /ug=Hs.281956 /len=356 | BE503478 | Hs.281956 | |
| 14345 | 0.025981 | mRNA; cDNA DKFZp586E1624 (from clone DKFZp586E1624) /gb=AL110152 /gi=5817054 /ug=Hs.94030 /len=1341 | AL110152 | Hs.94030 | |
| 14353 | 0.035601 | cDNA FLJ31303 fis, clone LIVER1000082. /gb=AK055865 /gi=16550700 /ug=Hs.350200 /len=2801 | AK055865 | Hs.350200 | |
| 14390 | 0.008919 | BX097880 NCI_CGAP_Thy1 cDNA clone IMAGp998F242841, mRNA sequence /clone=IMAGp998F242841, IMAGE:11332 07 /gb=BX097880 /gi=27829041 /ug=Hs.208961 /len=354 | BX097880 | Hs.208961 | |
| 14415 | 0.004826 | ESTs, cDNA, 5' end /clone=IMAGE:4515481 /clone_end=5' /gb=BG292389 /gi=13051140 /ug=Hs.374490 /len=887 | BG292389 | Hs.374490 | |
| 14417 | 0.035601 | proteasome (prosome, macropain) subunit, alpha type, 4 (PSMA4), mRNA /cds=(137,922) /gb=NM_002789 /gi=23110940 /ug=Hs.251531 /len=1189 | NM_002789 | Hs.251531 | NP_002780 |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|-------|----------|--|--------------------|-----------------------|-----------------------|
| 14419 | 0.025981 | UI-H-ED0-awz-e-06-0-UI.s1 NCI_CGAP_ED0 cDNA clone IMAGE:5825645 3', mRNA sequence /clone=IMAGE:5825645 /clone_end=3' /gb=BM995013 /gi=19719914 /ug=Hs.23871 /len=1235 | BM995013 | Hs.23871 | |
| 14430 | 0.005961 | ib38b12.y1 HR85 islet cDNA 5', mRNA sequence /clone_end=5' /gb=BG656191 /gi=13793600 /ug=Hs.409469 /len=574 | BG656191 | Hs.409469 | |
| 14439 | 0.023482 | cDNA FLJ13571 fis, clone PLACE1008405. /gb=AK023633 /gi=10435617 /ug=Hs.116278 /len=2484 | AK023633 | Hs.116278 | |
| 14442 | 0.01859 | cDNA FLJ12924 fis, clone NT2RP2004709. /gb=AK022986 /gi=10434694 /ug=Hs.38034 /len=2667 | AK022986 | Hs.38034 | |
| 14443 | 0.025981 | nc77d11.s1 NCI_CGAP_Pr2 cDNA clone IMAGE:783381, mRNA sequence /clone=IMAGE:783381 /gb=AA468352 /gi=2194886 /ug=Hs.324201 /len=362 | AA468352 | Hs.324201 | |
| 14475 | 0.025981 | EST, cDNA: FLJ23266 fis, clone COL06676, highly similar to HUMFRCC Homo sapiens clone s153 mRNA | AK026919 | | |
| 14494 | 0.008919 | No significant match | SEQ.ID.No.70 | | |
| 14495 | 0.035601 | No significant match | SEQ.ID.No.74 | | |
| 14504 | 0.032841 | No significant match (ORF:none) | SEQ.ID.No.22 | | |
| 14533 | 0.01859 | cDNA FLJ33669 fis, clone BRAMY2028740. /cds=(1,456) /gb=AK090988 /gi=21749257 /ug=Hs.396949 /len=2106 | AK090988 | Hs.396949 | |
| 14537 | 0.030485 | EST (zv14e11.r1 Soares_NhHMPu_S1 cDNA clone IMAGE:753644 5') | AA479436 | | |
| 14552 | 0.011207 | hypothetical protein MGC18257 (MGC18257), mRNA /cds=(39,1415) /gb=NM_138569 /gi=20070373 /ug=Hs.350860 /len=1740 | NM_138569 | Hs.350860 | NP_612636 |
| 14554 | 0.038534 | clone 24707 mRNA sequence /gb=AF055007 /gi=3005728 /ug=Hs.124969 /len=1729 | AF055007 | Hs.124969 | |
| 14564 | 0.041383 | mRNA for KIAA2019 protein. /cds=(15,8408) /gb=AB095939 /gi=24899201 /ug=Hs.57548 /len=9217 | AB095939 | Hs.57548 | |
| 14565 | 0.025981 | oq98a10.x1 NCI_CGAP_Co12 cDNA clone IMAGE:1594362 3' similar to contains Alu repetitive element; mRNA sequence /clone=IMAGE:1594362 /clone_end=3' /gb=AI074369 /gi=3401013 /ug=Hs.386367 /len=478 | AI074369 | Hs.386367 | |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
|-------|----------|---|--------------------|-----------------------|-----------------------|
| 14567 | 0.04789 | UI-H-FH1-bfp-m-06-0-UI.s1 NCI_CGAP_FH1 cDNA clone UI-H-FH1-bfp-m-06-0-UI 3', mRNA sequence /clone=UI-H-FH1-bfp-m-06-0-UI /clone_end=3' /gb=BU619573 /gi=23285788 /ug=Hs.312629 /len=1168 | BU619573 | Hs.312629 | |
| 14579 | 0.016419 | EST(yv47g01.s1 Soares fetal liver spleen 1NFLS cDNA clone IMAGE:245904 3') | N55367 | | NP_004388 |
| 14612 | 0.04789 | EST (AL536815 LTI_FL013_FBrn1 clone CS0DF020YK05 5') | AL536815 | | |
| 14633 | 0.035601 | EST(no86d01.s1 NCI_CGAP_AA1 cDNA clone IMAGE:1113697 3') | AA614000 | | |
| 14637 | 0.002454 | hypothetical protein PRO1331 (PRO1331), mRNA /cds=(423,617) /gb=NM_030778 /gi=13562115 /ug=Hs.301824 /len=1634 | NM_030778 | Hs.301824 | NP_110405 |
| 14666 | 0.030485 | EST(QV4-DT0021-281299-070-a12 DT0021) | AW936306 | | |
| 14672 | 0.01081 | EST (xq76f01.x1 NCI_CGAP_HN11 cDNA clone IMAGE:2756569 3') | AW265747 | | |
| 14675 | 0.035601 | EST (wi81d01.x1 NCI_CGAP_Kid12 cDNA clone IMAGE:2399713 3') | AI765544 | | |
| 14717 | 0.035601 | cDNA FLJ32589 fis, clone SPLEN2000443. /gb=AK057151 /gi=16552741 /ug=Hs.21342 /len=2178 | AK057151 | Hs.21342 | |
| 14722 | 0.032841 | cDNA FLJ11439 fis, clone HEMBA1001299. /gb=AK021501 /gi=10432697 /ug=Hs.287416 /len=1500 | AK021501 | Hs.287416 | |
| 14741 | 0.025981 | FLJ13882 fis, clone THYRO1001480 /cds=UNKNOWN /gb=AK023944 /gi=10436040 /ug=Hs.301435 /len=2446 | AK023944 | Hs.301435 | |
| 14760 | 0.00302 | control | | | |
| 14763 | 0.004826 | EST(cDNA clone IMAGE:2224205 3'.) | AI589443 | | |
| 14766 | 0.035601 | cDNA FLJ30301.fis, clone BRACE2003217. /gb=AK054863 /gi=16549482 /ug=Hs.285728 /len=2186 | AK054863 | Hs.285728 | |
| 14770 | 0.041383 | EST48277 Fetal spleen cDNA 3' end similar to EST containing Alu repeat, mRNA sequence /clone_end=3' /gb=AA342474 /gi=1994946 /ug=Hs.291585 /len=430 | AA342474 | Hs.291585 | |
| 14774 | 0.013024 | clone IMAGE:5274897, mRNA /gb=BC037888 /gi=23138738 /ug=Hs.351680 /len=4246 | BC037888 | Hs.351680 | |
| 14775 | 0.01081 | ESTs, cDNA /gb=AW963042 /gi=8152878 /ug=Hs.53455 /len=769 | AW963042 | Hs.53455 | NP_003401 |
| 14777 | 0.015602 | UI-E-EJ0-ahn-c-06-0-UI.s1 UI-E-EJ0 cDNA clone UI-E-EJ0-ahn-c-06-0-UI 3', mRNA sequence /clone=UI-E-EJ0-ahn-c-06-0-UI /clone_end=3' /gb=BM674956 /gi=18984854 /ug=Hs.131705 /len=1017 | BM674956 | Hs.131705 | |

| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Prot in Accession No. |
|-------|----------|--|--------------------|-----------------------|-----------------------|
| 14830 | 0.04789 | EST(MR1-MT0282-151200-003-e12 MT0282 cDNA, mRNA sequence) | BF903180 | | |
| 14835 | 0.022033 | BX115107 Soares fetal liver spleen 1NFLS cDNA clone IMAGp998G12373, mRNA sequence /clone=IMAGp998G12373 _IMAGE:19587 5 /gb=BX115107 /gi=27839238 /ug=Hs.431087 /len=758 | BX115107 | Hs.431087 | |
| 14847 | 0.01859 | EST(UI-CF-DU1-aae-h-20-0-UI.s1 UI-CF-DU1 cDNA clone UI-CF-DU1-aae-h-20-0-UI 3') | BU674998 | | |
| 14871 | 0.022033 | EST, cDNA, 3' end /clone=IMAGE:2488402 /clone_end=3' /gb=AI970954 /gi=5767780 /ug=Hs.311478 /len=509 | AI970954 | Hs.311478 | |
| 14874 | 0.022033 | yp52f01.s1 Soares retina N2b4HR cDNA clone IMAGE:191065 3', mRNA sequence /clone=IMAGE:191065 /clone_end=3' /gb=H40700 /gi=916752 /ug=Hs.33792 /len=504 | H40700 | Hs.33792 | |
| 14884 | 0.022033 | 602043661F1 NCI_CGAP_Brn67 cDNA clone IMAGE:4181462 5', mRNA sequence /clone=IMAGE:4181462 /clone_end=5' /gb=BF528488 /gi=11615851 /ug=Hs.433462 /len=885 | BF528488 | Hs.433462 | |
| 14893 | 0.013024 | EST375707 MAGE resequences, MAGH cDNA, mRNA sequence /gb=AW963634 /gi=8153470 /ug=Hs.429581 /len=750 | AW963634 | Hs.429581 | |
| 14902 | 0.041383 | poly(rC) binding protein 2 (PCBP2), transcript variant 1, mRNA /cds=(89,1189) /gb=NM_005016 /gi=14141167 /ug=Hs.63525 /len=1362 | NM_005016 | Hs.63525 | NP_114366 |
| 14903 | 0.030485 | Saccharomyces cerevisiae chromosome XII, complete chromosome sequence | NC_001144 | | |
| 14924 | 0.001929 | No significant match, ORF-3(1~195) | SEQ.ID.No.57 | | |
| 14951 | 0.025981 | clone IMAGE:4820928, mRNA /gb=BC033530 /gi=23272327 /ug=Hs.324359 /len=2018 | BC033530 | Hs.324359 | |
| 14971 | 0.007315 | No significant match (ORF:+3: 3~180[179]) | SEQ.ID.No.20 | | |

| TABLE 3D | | | | | |
|--|----------|--|--------------------|-----------------------|-----------------------|
| Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids | | | | | |
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 21 | 0.011824 | telomeric repeat binding factor (NIMA-interacting) 1 (TERF1), transcript variant 1, mRNA /cds=(16,1335) /gb=NM_017489 /gi=9257245 /ug=Hs.194562 /len=2686 | NM_017489 | Hs.194562 | NP_059523 |
| 75 | 0.044639 | GC20 protein (=AF077052 protein translation factor sui1 homologue) | AF064607 | | NP_005866 |
| 201 | 0.026896 | Saccharomyces cerevisiae chromosome XII, complete chromosome sequence | NC_001144 | | |
| 233 | 0.034264 | mitochondrion, complete genome | NC_001807 | | |
| 328 | 0.020878 | EST(yj40f11.r1 clone 151245 5') | H02533 | | NP_705833 |
| 358 | 0.043185 | hypothetical protein FLJ35613 (FLJ35613), mRNA /cds=(126,2063) /gb=NM_173653 /gi=27734934 /ug=Hs.30022 /len=3568 | NM_173653 | Hs.30022 | NP_775924 |
| 368 | 0.043185 | mitochondrion, complete genome | NC_001807 | | |
| 467 | 0.026896 | small nuclear ribonucleoprotein polypeptide G (SNRPG), mRNA /cds=(89,319) /gb=NM_003096 /gi=21359839 /ug=Hs.77496 /len=606 | NM_003096 | Hs.77496 | NP_003087 |
| 662 | 0.048295 | insulin-like growth factor binding protein 5 (IGFBP5), mRNA /cds=(752,1570) /gb=NM_000599 /gi=10834981 /ug=Hs.380833 /len=1722 | NM_000599 | Hs.380833 | NP_000590 |
| 674 | 0.011207 | SMART/HDAC1 associated repressor protein (SHARP), mRNA /cds=(205,11199) /gb=NM_015001 /gi=14790189 /ug=Hs.184245 /len=12227 | NM_015001 | Hs.184245 | NP_055816 |
| 678 | 0.038517 | clone alpha_est218/52C1 mRNA sequence /gb=AF001542 /gi=2529714 /ug=Hs.356442 /len=2992 | AF001542 | Hs.356442 | |
| 690 | 0.043185 | mRNA for KIAA0518 protein, partial cds. /cds=(1,1953) /gb=AB011090 /gi=3043559 /ug=Hs.23763 /len=4617 | AB011090 | Hs.23763 | |
| 700 | 0.038517 | major histocompatibility complex, class II, DR alpha (HLA-DRA), mRNA /cds=(65,829) /gb=NM_019111 /gi=18641378 /ug=Hs.409805 /len=1237 | NM_019111 | Hs.409805 | NP_061984 |
| 721 | 0.002459 | mitochondrion, complete genome | NC_001807 | | |
| 726 | 0.002051 | tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide (YWHAG), mRNA /cds=(192,935) /gb=NM_012479 /gi=21464100 /ug=Hs.25001 /len=3747 | NM_012479 | Hs.25001 | NP_036611 |

| Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids | | | | | |
|--|----------|--|--------------------|---------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession N | Protein Accession No. |
| 736 | 0.034264 | myosin, heavy polypeptide 11, smooth muscle (MYH11), transcript variant SM2, mRNA /cds=(89,5905) /gb=NM_022844 /gi=13124874 /ug=Hs.78344 /len=6900 | NM_022844 | Hs.78344 | NP_074035 |
| 806 | 0.043185 | ring finger protein 19 (RNF19), mRNA /cds=(318,2834) /gb=NM_015435 /gi=19923421 /ug=Hs.48320 /len=4357 | NM_015435 | Hs.48320 | NP_056250 |
| 807 | 0.007812 | KIAA0102 gene product (KIAA0102), mRNA /cds=(308,679) /gb=NM_014752 /gi=7661907 /ug=Hs.77665 /len=1370 | NM_014752 | Hs.77665 | NP_055567 |
| 808 | 0.043185 | PIX1 mRNA (ORF) | AF037219 | | NP_570854 |
| 829 | 0.026896 | zinc finger protein 103 (mouse) (ZFP103), mRNA /cds=(923,2980) /gb=NM_005667 /gi=5031824 /ug=Hs.155968 /len=3423 | NM_005667 | Hs.155968 | NP_005658 |
| 834 | 0.048295 | tetraspan 3 (TSPAN-3), mRNA /cds=(218,979) /gb=NM_005724 /gi=21264581 /ug=Hs.100090 /len=1842 | NM_005724 | Hs.100090 | NP_005715 |
| 837 | 0.034264 | serine/arginine repetitive matrix 2 (SRRM2), mRNA /cds=(226,8484) /gb=NM_016333 /gi=19923465 /ug=Hs.197114 /len=9027 | NM_016333 | Hs.197114 | NP_057417 |
| 846 | 0.048295 | LAG1 longevity assurance 2 (S. cerevisiae) (LASS2), mRNA /cds=(50,742) /gb=NM_013384 /gi=9937997 /ug=Hs.285976 /len=1646 | NM_013384 | Hs.285976 | NP_071358 |
| 923 | 0.001703 | eukaryotic translation initiation factor 3, subunit 3 gamma, 40kDa (EIF3S3), mRNA /cds=(6,1064) /gb=NM_003756 /gi=4503514 /ug=Hs.58189 /len=1280 | NM_003756 | Hs.58189 | NP_003747 |
| 980 | 0.038517 | cleavage and polyadenylation specific factor 6, 68kDa (CPSF6), mRNA /cds=(35,1690) /gb=NM_007007 /gi=5901927 /ug=Hs.64542 /len=3426 | NM_007007 | Hs.64542 | NP_008938 |
| 1008 | 0.038517 | Alg5, S. cerevisiae, of (ALG5), mRNA /cds=(28,1002) /gb=NM_013338 /gi=9665250 /ug=Hs.227933 /len=1125 | NM_013338 | Hs.227933 | NP_037470 |
| 1058 | 0.006699 | Williams-Beuren syndrome chromosome region 1 (WBSCR1), transcript variant 1, mRNA /cds=(9,755) /gb=NM_022170 /gi=11559922 /ug=Hs.180900 /len=2546 | NM_022170 | Hs.180900 | NP_114381 |
| 1122 | 0.043185 | RAB1B, member RAS oncogene family (RAB1B), mRNA /cds=(48,653) /gb=NM_030981 /gi=13569961 /ug=Hs.300816 /len=1985 | NM_030981 | Hs.300816 | NP_112243 |

| Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids | | | | | |
|--|----------|---|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | UniGene Accession No. | Protein Accession No. |
| 1168 | 0.048295 | thymosin, beta 4, X chromosome (TMSB4X), mRNA /cds=(78,212) /gb=NM_021109 /gi=11056060 /ug=Hs.75968 /len=556 | NM_021109 | Hs.75968 | NP_066932 |
| 1196 | 0.012137 | FK506 binding protein 14, 22 kDa (FKBP14), mRNA /cds=(146,781) /gb=NM_017946 /gi=8923658 /ug=Hs.264636 /len=2248 | NM_017946 | Hs.264636 | NP_060416 |
| 1236 | 0.018314 | matrix metalloproteinase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV collagenase) (MMP9), mRNA /cds=(20,2143) /gb=NM_004994 /gi=4826835 /ug=Hs.151738 /len=2334 | NM_004994 | Hs.151738 | NP_004985 |
| 1301 | 0.001408 | actin, beta (ACTB), mRNA /cds=(74,1201) /gb=NM_001101 /gi=5016088 /ug=Hs.426930 /len=1793 | NM_001101 | Hs.426930 | NP_001092 |
| 1313 | 0.046968 | Similar to LYRIC, clone MGC.41931 IMAGE:5298467, mRNA, complete cds /cds=(329,2077) /gb=BC045642 /gi=28277146 /ug=Hs.243901 /len=3729 | BC045642 | Hs.243901 | |
| 1375 | 0.020878 | similar to embryonic seven-span transmembrane protein-like protein (H. sapiens) (LOC135428), mRNA | XM_059770 | | |
| 1419 | 0.012137 | CD74 antigen (invariant polypeptide of major histocompatibility complex, class II antigen-associated) (CD74), mRNA /cds=(8,706) /gb=NM_004355 /gi=10835070 /ug=Hs.84298 /len=1304 | NM_004355 | Hs.84298 | NP_004346 |
| 1455 | 0.026896 | CDC5 cell division cycle 5-like (S. pombe) (CDC5L), mRNA /cds=(260,2668) /gb=NM_001253 /gi=16357499 /ug=Hs.155174 /len=3012 | NM_001253 | Hs.155174 | NP_001244 |
| 1456 | 0.012137 | CGI-74 protein (CGI-59), mRNA /cds=(1,1209) /gb=NM_016019 /gi=7706309 /ug=Hs.7194 /len=2296 | NM_016019 | Hs.7194 | NP_057103 |
| 1497 | 0.030399 | hypothetical protein MGC45474 (MGC45474), mRNA /cds=(218,2035) /gb=NM_152369 /gi=22748794 /ug=Hs.234101 /len=2384 | NM_152369 | Hs.234101 | |
| 1520 | 0.034264 | mRNA; cDNA DKFZp686G1167 (from clone DKFZp686G1167) /gb=AL833600 /gi=21734246 /ug=Hs.7720 /len=8355 | AL833600 | Hs.7720 | NP_001367 |
| 1565 | 0.016017 | NADH dehydrogenase (ubiquinone) flavoprotein 3, 10kDa (NDUFV3), mRNA /cds=(575,1945) /gb=NM_021075 /gi=21361323 /ug=Hs.59745 /len=2023 | NM_021075 | Hs.59745 | NP_066553 |
| 1599 | 0.048295 | protein XP_037672 (aa, 58%) | XP_037672 | | |

| Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids | | | | | |
|--|----------|---|--------------------------|-----------------------------|-----------------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 1647 | 0.038517 | asporin (LRR class 1) (ASPN), mRNA /cds=(228,1373) /gb=NM_017680 /gi=16596677 /ug=Hs.10760 /len=2466 | NM_017680 | Hs.10760 | NP_060150 |
| 1673 | 0.026896 | endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1 (HERPUD1), mRNA /cds=(96,1271) /gb=NM_014685 /gi=7661869 /ug=Hs.146393 /len=1884 | NM_014685 | Hs.146393 | NP_055500 |
| 1682 | 0.030399 | mRNA; cDNA DKFZp586A061 (from clone DKFZp586A061) /gb=AL080232 /gi=5262725 /ug=Hs.220696 /len=3052 | AL080232 | Hs.220696 | |
| 1683 | 0.038517 | mitochondrion, complete genome | NC_001807 | | |
| 1722 | 0.004872 | S100 calcium binding protein A11 (calgizzarin) (S100A11), mRNA /cds=(121,438) /gb=NM_005620 /gi=5032056 /ug=Hs.417004 /len=595 | NM_005620 | Hs.417004 | NP_005611 |
| 1741 | 0.048295 | mRNA; cDNA DKFZp586F1822 (from clone DKFZp586F1822) /gb=AL117461 /gi=5911922 /ug=Hs.82719 /len=3943 | AL117461 | Hs.82719 | |
| 1763 | 0.009079 | zinc finger protein 36, C3H type-like 1 (ZFP36L1), mRNA /cds=(131,1147) /gb=NM_004926 /gi=15812179 /ug=Hs.85155 /len=3022 | NM_004926 | Hs.85155 | NP_004917 |
| 1787 | 0.043185 | ras gene family, member E (ARHE), mRNA /cds=(141,875) /gb=NM_005168 /gi=21361257 /ug=Hs.6838 /len=2685 | NM_005168 | Hs.6838 | NP_005159 |
| 1954 | 0.043185 | glycolipid transfer protein (GLTP), mRNA /cds=(115,744) /gb=NM_016433 /gi=20357594 /ug=Hs.381256 /len=1449 | NM_016433 | Hs.381256 | NP_057517 |
| 1999 | 0.005723 | chromosome 20 open reading frame 40 (C20orf40), mRNA /cds=(208,396) /gb=NM_014054 /gi=7661709 /ug=Hs.105379 /len=417 | NM_014054 | Hs.105379 | NP_054773 |
| 2032 | 0.024701 | histone acetyltransferase (HBOA), mRNA /cds=(43,1878) /gb=NM_007067 /gi=5901961 /ug=Hs.21907 /len=3504 | NM_007067 | Hs.21907 | NP_008998 |
| 2062 | 0.048295 | ovarian carcinoma immunoreactive antigen (OCIA), mRNA /cds=(168,905) /gb=NM_017830 /gi=8923426 /ug=Hs.132071 /len=1434 | NM_017830 | Hs.132071 | NP_060300 |
| 2064 | 0.010515 | FK506 binding protein 5 (FKBP5), mRNA /cds=(154,1527) /gb=NM_004117 /gi=17149847 /ug=Hs.7557 /len=3781 | NM_004117 | Hs.7557 | NP_004108 |
| 2103 | 0.004131 | SRY (sex determining region Y)-box 12 (SOX12), mRNA /cds=(331,1278) /gb=NM_006943 /gi=21264338 /ug=Hs.43627 /len=4645 | NM_006943 | Hs.43627 | NP_008874 |

| Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids | | | | | |
|--|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 2104 | 0.010245 | hPMS3 mRNA, partial cds. /cds=(1,773) /gb=D38435 /gi=600590 /ug=Hs.334451 /len=846 | D38435 | Hs.334451 | |
| 2112 | 0.026896 | NRH:quinone oxidoreductase 2 gene (NQO2) | AB050248 | | |
| 2150 | 0.043185 | ferritin, heavy polypeptide 1 (FTH1), mRNA /cds=(92,664) /gb=NM_002032 /gi=4503794 /ug=Hs.418650 /len=801 | NM_002032 | Hs.418650 | NP_002023 |
| 2171 | 0.043185 | zinc finger protein 202 (ZNF202), mRNA /cds=(11,1957) /gb=NM_003455 /gi=10835040 /ug=Hs.9443 /len=4053 | NM_003455 | Hs.9443 | NP_003446 |
| 2190 | 0.043185 | Deleted in split-hand/split-foot 1 region (DSS1), mRNA /cds=(129,341) /gb=NM_006304 /gi=5453639 /ug=Hs.333495 /len=509 | NM_006304 | Hs.333495 | NP_006295 |
| 2212 | 0.018314 | chromosome 21 open reading frame 4 (C21orf4), mRNA /cds=(159,635) /gb=NM_006134 /gi=8659558 /ug=Hs.284142 /len=750 | NM_006134 | Hs.284142 | NP_006125 |
| 2213 | 0.005723 | CGI-99 protein (CGI-99), mRNA /cds=(162,896) /gb=NM_016039 /gi=7706321 /ug=Hs.110803 /len=1105 | NM_016039 | Hs.110803 | NP_057123 |
| 2237 | 0.043185 | mRNA; cDNA DKFZp667F074 (from clone DKFZp667F074) /cds=(1,2388) /gb=AL834362 /gi=21740016 /ug=Hs.378933 /len=4245 | AL834362 | Hs.378933 | |
| 2242 | 0.030399 | uncharacterized hypothalamus protein HT010 (HT010), mRNA /cds=(227,1420) /gb=NM_018471 /gi=8923807 /ug=Hs.6375 /len=2140 | NM_018471 | Hs.6375 | NP_060941 |
| 2313 | 0.034264 | Putative prostate cancer tumor suppressor (N33), mRNA /cds=(149,1195) /gb=NM_006765 /gi=6996933 /ug=Hs.71119 /len=1521 | NM_006765 | Hs.71119 | NP_839952 |
| 2319 | 0.002459 | retinol dehydrogenase 11 (all-trans and 9-cis) (RDH11), mRNA /cds=(41,997) /gb=NM_016026 /gi=20070271 /ug=Hs.179817 /len=2538 | NM_016026 | Hs.179817 | NP_057110 |
| 2399 | 0.009079 | mitochondrion, complete genome | NC_001807 | | |
| 2404 | 0.048295 | keratan sulfate proteoglycan | AF063301 | | NP_008966 |
| 2498 | 0.034264 | ORF2 [Canis familiaris](60%) | AB012223 | | |
| 2499 | 0.026896 | dynein, cytoplasmic, light intermediate polypeptide 1 (DNCL1), mRNA /cds=(81,1652) /gb=NM_016141 /gi=7705852 /ug=Hs.266483 /len=2487 | NM_016141 | Hs.266483 | NP_057225 |
| 2501 | 0.048295 | replication protein A2, 32kDa (RPA2), mRNA /cds=(292,1104) /gb=NM_002946 /gi=21314636 /ug=Hs.79411 /len=1750 | NM_002946 | Hs.79411 | NP_002937 |

| Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids | | | | | |
|--|----------|---|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 2507 | 0.007812 | cDNA FLJ13552 fis, clone PLACE1007218. /gb=AK023614 /gi=10435594 /ug=Hs.204945 /len=1850 | AK023614 | Hs.204945 | |
| 2534 | 0.016017 | dendritic cell protein (GA17), mRNA /cds=(53,1177) /gb=NM_006360 /gi=23397428 /ug=Hs.406648 /len=1268 | NM_006360 | Hs.406648 | NP_006351 |
| 2549 | 0.030399 | Tax1 T-cell leukemia virus type I) binding protein 1 (TAX1BP1), mRNA /cds=(89,2458) /gb=NM_006024 /gi=21361681 /ug=Hs.5437 /len=3028 | NM_006024 | Hs.5437 | NP_006015 |
| 2557 | 0.016017 | leucine-rich PPR-motif containing (LRPPRC), mRNA /cds=(46,3867) /gb=NM_133259 /gi=18959201 /ug=Hs.182490 /len=4782 | NM_133259 | Hs.182490 | NP_573566 |
| 2578 | 0.034264 | G protein Golf alpha gene | U55184 | | |
| 2617 | 0.026896 | collagen, type I, alpha 1 (COL1A1), mRNA /cds=(120,4514) /gb=NM_000088 /gi=14719826 /ug=Hs.172928 /len=5921 | NM_000088 | Hs.172928 | NP_000079 |
| 2624 | 0.012137 | RAB27A, member RAS oncogene family (RAB27A), mRNA /cds=(246,911) /gb=NM_004580 /gi=19923263 /ug=Hs.50477 /len=2496 | NM_004580 | Hs.50477 | NP_004571 |
| 2681 | 0.038517 | HBS1-like (S. cerevisiae) (HBS1L), mRNA /cds=(194,2248) /gb=NM_006620 /gi=24431963 /ug=Hs.221040 /len=7163 | NM_006620 | Hs.221040 | NP_006611 |
| 2703 | 0.010515 | clone IMAGE:5259179, mRNA /gb=BC035034 /gi=23958339 /ug=Hs.174905 /len=3863 | BC035034 | Hs.174905 | |
| 2747 | 0.048295 | signal transducing adaptor molecule (SH3 domain and ITAM motif) 1 (STAM) | NM_003473 | | NP_003464 |
| 2790 | 0.023731 | choroideremia (Rab escort protein 1) (CHM), transcript variant 2950156, mRNA /cds=(31,1992) /gb=NM_000390 /gi=9966760 /ug=Hs.2010 /len=2115 | NM_000390 | Hs.2010 | NP_000381 |
| 2801 | 0.034264 | Rattus norvegicus mitochondrial genome | NC_001665 | | |
| 2824 | 0.034264 | xeroderma pigmentosum, complementation group C (XPC), mRNA /cds=(16,2838) /gb=NM_004628 /gi=20127459 /ug=Hs.320 /len=3658 | NM_004628 | Hs.320 | NP_004619 |
| 2830 | 0.004131 | stem-loop (histone) binding protein (SLBP), mRNA /cds=(116,928) /gb=NM_006527 /gi=19913344 /ug=Hs.75257 /len=1743 | NM_006527 | Hs.75257 | NP_006518 |

| Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids | | | | | |
|--|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 2839 | 0.043185 | synovial sarcoma translocation gene on chromosome 18-like 1 (SS18L1), mRNA /cds=(61,1251) /gb=NM_015558 /gi=27754185 /ug=Hs.154429 /len=3723 | NM_015558 | Hs.154429 | NP_056373 |
| 2843 | 0.020878 | UI-E-EJ0-ahj-n-19-0-UI.r1 UI-E-EJ0 cDNA clone UI-E-EJ0-ahj-n-19-0-UI 5', mRNA sequence /clone=UI-E-EJ0-ahj-n-19-0-UI /clone_end=5' /gb=BM701108 /gi=19014366 /ug=Hs.401941 /len=1923 | BM701108 | Hs.401941 | |
| 2855 | 0.043185 | likely ortholog of mouse dynactin 6 (DCTN6), mRNA /cds=(88,660) /gb=NM_006571 /gi=18426895 /ug=Hs.39913 /len=1044 | NM_006571 | Hs.39913 | NP_006562 |
| 2859 | 0.020878 | lysyl-tRNA synthetase (KARS), mRNA /cds=(41,1834) /gb=NM_005548 /gi=5031814 /ug=Hs.3100 /len=1997 | NM_005548 | Hs.3100 | NP_005539 |
| 2870 | 0.043185 | threonyl-tRNA synthetase (TARS), mRNA /cds=(135,2270) /gb=NM_152295 /gi=25054078 /ug=Hs.84131 /len=2662 | NM_152295 | Hs.84131 | NP_689508 |
| 2926 | 0.030399 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 24 (DDX24), mRNA /cds=(100,2679) /gb=NM_020414 /gi=14251213 /ug=Hs.155986 /len=2967 | NM_020414 | Hs.155986 | NP_065147 |
| 2932 | 0.018314 | cyclin D binding myb-like transcription factor 1 (DMTF1), mRNA /cds=(276,2558) /gb=NM_021145 /gi=10863946 /ug=Hs.5671 /len=3767 | NM_021145 | Hs.5671 | NP_066968 |
| 2946 | 0.003489 | CD164 antigen, sialomucin (CD164), mRNA /cds=(94,687) /gb=NM_006016 /gi=21361273 /ug=Hs.43910 /len=3038 | NM_006016 | Hs.43910 | NP_006007 |
| 2976 | 0.043185 | myosin, light polypeptide 6, alkali, smooth muscle and non-muscle (MYL6), transcript variant 3, mRNA /cds=(41,514) /gb=NM_079425 /gi=17986263 /ug=Hs.77385 /len=717 | NM_079425 | Hs.77385 | NP_524149 |
| 2980 | 0.009079 | mRNA for KIAA0121 protein, partial cds. /cds=(411,1301) /gb=D50911 /gi=6633996 /ug=Hs.155584 /len=3787 | D50911 | Hs.155584 | |
| 3013 | 0.012137 | uncharacterized hematopoietic stem/progenitor cells protein MDS031 (MDS031), mRNA /cds=(35,532) /gb=NM_018466 /gi=20070304 /ug=Hs.110853 /len=1358 | NM_018466 | Hs.110853 | NP_060936 |
| 3024 | 0.043185 | mRNA; cDNA DKFZp434J214 (from clone DKFZp434J214); partial cds /cds=(1,1082) /gb=AL080156 /gi=5262614 /ug=Hs.12813 /len=2749 | AL080156 | Hs.12813 | NP_056323 |

| Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids | | | | | |
|--|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 3050 | 0.043185 | DnaJ (Hsp40) subfamily B, member 9 (DNAJB9), mRNA /cds=(203,874) /gb=NM_012328 /gi=9558754 /ug=Hs.6790 /len=2371 | NM_012328 | Hs.6790 | NP_036460 |
| 3051 | 0.038517 | clone MGC:45564 IMAGE:4384472, mRNA, complete cds /cds=(188,1123) /gb=BC036746 /gi=22477830 /ug=Hs.132230 /len=3767 | BC036746 | Hs.132230 | |
| 3052 | 0.034264 | NADH dehydrogenase (ubiquinone) 1, beta subcomplex, 6, 17kDa (NDUFB6), mRNA /cds=(104,490) /gb=NM_002493 /gi=20149518 /ug=Hs.109646 /len=733 | NM_002493 | Hs.109646 | NP_002484 |
| 3062 | 0.010515 | myosin, light polypeptide, regulatory, non-sarcomeric (20kD) (MLCB), mRNA /cds=(115,630) /gb=NM_006471 /gi=5453739 /ug=Hs.180224 /len=944 | NM_006471 | Hs.180224 | NP_006462 |
| 3067 | 0.043185 | mitochondrion, complete genome | NC_001807 | | |
| 3088 | 0.034264 | sulfotransferase family, cytosolic, 1C, member 2 (SULT1C2), mRNA /cds=(330,1238) /gb=NM_006588 /gi=5730070 /ug=Hs.312644 /len=2143 | NM_006588 | Hs.312644 | NP_006579 |
| 3098 | 0.030399 | malate dehydrogenase 1, NAD (soluble) (MDH1), mRNA /cds=(57,1061) /gb=NM_005917 /gi=21735619 /ug=Hs.75375 /len=1268 | NM_005917 | Hs.75375 | NP_005908 |
| 3100 | 0.013965 | polymerase (DNA-directed) kappa (POLK), mRNA /cds=(173,2785) /gb=NM_016218 /gi=7705343 /ug=Hs.135756 /len=4074 | NM_016218 | Hs.135756 | NP_057302 |
| 3116 | 0.034264 | Hypothetical protein(cDNA FLJ11299 fis, clone PLACE1009845, highly similar to KIAA0905 protein) | AK002161 | | NP_057295 |
| 3140 | 0.034264 | DKFZp451H2115_r1 451 (synonym: hlcc1) spinal cord cDNA clone DKFZp451H2115 5', mRNA sequence /clone=DKFZp451H2115 /clone_end=5' /gb=AL589315 /gi=13243087 /ug=Hs.332004 /len=517 | AL589315 | Hs.332004 | |
| 3144 | 0.016017 | solute carrier family 20 (phosphate transporter), member 1 (SLC20A1), mRNA /cds=(371,2410) /gb=NM_005415 /gi=7382462 /ug=Hs.78452 /len=3220 | NM_005415 | Hs.78452 | NP_005406 |
| 3147 | 0.005723 | PRO0659 protein (PRO0659), mRNA /cds=(60,584) /gb=NM_014138 /gi=7662583 /ug=Hs.6451 /len=1416 | NM_014138 | Hs.6451 | NP_054857 |
| 3187 | 0.034264 | clone IMAGE:5229459, mRNA /gb=BC044229 /gi=28277403 /ug=Hs.266263 /len=2044 | BC044229 | Hs.266263 | |

| Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids | | | | | |
|--|----------|---|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 3207 | 0.038517 | hypothetical protein LOC51240 (LOC51240), mRNA /cds=(59,520) /gb=NM_016467 /gi=24475967 /ug=Hs.7870 /len=1017 | NM_016467 | Hs.7870 | NP_057551 |
| 3228 | 0.006699 | cDNA FLJ13234 fis, clone OVARC1000302. /gb=AK023296 /gi=10435170 /ug=Hs.240075 /len=1713 | AK023296 | Hs.240075 | |
| 3291 | 0.018314 | clathrin, light polypeptide (Lca) (CLTA), transcript variant brain-specific, mRNA /cds=(75,821) /gb=NM_007096 /gi=6005992 /ug=Hs.104143 /len=1105 | NM_007096 | Hs.104143 | NP_009027 |
| 3318 | 0.026896 | endothelial protein C receptor | AB026584 | | |
| 3334 | 0.016017 | cDNA: FLJ23307 fis, clone HEP11549, highly similar to AF041037 novel antagonist of FGF signaling (sprouty-1) mRNA. /gb=AK026960 /gi=10439945 /ug=Hs.88044 /len=2520 | AK026960 | Hs.88044 | |
| 3354 | 0.006699 | ribosomal protein L23 (RPL23), mRNA /cds=(27,449) /gb=NM_000978 /gi=14591907 /ug=Hs.234518 /len=493 | NM_000978 | Hs.234518 | NP_000969 |
| 3390 | 0.023731 | phosphoribosyl pyrophosphate synthetase-associated protein 2 (PRPSAP2), mRNA /cds=(212,1321) /gb=NM_002767 /gi=22538484 /ug=Hs.13339 /len=1890 | NM_002767 | Hs.13339 | NP_002758 |
| 3420 | 0.026896 | heat shock 70kDa protein 8 (HSPA8), transcript variant 1, mRNA /cds=(79,2019) /gb=NM_006597 /gi=24234684 /ug=Hs.180414 /len=2276 | NM_006597 | Hs.180414 | NP_694881 |
| 3426 | 0.038517 | Escherichia coli K-12 MG1655 section 343 of 400 of the complete genome | AE000453 | | |
| 3433 | 0.048295 | interferon induced transmembrane protein 3 (1-8U) (IFITM3), mRNA /cds=(238,639) /gb=NM_021034 /gi=11995467 /ug=Hs.381234 /len=808 | NM_021034 | Hs.381234 | NP_066362 |
| 3471 | 0.018314 | RAN, member RAS oncogene family (RAN), mRNA /cds=(115,765) /gb=NM_006325 /gi=6042206 /ug=Hs.10842 /len=1656 | NM_006325 | Hs.10842 | NP_006316 |
| 3521 | 0.048295 | ubiquitin-like, containing PHD and RING finger domains 2 (URF2), transcript variant 1, mRNA /cds=(341,1852) /gb=NM_152306 /gi=23312361 /ug=Hs.348602 /len=3720 | NM_152306 | Hs.348602 | NP_690856 |
| 3535 | 0.004131 | mRNA; cDNA DKFZp761C169 (from clone DKFZp761C169); partial cds /cds=(997,2475) /gb=AL161991 /gi=7328122 /ug=Hs.71252 /len=3324 | AL161991 | Hs.71252 | NP_075064 |
| 3564 | 0.018314 | SOX6 (SOX6) gene | AF309471 | | |

| Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids | | | | | |
|--|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 3607 | 0.016017 | mitochondrion, complete genome | NC_001807 | | |
| 3650 | 0.023731 | hypothetical protein FLJ10326 (FLJ10326), mRNA /cds=(3,2297) /gb=NM_018060 /gi=8922355 /ug=Hs.262823 /len=3016 | NM_018060 | Hs.262823 | NP_060530 |
| 3751 | 0.018314 | S100 calcium binding protein A11 (calgizzarin) (S100A11), mRNA /cds=(121,438) /gb=NM_005620 /gi=5032056 /ug=Hs.417004 /len=595 | NM_005620 | Hs.417004 | NP_005611 |
| 3755 | 0.010515 | zinc finger protein 84 (HPF2) (ZNF84), mRNA /cds=(352,2568) /gb=NM_003428 /gi=4508036 /ug=Hs.9450 /len=3257 | NM_003428 | Hs.9450 | NP_003419 |
| 3793 | 0.043185 | myosin, light polypeptide 5, regulatory (MYL5), mRNA /cds=(106,627) /gb=NM_002477 /gi=4505304 /ug=Hs.170482 /len=661 | NM_002477 | Hs.170482 | NP_002468 |
| 3840 | 0.009079 | sorcin (SRI), mRNA /cds=(13,609) /gb=NM_003130 /gi=4507206 /ug=Hs.422340 /len=952 | NM_003130 | Hs.422340 | NP_003121 |
| 3852 | 0.048295 | matrilin 3 (MATN3) precursor, mRNA /cds=(64,1524) /gb=NM_002381 /gi=13518040 /ug=Hs.278461 /len=2599 | NM_002381 | Hs.278461 | NP_002372 |
| 3861 | 0.007812 | basigin (BSG), mRNA /cds=(58,867) /gb=NM_001728 /gi=4502458 /ug=Hs.74631 /len=1638 | NM_001728 | Hs.74631 | NP_001719 |
| 3888 | 0.030399 | SAC2 suppressor of actin mutations 2-like (yeast) (SACM2L), transcript variant 1, mRNA /cds=(245,2416) /gb=NM_080564 /gi=18379336 /ug=Hs.169407 /len=2985 | NM_080564 | Hs.169407 | NP_542131 |
| 3911 | 0.012137 | mitochondrion, complete genome | NC_001807 | | |
| 3938 | 0.023731 | mitochondrion, complete genome | NC_001807 | | |
| 3944 | 0.013965 | mitochondrion, complete genome | NC_001807 | | |
| 3951 | 0.034264 | ATP synthase, H transporting, mitochondrial F1 complex, gamma polypeptide 1 (ATP5C1), mRNA /cds=(32,925) /gb=NM_005174 /gi=4885078 /ug=Hs.155433 /len=1078 | NM_005174 | Hs.155433 | NP_005165 |
| 3991 | 0.001703 | LGMD2B | AJ007973 | | |
| 4004 | 0.043185 | bromodomain containing 2 (BRD2), mRNA /cds=(1702,4107) /gb=NM_005104 /gi=12408641 /ug=Hs.75243 /len=4693 | NM_005104 | Hs.75243 | NP_005095 |
| 4046 | 0.030399 | polymerase (RNA) II (DNA directed) polypeptide C, 33kDa (POLR2C), transcript variant gamma, mRNA /cds=(58,885) /gb=NM_032940 /gi=14702170 /ug=Hs.79402 /len=1782 | NM_032940 | Hs.79402 | NP_116558 |

| Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids | | | | | |
|--|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 4051 | 0.020878 | methyl CpG binding protein 2 (Rett syndrome) (MECP2), mRNA /cds=(168,1628) /gb=NM_004992 /gi=7710148 /ug=Hs.3239 /len=10182 | NM_004992 | Hs.3239 | NP_004983 |
| 4054 | 0.010515 | histamine N-methyltransferase (HNMT), mRNA /cds=(253,1131) /gb=NM_006895 /gi=5901969 /ug=Hs.81182 /len=1667 | NM_006895 | Hs.81182 | NP_008826 |
| 4090 | 0.048295 | AGENCOURT_6413683 NIH_MGC_85 cDNA clone IMAGE:5497620 5', mRNA sequence /clone=IMAGE:5497620 /clone_end=5' /gb=BM458572 /gi=18507612 /ug=Hs.194215 /len=1106 | BM458572 | Hs.194215 | |
| 4092 | 0.003489 | NADH dehydrogenase (ubiquinone) Fe-S protein 3, 30kDa (NADH-coenzyme Q reductase) (NDUFS3), mRNA /cds=(13,807) /gb=NM_004551 /gi=4758787 /ug=Hs.429506 /len=899 | NM_004551 | Hs.429506 | NP_004542 |
| 4159 | 0.043185 | suppressor of Ty 3 (S. cerevisiae) (SUPT3H), mRNA /cds=(72,1025) /gb=NM_003599 /gi=4507308 /ug=Hs.304173 /len=1165 | NM_003599 | Hs.304173 | NP_003590 |
| 4191 | 0.009079 | signal sequence receptor, alpha (translocon-associated protein alpha) (SSR1), mRNA /cds=(112,972) /gb=NM_003144 /gi=6552340 /ug=Hs.250773 /len=3285 | NM_003144 | Hs.250773 | NP_003135 |
| 4202 | 0.013965 | serum/glucocorticoid regulated kinase-like (SGKL), transcript variant 1, mRNA /cds=(416,1705) /gb=NM_013257 /gi=25168264 /ug=Hs.380877 /len=4155 | NM_013257 | Hs.380877 | NP_733827 |
| 4223 | 0.006699 | solute carrier family 25 (carnitine/acylcarnitine translocase), member 20 (SLC25A20), mitochondrial protein encoded by nuclear gene, mRNA /cds=(37,942) /gb=NM_000387 /gi=6006040 /ug=Hs.13845 /len=1219 | NM_000387 | Hs.13845 | NP_000378 |
| 4256 | 0.043185 | retinoic acid receptor, alpha (RARA), mRNA /cds=(103,1491) /gb=NM_000964 /gi=4506418 /ug=Hs.361071 /len=2907 | NM_000964 | Hs.361071 | NP_000955 |
| 4301 | 0.016017 | mRNA for KIAA1404 protein, partial cds. /cds=(65,5842) /gb=AB037825 /gi=7243188 /ug=Hs.200317 /len=7204 | AB037825 | Hs.200317 | NP_066363 |
| 4376 | 0.016017 | KIAA0089 protein (KIAA0089), mRNA /cds=(66,1121) /gb=NM_015141 /gi=24307998 /ug=Hs.82432 /len=3959 | NM_015141 | Hs.82432 | NP_055956 |

| Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids | | | | | |
|--|----------|---|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 4390 | 0.026896 | ataxia telangiectasia and Rad3 related (ATR), mRNA /cds=(106,8040) /gb=NM_001184 /gi=20143978 /ug=Hs.77613 /len=8265 | NM_001184 | Hs.77613 | NP_001175 |
| 4406 | 0.038517 | mitochondrion, complete genome | NC_001807 | | |
| 4425 | 0.018314 | gene amplified in squamous cell carcinoma 1 (GASC1), mRNA /cds=(151,3321) /gb=NM_015061 /gi=24307986 /ug=Hs.149918 /len=4239 | NM_015061 | Hs.149918 | NP_055876 |
| 4442 | 0.030399 | SGT1, suppressor of G2 allele of SKP1 (S. cerevisiae) (SUGT1), mRNA /cds=(56,1057) /gb=NM_006704 /gi=14165471 /ug=Hs.421239 /len=1535 | NM_006704 | Hs.421239 | NP_006695 |
| 4465 | 0.005723 | HIV-1 rev binding protein 2 (HRB2), mRNA /cds=(30,1175) /gb=NM_007043 /gi=21359979 /ug=Hs.154762 /len=1527 | NM_007043 | Hs.154762 | NP_008974 |
| 4498 | 0.048295 | mRNA for KIAA0265 gene, partial cds. /cds=(1,1206) /gb=D87454 /gi=1665796 /ug=Hs.192966 /len=5551 | D87454 | Hs.192966 | |
| 4511 | 0.030399 | syndecan binding protein (syntenin) (SDCBP), mRNA /cds=(149,1045) /gb=NM_005625 /gi=5032082 /ug=Hs.8180 /len=2193 | NM_005625 | Hs.8180 | NP_005616 |
| 4513 | 0.020878 | hepatitis B virus x interacting protein (HBXIP), mRNA /cds=(56,331) /gb=NM_006402 /gi=5454169 /ug=Hs.433355 /len=605 | NM_006402 | Hs.433355 | NP_006393 |
| 4530 | 0.043185 | I factor (complement) (IF), mRNA /cds=(15,1766) /gb=NM_000204 /gi=4504578 /ug=Hs.36602 /len=1963 | NM_000204 | Hs.36602 | NP_000195 |
| 4538 | 0.048295 | CGI-49 protein (CGI-49), mRNA /cds=(1,1287) /gb=NM_016002 /gi=7705766 /ug=Hs.238126 /len=2127 | NM_016002 | Hs.238126 | NP_057086 |
| 4540 | 0.016017 | decay accelerating factor for complement (CD55, Cromer blood group system) (DAF), mRNA /cds=(66,1211) /gb=NM_000574 /gi=10835142 /ug=Hs.1369 /len=2102 | NM_000574 | Hs.1369 | NP_000565 |
| 4592 | 0.030399 | CC chemokine gene cluster | AF088219 | | |
| 4641 | 0.009079 | major histocompatibility complex, class II, DR beta 1 (HLA-DRB1), mRNA /cds=(63,863) /gb=NM_002124 /gi=4504410 /ug=Hs.375570 /len=1182 | NM_002124 | Hs.375570 | NP_002115 |
| 4651 | 0.009079 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 9 (RNA helicase A, nuclear DNA helicase II; leukophysin) (DDX9), transcript variant 1, mRNA /cds=(81,3920) /gb=NM_001357 /gi=13514819 /ug=Hs.74578 /len=4199 | NM_001357 | Hs.74578 | NP_085077 |

| Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids | | | | | |
|--|----------|---|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 4655 | 0.013965 | tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin) (TNFRSF11B), mRNA /cds=(252,1457) /gb=NM_002546 /gi=22547122 /ug=Hs.81791 /len=2291 | NM_002546 | Hs.81791 | NP_002537 |
| 4670 | 0.001158 | UI-E-DW0-agg-j-14-0-UI.r1 UI-E-DW0 cDNA clone UI-E-DW0-agg-j-14-0-UI 5', mRNA sequence /clone=UI-E-DW0-agg-j-14-0-UI /clone_end=5' /gb=BM706185 /gi=19019443 /ug=Hs.433563 /len=949 | BM706185 | Hs.433563 | |
| 4672 | 0.002935 | coronin, actin binding protein, 1C (CORO1C), mRNA /cds=(97,1521) /gb=NM_014325 /gi=27477119 /ug=Hs.17377 /len=3828 | NM_014325 | Hs.17377 | NP_055140 |
| 4681 | 0.023731 | RNA binding motif protein 8A (RBM8A), mRNA /cds=(30,554) /gb=NM_005105 /gi=15812217 /ug=Hs.10283 /len=2787 | NM_005105 | Hs.10283 | NP_005096 |
| 4694 | 0.004131 | hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor) (HIF1A), mRNA /cds=(265,2745) /gb=NM_001530 /gi=4504384 /ug=Hs.197540 /len=3933 | NM_001530 | Hs.197540 | NP_851397 |
| 4701 | 0.023731 | ubiquitin-like 5 (UBL5), mRNA /cds=(66,287) /gb=NM_024292 /gi=13236509 /ug=Hs.13836 /len=413 | NM_024292 | Hs.13836 | NP_077268 |
| 4726 | 0.018314 | fucosyltransferase 8 (alpha (1,6) fucosyltransferase) (FUT8), mRNA /cds=(717,2444) /gb=NM_004480 /gi=4758407 /ug=Hs.118722 /len=3280 | NM_004480 | Hs.118722 | NP_835370 |
| 4747 | 0.030399 | leucine zipper transcription factor-like 1 (LZTF1), mRNA /cds=(125,1024) /gb=NM_020347 /gi=9966792 /ug=Hs.30824 /len=3384 | NM_020347 | Hs.30824 | NP_065080 |
| 4758 | 0.026896 | inhibin, beta A (activin A, activin AB alpha polypeptide) (INHBA), mRNA /cds=(86,1366) /gb=NM_002192 /gi=4504698 /ug=Hs.727 /len=1840 | NM_002192 | Hs.727 | NP_002183 |
| 4794 | 0.018314 | mitochondrion, complete genome | NC_001807 | | |
| 4797 | 0.026896 | tRNA nucleotidyl transferase, CCA-adding, 1 (TRNT1), mRNA /cds=(141,1358) /gb=NM_016000 /gi=20070270 /ug=Hs.102897 /len=1865 | NM_016000 | Hs.102897 | NP_057084 |
| 4880 | 0.048295 | cDNA FLJ12776 fis, clone NT2RP2001678. /gb=AK022838 /gi=10434465 /ug=Hs.372558 /len=2629 | AK022838 | Hs.372558 | |
| 4885 | 0.006699 | clone alpha_est218/52C1 mRNA sequence /gb=AF001542 /gi=2529714 /ug=Hs.356442 /len=2992 | AF001542 | Hs.356442 | |

| Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids | | | | | |
|--|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 4916 | 0.001408 | collagen, type X, alpha 1 (Schmid metaphyseal chondrodysplasia) (COL10A1), mRNA /cds=(97,2139) /gb=NM_000493 /gi=18105031 /ug=Hs.179729 /len=3285 | NM_000493 | Hs.179729 | NP_000484 |
| 4919 | 0.001158 | KIAA0436 mRNA, partial cds. /cds=(1,2070) /gb=AB007896 /gi=2662152 /ug=Hs.110 /len=4661 | AB007896 | Hs.110 | |
| 4925 | 0.001158 | tm68a09.x1 NCI_CGAP_Brn25 cDNA clone IMAGE:2163256 3', mRNA sequence /clone=IMAGE:2163256 /clone_end=3' /gb=AI498805 /gi=4390787 /ug=Hs.436349 /len=460 | AI498805 | Hs.436349 | |
| 4941 | 0.002051 | mRNA; cDNA DKFZp451P176 (from clone DKFZp451P176) /gb=AL832365 /gi=21732928 /ug=Hs.159471 /len=5559 | AL832365 | Hs.159471 | |
| 4963 | 0.048295 | cytochrome c oxidase subunit VIIa polypeptide 2 (liver) (COX7A2), nuclear gene encoding mitochondrial protein, mRNA /cds=(76,327) /gb=NM_001865 /gi=18105035 /ug=Hs.70312 /len=470 | NM_001865 | Hs.70312 | NP_001856 |
| 4968 | 0.004131 | thioredoxin (TXN), mRNA /cds=(64,381) /gb=NM_003329 /gi=4507744 /ug=Hs.432922 /len=501 | NM_003329 | Hs.432922 | NP_003320 |
| 5000 | 0.038517 | diphtheria toxin receptor (heparin-binding epidermal growth factor-like growth factor) (DTR), mRNA /cds=(262,888) /gb=NM_001945 /gi=4503412 /ug=Hs.799 /len=2360 | NM_001945 | Hs.799 | NP_001936 |
| 5002 | 0.016017 | mitochondrion, complete genome | NC_001807 | | |
| 5004 | 0.048295 | cytochrome P450, family 1, subfamily B, polypeptide 1 (CYP1B1), mRNA /cds=(373,2004) /gb=NM_000104 /gi=13325059 /ug=Hs.154654 /len=5128 | NM_000104 | Hs.154654 | NP_000095 |
| 5018 | 0.018314 | mRNA; cDNA DKFZp762B195 (from clone DKFZp762B195) /gb=AL359585 /gi=8655645 /ug=Hs.356766 /len=2183 | AL359585 | Hs.356766 | |
| 5026 | 0.023731 | hect domain and RLD 2 (HERC2), mRNA /cds=(62,14566) /gb=NM_004667 /gi=5729867 /ug=Hs.266933 /len=15304 | NM_004667 | Hs.266933 | NP_004658 |
| 5027 | 0.034264 | nucleobindin 1 (NUCB1), mRNA /cds=(27,1412) /gb=NM_006184 /gi=20070227 /ug=Hs.172609 /len=2311 | NM_006184 | Hs.172609 | NP_006175 |
| 5074 | 0.026896 | mRNA; cDNA DKFZp762B195 (from clone DKFZp762B195) /gb=AL359585 /gi=8655645 /ug=Hs.356766 /len=2183 | AL359585 | Hs.356766 | |

| Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids | | | | | |
|--|----------|---|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 5102 | 0.007812 | cofilin 1 (non-muscle) (CFL1), mRNA /cds=(52,552) /gb=NM_005507 /gi=5031634 /ug=Hs.180370 /len=1059 | NM_005507 | Hs.180370 | NP_005498 |
| 5104 | 0.026896 | T-cell activation leucine repeat-rich protein (TA-LRRP), mRNA /cds=(565,2976) /gb=NM_015350 /gi=21245133 /ug=Hs.199243 /len=3588 | NM_015350 | Hs.199243 | NP_056165 |
| 5111 | 0.043185 | chromosome 14 open reading frame 94 (C14orf94), mRNA /cds=(211,1302) /gb=NM_017815 /gi=8923395 /ug=Hs.8886 /len=1618 | NM_017815 | Hs.8886 | NP_060285 |
| 5139 | 0.034264 | nuclear receptor coactivator 4 (NCOA4), mRNA /cds=(141,1985) /gb=NM_005437 /gi=14149616 /ug=Hs.99908 /len=3506 | NM_005437 | Hs.99908 | NP_005428 |
| 5192 | 0.020878 | mRNA for KIAA0232 protein, partial cds. /cds=(435,4643) /gb=D86985 /gi=20521849 /ug=Hs.79276 /len=7840 | D86985 | Hs.79276 | |
| 5230 | 0.016017 | CDC28 protein kinase regulatory subunit 2 (CKS2), mRNA /cds=(96,335) /gb=NM_001827 /gi=4502858 /ug=Hs.83758 /len=627 | NM_001827 | Hs.83758 | NP_001818 |
| 5250 | 0.002459 | SFRS protein kinase 1 (SRPK1), mRNA /cds=(10,1974) /gb=NM_003137 /gi=15834623 /ug=Hs.75761 /len=4244 | NM_003137 | Hs.75761 | NP_003128 |
| 5257 | 0.026896 | likely ortholog of mouse hypoxia induced gene 1 (HIG1), mRNA /cds=(93,374) /gb=NM_014056 /gi=7661619 /ug=Hs.7917 /len=1362 | NM_014056 | Hs.7917 | NP_054775 |
| 5261 | 0.043185 | replication factor C (activator 1) 4, 37kDa (RFC4), mRNA /cds=(284,1375) /gb=NM_002916 /gi=4506490 /ug=Hs.35120 /len=1446 | NM_002916 | Hs.35120 | NP_002907 |
| 5262 | 0.018314 | ALL1-fused gene from chromosome 1q (AF1Q), mRNA /cds=(353,625) /gb=NM_006818 /gi=21626459 /ug=Hs.75823 /len=1653 | NM_006818 | Hs.75823 | NP_006809 |
| 5283 | 0.009079 | transforming, acidic coiled-coil containing protein 2 (TACC2), mRNA /cds=(87,3167) /gb=NM_006997 /gi=11119413 /ug=Hs.272023 /len=3686 | NM_006997 | Hs.272023 | NP_008928 |
| 5327 | 0.043185 | zinc finger, DHHC domain containing 14 (ZDHHC14), mRNA /cds=(498,1964) /gb=NM_024630 /gi=24371240 /ug=Hs.38270 /len=2821 | NM_024630 | Hs.38270 | NP_714968 |
| 5342 | 0.013965 | KIAA0308 gene, partial cds /cds=UNKNOWN /gb=AB002306 /gi=2224556 /ug=Hs.10351 /len=6452 | AB002306 | Hs.10351 | NP_525127 |

| Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids | | | | | |
|--|----------|---|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 5370 | 0.014664 | laminin receptor 1 (ribosomal protein SA, 67kDa) (LAMR1), mRNA /cds=(86,973) /gb=NM_002295 /gi=9845501 /ug=Hs.181357 /len=1039 | NM_002295 | Hs.181357 | NP_002286 |
| 5392 | 0.001703 | clone IMAGE:5398100, mRNA /gb=BC035584 /gi=23273438 /ug=Hs.407477 /len=1570 | BC035584 | Hs.407477 | |
| 5394 | 0.004872 | hypothetical protein FLJ11294 (FLJ11294), mRNA /cds=(160,4170) /gb=NM_018383 /gi=19923528 /ug=Hs.107000 /len=4602 | NM_018383 | Hs.107000 | NP_060853 |
| 5438 | 0.007812 | mitochondrion, complete genome | NC_001807 | | |
| 5445 | 0.030399 | hypothetical protein FLJ20312 (FLJ20312), mRNA /cds=(384,803) /gb=NM_017761 /gi=20127576 /ug=Hs.7862 /len=2382 | NM_017761 | Hs.7862 | NP_060231 |
| 5503 | 0.038517 | HSPC142 protein (HSPC142), mRNA /cds=(127,1230) /gb=NM_014173 /gi=7661801 /ug=Hs.190722 /len=1432 | NM_014173 | Hs.190722 | NP_054892 |
| 5504 | 0.030399 | hypothetical protein FLJ22329 (FLJ22329), mRNA /cds=(36,767) /gb=NM_024656 /gi=13375904 /ug=Hs.367653 /len=2501 | NM_024656 | Hs.367653 | NP_078932 |
| 5580 | 0.048295 | PTK9L protein tyrosine kinase 9-like (A6-related protein) (PTK9L), mRNA /cds=(105,1154) /gb=NM_007284 /gi=6005845 /ug=Hs.6780 /len=1574 | NM_007284 | Hs.6780 | NP_009215 |
| 5629 | 0.018314 | folliculin (FST), transcript variant FST317, mRNA /cds=(28,981) /gb=NM_006350 /gi=7242223 /ug=Hs.9914 /len=1386 | NM_006350 | Hs.9914 | NP_037541 |
| 5666 | 9.48E-04 | KNP-1a (=U53007 GT335) | D86061 | | NP_004640 |
| 5671 | 0.002051 | EPC-1 (=M76979 PEDF;U29953;M90493) | U57446 | | |
| 5672 | 0.026896 | clone IMAGE:5265581, mRNA /gb=BC035165 /gi=23272508 /ug=Hs.400548 /len=2237 | BC035165 | Hs.400548 | |
| 5723 | 0.003489 | cytoskeleton-associated protein 4 (CKAP4), mRNA /cds=(85,1893) /gb=NM_006825 /gi=19920316 /ug=Hs.74368 /len=2913 | NM_006825 | Hs.74368 | NP_006816 |
| 5744 | 0.023731 | DNA segment on chromosome X (unique) 9928 expressed sequence (DXS9928E), mRNA /cds=(76,1095) /gb=NM_004699 /gi=4758219 /ug=Hs.54277 /len=1311 | NM_004699 | Hs.54277 | NP_004690 |

| Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids | | | | | |
|--|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 5748 | 0.030399 | vasoactive intestinal peptide receptor 1 (VIPR1), mRNA /cds=(111,1484) /gb=NM_004624 /gi=15619005 /ug=Hs.348500 /len=2771 | NM_004624 | Hs.348500 | NP_004615 |
| 5780 | 0.030399 | chondroitin 4-O-sulfotransferase 2 (C4S-2), mRNA /cds=(145,1389) /gb=NM_018641 /gi=20070291 /ug=Hs.25204 /len=2117 | NM_018641 | Hs.25204 | NP_061111 |
| 5787 | 0.034264 | ADP-ribosylation factor guanine nucleotide factor 6 (EFA6R), mRNA /cds=(53,1657) /gb=NM_015310 /gi=7662395 /ug=Hs.6763 /len=6722 | NM_015310 | Hs.6763 | NP_056125 |
| 5793 | 0.016017 | zinc finger protein 265 (ZNF265), mRNA /gb=NM_005455 /gi=19923317 /ug=Hs.194718 /len=2837 | NM_005455 | Hs.194718 | NP_005446 |
| 5812 | 0.038517 | hypothetical protein FLJ12439 (FLJ12439), mRNA /cds=(41,736) /gb=NM_023077 /gi=12751490 /ug=Hs.349905 /len=1614 | NM_023077 | Hs.349905 | NP_075565 |
| 5815 | 0.043185 | at74h07.x1 Barstead colon HPLRB7 cDNA clone IMAGE:2377789 3' similar to contains Alu repetitive element; contains element MER22 repetitive element ;, mRNA sequence /clone=IMAGE:2377789 /clone_end=3' /gb=AI833064 /gi=5455044 /ug=Hs.369949 /len=553 | AI833064 | Hs.369949 | |
| 5822 | 0.023731 | enhancer of zeste 1 (Drosophila) (EZH1), mRNA /cds=(123,2366) /gb=NM_001991 /gi=19923201 /ug=Hs.194669 /len=4640 | NM_001991 | Hs.194669 | NP_001982 |
| 5863 | 0.020878 | polypyrimidine tract binding protein 2 (PTBP2), mRNA /cds=(53,1648) /gb=NM_021190 /gi=10863996 /ug=Hs.34956 /len=3054 | NM_021190 | Hs.34956 | NP_067013 |
| 5873 | 0.004872 | blood-stage membrane protein Ag-1 [Plasmodium yoelii] | AF103869 | | |
| 5919 | 0.012137 | chromosome 4 open reading frame 1 (C4orf1), mRNA /cds=(121,1827) /gb=NM_006345 /gi=7656945 /ug=Hs.270956 /len=3250 | NM_006345 | Hs.270956 | NP_006336 |
| 5997 | 0.038517 | NTT gene (L1 Alu and MER 38 repeat regions) | U54776 | | |
| 6009 | 0.034264 | methylmalonyl Coenzyme A mutase (MUT), nuclear gene encoding mitochondrial protein, mRNA /cds=(77,2329) /gb=NM_000255 /gi=4557766 /ug=Hs.155212 /len=2798 | NM_000255 | Hs.155212 | NP_000246 |

| Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids | | | | | |
|--|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 6013 | 0.016017 | Similar to hect domain and RLD 2, clone IMAGE:4830978, mRNA /gb=BC033888 /gi=21706785 /ug=Hs.429904 /len=4297 | BC033888 | Hs.429904 | |
| 6028 | 0.034264 | protein-tyrosine kinase, trkB | X75958 | | NP_006171 |
| 6063 | 0.018314 | eukaryotic translation initiation factor 4A, isoform 2 (EIF4A2), mRNA /cds=(16,1239) /gb=NM_001967 /gi=9945313 /ug=Hs.173912 /len=1864 | NM_001967 | Hs.173912 | NP_001958 |
| 6068 | 0.013965 | mitochondrial ribosomal protein L27 (MRPL27), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA /cds=(32,316) /gb=NM_148571 /gi=22547130 /ug=Hs.7736 /len=2472 | NM_148571 | Hs.7736 | NP_683412 |
| 6081 | 0.020878 | mitochondrial ribosomal protein L33 (MRPL33), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA /cds=(60,257) /gb=NM_004891 /gi=21735607 /ug=Hs.14454 /len=541 | NM_004891 | Hs.14454 | NP_663303 |
| 6082 | 0.016017 | proteasome (prosome, macropain) subunit, alpha type, 4 (PSMA4), mRNA /cds=(137,922) /gb=NM_002789 /gi=23110940 /ug=Hs.251531 /len=1189 | NM_002789 | Hs.251531 | NP_002780 |
| 6083 | 0.006699 | NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (NADH-coenzyme Q reductase) (NDUFS4), mRNA /cds=(9,536) /gb=NM_002495 /gi=4505368 /ug=Hs.10758 /len=668 | NM_002495 | Hs.10758 | NP_002486 |
| 6129 | 0.012137 | myosin, light polypeptide 3, alkali; ventricular, skeletal, slow (MYL3), mRNA /cds=(51,638) /gb=NM_000258 /gi=4557776 /ug=Hs.1815 /len=872 | NM_000258 | Hs.1815 | NP_000249 |
| 6139 | 0.048295 | cofilin 1 (non-muscle) (CFL1), mRNA /cds=(52,552) /gb=NM_005507 /gi=5031634 /ug=Hs.180370 /len=1059 | NM_005507 | Hs.180370 | NP_005498 |
| 6191 | 0.004872 | calsyntenin 3 (CLSTN3), mRNA /cds=(539,3445) /gb=NM_014718 /gi=7662267 /ug=Hs.107809 /len=4300 | NM_014718 | Hs.107809 | NP_055533 |
| 6237 | 0.012137 | cDNA FLJ12807 fis, clone NT2RP2002316. /gb=AK022869 /gi=10434511 /ug=Hs.188361 /len=2697 | AK022869 | Hs.188361 | |
| 6244 | 0.020674 | lumican (LUM), mRNA /cds=(142,1158) /gb=NM_002345 /gi=21359858 /ug=Hs.79914 /len=1804 | NM_002345 | Hs.79914 | NP_002336 |
| 6248 | 0.046968 | tumor differentially expressed 1 (TDE1), mRNA /cds=(78,1499) /gb=NM_006811 /gi=5803192 /ug=Hs.272168 /len=1892 | NM_006811 | Hs.272168 | NP_006802 |

| Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids | | | | | |
|--|----------|---|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 6258 | 0.004872 | deleted in liver cancer 1 (DLC1), mRNA /cds=(296,3571) /gb=NM_006094 /gi=6633799 /ug=Hs.8700 /len=3821 | NM_006094 | Hs.8700 | NP_006085 |
| 6267 | 0.012678 | mRNA for KIAA1965 protein. /cds=(1,1699) /gb=AB075845 /gi=18916817 /ug=Hs.71730 /len=4299 | AB075845 | Hs.71730 | |
| 6295 | 0.016017 | Notch 2 (Drosophila) (NOTCH2), mRNA /cds=(257,7672) /gb=NM_024408 /gi=24041034 /ug=Hs.8121 /len=11433 | NM_024408 | Hs.8121 | NP_077719 |
| 6297 | 0.009079 | 5'-nucleotidase, cytosolic II (NT5C2), mRNA /cds=(145,1830) /gb=NM_012229 /gi=20149601 /ug=Hs.138593 /len=3364 | NM_012229 | Hs.138593 | NP_036361 |
| 6302 | 0.041767 | diphtheria toxin receptor (heparin-binding epidermal growth factor-like growth factor) (DTR), mRNA /cds=(262,888) /gb=NM_001945 /gi=4503412 /ug=Hs.799 /len=2360 | NM_001945 | Hs.799 | NP_001936 |
| 6307 | 0.032747 | cDNA FLJ37296 fis, clone BRAMY2015420. /gb=AK094615 /gi=21753707 /ug=Hs.4983 /len=3181 | AK094615 | Hs.4983 | |
| 6365 | 0.010515 | epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene avian) (EGFR), mRNA /cds=(187,3819) /gb=NM_005228 /gi=4885198 /ug=Hs.77432 /len=5532 | NM_005228 | Hs.77432 | NP_005219 |
| 6382 | 0.026896 | hypothetical protein HSPC210 (HSPC210), mRNA /cds=(138,605) /gb=NM_016472 /gi=24475986 /ug=Hs.4104 /len=1152 | NM_016472 | Hs.4104 | NP_057556 |
| 6385 | 0.013965 | RAB32, member RAS oncogene family (RAB32), mRNA /cds=(183,860) /gb=NM_006834 /gi=20127508 /ug=Hs.32217 /len=1236 | NM_006834 | Hs.32217 | NP_006825 |
| 6386 | 0.002935 | mitochondrion, complete genome | NC_001807 | | |
| 6395 | 0.038517 | SOCS box-containing WD protein SWIP-1 (WSB1), transcript variant 3, mRNA /cds=(317,1051) /gb=NM_134264 /gi=20143909 /ug=Hs.187991 /len=4243 | NM_134264 | Hs.187991 | NP_599027 |
| 6402 | 0.026896 | actin, gamma 1 (ACTG1), mRNA /cds=(75,1202) /gb=NM_001614 /gi=11038618 /ug=Hs.14376 /len=1919 | NM_001614 | Hs.14376 | NP_001605 |
| 6405 | 0.043185 | cyclic AMP-regulated phosphoprotein (90% match) | AF112220 | | NP_057384 |
| 6442 | 0.007812 | 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3 (PFKFB3), mRNA /cds=(115,1677) /gb=NM_004566 /gi=4758899 /ug=Hs.195471 /len=4322 | NM_004566 | Hs.195471 | NP_004557 |

| Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids | | | | | |
|--|----------|---|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 6464 | 0.038517 | KIAA0250 gene | NM_014837 | | NP_055652 |
| 6469 | 0.034264 | protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha) (PPP3CA), mRNA /cds=(407,1972) /gb=NM_000944 /gi=19923130 /ug=Hs.272458 /len=4425 | NM_000944 | Hs.272458 | NP_000935 |
| 6522 | 0.030399 | Rattus norvegicus mitochondrial genome | NC_001665 | | |
| 6530 | 0.034264 | pleckstrin domain containing, family A (phosphoinositide binding specific) member 4 (PLEKHA4), mRNA /cds=(526,2865) /gb=NM_020904 /gi=10190743 /ug=Hs.9469 /len=3056 | NM_020904 | Hs.9469 | NP_065955 |
| 6543 | 0.020878 | general transcription factor IIH, polypeptide 1 (62kD subunit) (GTF2H1), mRNA /cds=(161,1807) /gb=NM_005316 /gi=19923304 /ug=Hs.89578 /len=2989 | NM_005316 | Hs.89578 | NP_005307 |
| 6550 | 0.023731 | t-complex-associated-testis-expressed 1-like 1 (TCTEL1), mRNA /cds=(1,342) /gb=NM_006519 /gi=5730084 /ug=Hs.266940 /len=713 | NM_006519 | Hs.266940 | NP_006510 |
| 6574 | 0.012137 | RCC1 | D00591 | | |
| 6577 | 0.048295 | ornithine decarboxylase antizyme 1 (OAZ1), mRNA /gb=NM_004152 /gi=9845504 /ug=Hs.281960 /len=986 | NM_004152 | Hs.281960 | NP_004143 |
| 6581 | 0.007812 | mitogen inducible gene mig-2, complete CDS. /cds=(1,2165) /gb=Z24725 /gi=505032 /ug=Hs.75260 /len=3270 | Z24725 | Hs.75260 | NP_006823 |
| 6584 | 0.012137 | likely ortholog of mouse monocyte macrophage 19 (MMRP19), mRNA /cds=(78,806) /gb=NM_015957 /gi=7705723 /ug=Hs.104058 /len=1226 | NM_015957 | Hs.104058 | NP_057041 |
| 6590 | 0.020878 | mRNA for KIAA0981 protein, partial cds. /cds=(1,1738) /gb=AB023198 /gi=4589605 /ug=Hs.158135 /len=5182 | AB023198 | Hs.158135 | |
| 6598 | 0.026896 | phosphomannomutase 2 (PMM2) gene (5e-10 match) | AF157794 | | |
| 6603 | 0.026896 | tm68a09.x1 NCI_CGAP_Brn25 cDNA clone IMAGE:2163256 3', mRNA sequence /clone=IMAGE:2163256 /clone_end=3' /gb=AI498805 /gi=4390787 /ug=Hs.436349 /len=460 | AI498805 | Hs.436349 | |
| 6619 | 0.001703 | phosphodiesterase 1A, calmodulin-dependent (PDE1A) mRNA | NM_005019 | | NP_005010 |

| Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids | | | | | |
|--|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 6630 | 9.48E-04 | NADH dehydrogenase (ubiquinone) Fe-S protein 6, 13kDa (NADH-coenzyme Q reductase) (NDUFS6), mRNA /cds=(11,385) /gb=NM_004553 /gi=4758791 /ug=Hs.49767 /len=547 | NM_004553 | Hs.49767 | NP_004544 |
| 6661 | 0.043185 | stromal antigen 1 (STAG1), mRNA /cds=(401,4177) /gb=NM_005862 /gi=5032062 /ug=Hs.286148 /len=4337 | NM_005862 | Hs.286148 | NP_005853 |
| 6666 | 0.016017 | tigger transposable element derived 1 (TIGD1), mRNA /cds=(635,2410) /gb=NM_145702 /gi=22209000 /ug=Hs.351348 /len=2448 | NM_145702 | Hs.351348 | NP_663748 |
| 6687 | 0.020878 | qe80a05.x1 Soares_fetal_lung_NbHL19W cDNA clone IMAGE:1745264 3' similar to Q04323 HYPOTHETICAL 33.4 KD PROTEIN.;, mRNA sequence /clone=IMAGE:1745264 /clone_end=3' /gb=AI193849 /gi=3745058 /ug=Hs.386662 /len=586 | AI193849 | Hs.386662 | |
| 6722 | 0.034264 | syndecan 1 (SDC1), mRNA /cds=(253,1185) /gb=NM_002997 /gi=21359855 /ug=Hs.82109 /len=2484 | NM_002997 | Hs.82109 | NP_002988 |
| 6732 | 0.005723 | dermatan-4-sulfotransferase-1 (D4ST-1), mRNA /cds=(1,1131) /gb=NM_130468 /gi=18497303 /ug=Hs.24947 /len=1960. | NM_130468 | Hs.24947 | NP_569735 |
| 6738 | 6.26E-04 | ankyrin repeat and SOCS box-containing 3 (ASB3), transcript variant 1, mRNA /cds=(136,1692) /gb=NM_016115 /gi=22208952 /ug=Hs.9893 /len=2214 | NM_016115 | Hs.9893 | NP_665862 |
| 6745 | 0.001408 | mRNA; cDNA DKFZp434A163 (from clone DKFZp434A163); partial cds /cds=(1,4964) /gb=AL110218 /gi=5817150 /ug=Hs.127401 /len=5084 | AL110218 | Hs.127401 | |
| 6754 | 0.002935 | TSC-22 related protein (TSC-22R) (=AF228339 glucocorticoid-induced GILZ) | AF153603 | | NP_004080 |
| 6795 | 0.003489 | KIAA0438 gene product (KIAA0438), mRNA /cds=(118,2244) /gb=NM_014819 /gi=7662123 /ug=Hs.279849 /len=4765 | NM_014819 | Hs.279849 | NP_055634 |
| 6825 | 0.034264 | hypothetical protein MGC4400 (MGC4400), mRNA /cds=(381,1817) /gb=NM_032679 /gi=14249251 /ug=Hs.130891 /len=3067 | NM_032679 | Hs.130891 | NP_116068 |

| Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids | | | | | |
|--|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 6836 | 0.038517 | UI-E-DW1-ahd-d-13-0-UI.s1 UI-E-DW1 cDNA clone UI-E-DW1-ahd-d-13-0-UI 3', mRNA sequence /clone=UI-E-DW1-ahd-d-13-0-UI /clone_end=3' /gb=BU737702 /gi=23673914 /ug=Hs.405983 /len=1215 | BU737702 | Hs.405983 | |
| 6883 | 0.001408 | platelet-derived growth factor receptor, alpha polypeptide (PDGFRA), mRNA /cds=(395,3664) /gb=NM_006206 /gi=15451787 /ug=Hs.74615 /len=6633 | NM_006206 | Hs.74615 | NP_006197 |
| 6891 | 0.034264 | protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B), mRNA /cds=(167,1423) /gb=NM_002736 /gi=4506064 /ug=Hs.77439 /len=3259 | NM_002736 | Hs.77439 | NP_002727 |
| 6914 | 0.038517 | gene trap ankyrin repeat (GTAR), mRNA /cds=(118,7926) /gb=NM_032217 /gi=27477106 /ug=Hs.12329 /len=9016 | NM_032217 | Hs.12329 | NP_115593 |
| 6950 | 0.038517 | splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated) (SFPQ), mRNA /cds=(86,2209) /gb=NM_005066 /gi=4826997 /ug=Hs.180610 /len=3071 | NM_005066 | Hs.180610 | NP_005057 |
| 6972 | 0.023731 | similar to zinc finger protein (LOC91172), mRNA (=FLJ12859,=FLJ11645) | XM_036627 | | |
| 7035 | 0.002935 | hypothetical protein (KIAA0238) | D87075 | | NP_005107 |
| 7077 | 0.048295 | mitochondrion, complete genome | NC_001807 | | |
| 7087 | 0.038517 | mitochondrion, complete genome | NC_001807 | | |
| 7098 | 0.012137 | inactive progesterone receptor, 23 kD (TEBP), mRNA /cds=(107,589) /gb=NM_006601 /gi=23308578 /ug=Hs.278270 /len=1490 | NM_006601 | Hs.278270 | NP_006592 |
| 7102 | 0.003489 | survival of motor neuron protein interacting protein 1 (SIP1), mRNA /cds=(84,926) /gb=NM_003616 /gi=4506960 /ug=Hs.102456 /len=1285 | NM_003616 | Hs.102456 | NP_003607 |
| 7116 | 0.010515 | 7i76f10.y1 NCI_CGAP_Brn20 cDNA clone IMAGE:3340651.5', mRNA sequence /clone=IMAGE:3340651 /clone_end=5' /gb=BF057907 /gi=10811803 /ug=Hs.439614 /len=133 | BF057907 | Hs.439614 | |
| 7178 | 0.013965 | supervillin (SVIL), transcript variant 2, mRNA /cds=(754,7398) /gb=NM_021738 /gi=11496981 /ug=Hs.154567 /len=8300 | NM_021738 | Hs.154567 | NP_068506 |

| Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids | | | | | |
|--|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 7217 | 0.004872 | ATPase, Na /K transporting, beta 3 polypeptide (ATP1B3), mRNA /cds=(1,840) /gb=NM_001679 /gi=4502280 /ug=Hs.76941 /len=1679 | NM_001679 | Hs.76941 | NP_001670 |
| 7221 | 0.043185 | 602410168F1 NIH_MGC_92 cDNA clone IMAGE:4538560 5', mRNA sequence /clone=IMAGE:4538560 /clone_end=5' /gb=BG394022 /gi=13287470 /ug=Hs.421597 /len=1059 | BG394022 | Hs.421597 | |
| 7222 | 0.013965 | REV3-like, catalytic subunit of DNA polymerase zeta (yeast) (REV3L), mRNA /cds=(823,9981) /gb=NM_002912 /gi=4506482 /ug=Hs.115521 /len=10919 | NM_002912 | Hs.115521 | NP_002903 |
| 7265 | 0.018314 | thioredoxin interacting protein (TXNIP), mRNA /cds=(222,1397) /gb=NM_006472 /gi=5454161 /ug=Hs.179526 /len=2704 | NM_006472 | Hs.179526 | NP_006463 |
| 7310 | 0.007812 | UI-H-BI2-agp-f-12-0-UI.s1 NCI_CGAP_Sub4 cDNA clone IMAGE:2725031 3', mRNA sequence /clone=IMAGE:2725031 /clone_end=3' /gb=AW292456 /gi=6699092 /ug=Hs.437793 /len=745 | AW292456 | Hs.437793 | |
| 7331 | 0.034264 | AGENCOURT_8856629 Lupski_sciatic_nerve cDNA clone IMAGE:6200636 5', mRNA sequence /clone=IMAGE:6200636 /clone_end=5' /gb=BQ947179 /gi=22362657 /ug=Hs.356605 /len=1277 | BQ947179 | Hs.356605 | |
| 7339 | 0.005723 | major histocompatibility complex, class II, DR beta 3 (HLA-DRB3), mRNA /cds=(41,841) /gb=NM_022555 /gi=18641371 /ug=Hs.308026 /len=1158 | NM_022555 | Hs.308026 | NP_072049 |
| 7341 | 0.048295 | peroxiredoxin 5 (PRDX5), mRNA /cds=(37,681) /gb=NM_012094 /gi=6912237 /ug=Hs.31731 /len=805 | NM_012094 | Hs.31731 | NP_036226 |
| 7382 | 0.018314 | cortactin binding protein 2 (CORTBP2), mRNA /cds=(93,5084) /gb=NM_033427 /gi=16975495 /ug=Hs.293539 /len=5975 | NM_033427 | Hs.293539 | NP_219499 |
| 7399 | 0.030399 | Similar to alpha-methylacyl-CoA racemase, clone MGC:3743 IMAGE:2958112, mRNA, complete cds | BC009471 | | NP_055139 |
| 7414 | 0.010515 | tetraspanin similar to TM4SF9 (DC-TM4F2), mRNA /cds=(79,891) /gb=NM_030927 /gi=13569888 /ug=Hs.101395 /len=2556 | NM_030927 | Hs.101395 | NP_112189 |

| Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids | | | | | |
|--|----------|---|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 7439 | 0.030399 | pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN), mRNA /cds=(396,902) /gb=NM_002825 /gi=27552761 /ug=Hs.44 /len=1029 | NM_002825 | Hs.44 | NP_002816 |
| 7450 | 0.030399 | KIAA0097 gene product (KIAA0097), mRNA /cds=(27,5945) /gb=NM_014756 /gi=24307972 /ug=Hs.76989 /len=6449 | NM_014756 | Hs.76989 | NP_055571 |
| 7581 | 0.043185 | FK506 binding protein 5 (FKBP5), mRNA /cds=(154,1527) /gb=NM_004117 /gi=17149847 /ug=Hs.7557 /len=3781 | NM_004117 | Hs.7557 | NP_004108 |
| 7611 | 0.038517 | RAB14, member RAS oncogene family (RAB14), mRNA /cds=(184,831) /gb=NM_016322 /gi=19923482 /ug=Hs.5807 /len=4106 | NM_016322 | Hs.5807 | NP_057406 |
| 7623 | 0.046968 | growth factor receptor-bound protein 10 (GRB10), mRNA /cds=(782,2548) /gb=NM_005311 /gi=19923302 /ug=Hs.81875 /len=5431 | NM_005311 | Hs.81875 | NP_005302 |
| 7632 | 0.030399 | nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha (NFKBIA), mRNA /cds=(95,1048) /gb=NM_020529 /gi=10092618 /ug=Hs.81328 /len=1550 | NM_020529 | Hs.81328 | NP_065390 |
| 7642 | 0.034264 | actin, beta (ACTB), mRNA /cds=(74,1201) /gb=NM_001101 /gi=5016088 /ug=Hs.426930 /len=1793 | NM_001101 | Hs.426930 | NP_001092 |
| 7651 | 0.013965 | DZIP3 mRNA, partial cds | AF279370 | | NP_055463 |
| 7660 | 3.22E-04 | bladder cancer overexpressed protein (BLOV1), mRNA /cds=(72,1136) /gb=NM_018656 /gi=8922084 /ug=Hs.125830 /len=2324 | NM_018656 | Hs.125830 | NP_061126 |
| 7672 | 0.030399 | solute carrier family 25 (mitochondrial carrier, brain), member 14 (SLC25A14), transcript variant long, nuclear gene encoding mitochondrial protein, mRNA /cds=(207,1184) /gb=NM_003951 /gi=6006039 /ug=Hs.194686 /len=1601 | NM_003951 | Hs.194686 | NP_073721 |
| 7694 | 0.004131 | cDNA FLJ25013 fis, clone CBL01365. /gb=AK057742 /gi=16553667 /ug=Hs.380091 /len=2200 | AK057742 | Hs.380091 | |
| 7723 | 0.001623 | yp24c06.s1 Soares breast 3NbHBst cDNA clone IMAGE:188362 3' similar to gb:M10942_cds1 metallothionein-1e gene mRNA sequence /clone=IMAGE:188362 /clone_end=3' /gb=H43642 /gi=919694 /ug=Hs.418241 /len=452 | H43642 | Hs.418241 | |

| Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids | | | | | |
|--|----------|---|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 7727 | 0.038517 | hypothetical protein FLJ13081 (FLJ13081), mRNA /cds=(171,2099) /gb=NM_024834 /gi=13376242 /ug=Hs.180638 /len=4113 | NM_024834 | Hs.180638 | NP_079110 |
| 7728 | 0.038517 | Down syndrome critical region gene 5 (DSCR5), transcript variant 3, mRNA /cds=(342,668) /gb=NM_016430 /gi=24497594 /ug=Hs.408790 /len=875 | NM_016430 | Hs.408790 | NP_710149 |
| 7741 | 0.026896 | major histocompatibility complex, class II, DR beta 3 (HLA-DRB3), mRNA /cds=(41,841) /gb=NM_022555 /gi=18641371 /ug=Hs.308026 /len=1158 | NM_022555 | Hs.308026 | NP_072049 |
| 7927 | 0.004414 | UI-H-EZ1-bca-n-05-0-UI.s1 NCI_CGAP_Ch2 cDNA clone UI-H-EZ1-bca-n-05-0-UI 3', mRNA sequence /clone=UI-H-EZ1-bca-n-05-0-UI /clone_end=3' /gb=BQ774356 /gi=21982825 /ug=Hs.43227 /len=1083 | BQ774356 | Hs.43227 | |
| 7946 | 0.038517 | EST (AV746410 NPA H.sapiens cDNA clone NPABDD10 5') | AV746410 | | NP_006463 |
| 8054 | 0.043185 | pyruvate dehydrogenase kinase 4 mRNA, 3' untranslated region, partial sequence /cds=UNKNOWN/gb=AF334710 /gi=12658438 /ug=Hs.8364 /len=1819 | AF334710 | Hs.8364 | NP_002603 |
| 8097 | 0.048295 | mRNA for KIAA1915 protein, partial cds. /cds=(356,2536) /gb=AB067502 /gi=15620888 /ug=Hs.12915 /len=7801 | AB067502 | Hs.12915 | |
| 8128 | 0.026896 | mRNA for KIAA1545 protein, partial cds. /cds=(1,2909) /gb=AB046765 /gi=20521935 /ug=Hs.127270 /len=4307 | AB046765 | Hs.127270 | |
| 8198 | 0.043185 | PHD zinc finger protein XAP135 (XAP135), transcript variant 2, mRNA /cds=(222,1448) /gb=NM_133325 /gi=19747275 /ug=Hs.7759 /len=1583 | NM_133325 | Hs.7759 | NP_579866 |
| 8201 | 0.048295 | KIAA1892 protein (KIAA1892), mRNA /cds=(308,1669) /gb=NM_015397 /gi=22218618 /ug=Hs.102669 /len=3636 | NM_015397 | Hs.102669 | NP_056212 |
| 8208 | 0.030399 | SPT3-associated factor 42 (STAF42), mRNA /cds=(22,1029) /gb=NM_053053 /gi=16596695 /ug=Hs.107968 /len=2122 | NM_053053 | Hs.107968 | NP_444281 |
| 8209 | 0.023731 | UI-E-EJ0-ahj-n-19-0-UI.r1 UI-E-EJ0 cDNA clone UI-E-EJ0-ahj-n-19-0-UI 5', mRNA sequence /clone=UI-E-EJ0-ahj-n-19-0-UI /clone_end=5' /gb=BM701108 /gi=19014366 /ug=Hs.401941 /len=1923 | BM701108 | Hs.401941 | |

| Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids | | | | | |
|--|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 8244 | 0.048295 | peptidylprolyl isomerase (cyclophilin)-like 4 (PPIL4), mRNA /cds=(31,1509) /gb=NM_139126 /gi=22538483 /ug=Hs.11065 /len=2481 | NM_139126 | Hs.11065 | NP_624311 |
| 8260 | 0.013965 | EST(zd17f12.r1 Soares fetal heart NbHH19W cDNA clone 340943 5') | W57908 | | |
| 8269 | 0.013965 | clone IMAGE:5243705, mRNA /gb=BC043383 /gi=27695948 /ug=Hs.439631 /len=2177 | BC043383 | Hs.439631 | |
| 8341 | 0.016017 | EST(we27d09.x1 NCI_CGAP_Lu24 clone IMAGE:2342321 3') | AI797144 | | NP_002877 |
| 8359 | 0.048295 | UI-H-BW1-amn-b-05-0-UI.s1 NCI_CGAP_Sub7 cDNA clone IMAGE:3070401 3', mRNA sequence /clone=IMAGE:3070401 /clone_end=3' /gb=BF513064 /gi=11598243 /ug=Hs.446233 /len=777 | BF513064 | Hs.446233 | |
| 8368 | 0.013965 | EST(qq29d09.x1 Soares_NhHMPu_S1 clone IMAGE:1933937 3') | AI338976 | | NP_001101 |
| 8376 | 0.009079 | EST(zk54c05.r1 Soares_pregnant_uterus_NbHPU cDNA clone IMAGE:486632 5') | AA044356 | | NP_001767 |
| 8381 | 0.023731 | Tho2 mRNA, complete cds /cds=(1,4437) /gb=AF441770 /gi=20799317 /ug=Hs.16411 /len=4452 | AF441770 | Hs.16411 | |
| 8399 | 0.038517 | EST(nc26d02.r1 NCI_CGAP_Pr1 cDNA clone IMAGE:1009251 similar to contains Alu repetitive element) | AA226526 | | |
| 8437 | 0.002459 | EST(yi83h07.r1 Soares infant brain 1NIB IMAGE:44845 5') | H06795 | | |
| 8454 | 0.043185 | EST ae93d05.s1 Stratagene schizo brain S11'H.sapiens cDNA clone IMAGE:1020489 3' | AA780434 | | |
| 8505 | 0.020878 | EST(hv67h07.x1 NCI_CGAP_Lu24 IMAGE:3178525 3') | BE220163 | | |
| 8518 | 0.032747 | clone IMAGE:5311197, mRNA /gb=BC042002 /gi=27469533 /ug=Hs.260395 /len=1498 | BC042002 | Hs.260395 | |
| 8529 | 0.018314 | EST(602645742F1 NIH_MGC_76 clone IMAGE:4767299 5') | BG618375 | | |
| 8571 | 0.002459 | AGENCOURT_6758988 NIH_MGC_115 cDNA clone IMAGE:5755234 5', mRNA sequence /clone=IMAGE:5755234 /clone_end=5' /gb=BQ067651 /gi=19896697 /ug=Hs.204354 /len=1385 | BQ067651 | Hs.204354 | |
| 8581 | 0.048295 | EST(AV718982 GLC cDNA clone GLCACH01 5') | AV718982 | | |
| 8590 | 0.048295 | EST(601509721F1 NIH_MGC_71 cDNA clone IMAGE:3911140 5') | BE886324 | | NP_777581 |

| Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids | | | | | |
|--|----------|---|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 8607 | 0.018314 | AGENCOURT_6796992 NIH_MGC_85 cDNA clone IMAGE:5787783 5', mRNA sequence /clone=IMAGE:5787783 /clone_end=5' /gb=BQ049841 /gi=19809181 /ug=Hs.292457 /len=1391 | BQ049841 | Hs.292457 | |
| 8621 | 0.023731 | ah42f05.s1 Soares_testis_NHT cDNA clone 1292193 3' similar to P54687 BRANCHED-CHAIN AMINO ACID AMINOTRANSFERASE, CYTOSOLIC ; mRNA sequence /clone=1292193 /clone_end=3' /gb=AA705851 /gi=2715769 /ug=Hs.443872 /len=412 | AA705851 | Hs.443872 | |
| 8657 | 0.010515 | UI-E-EJ1-ajj-p-12-0-UI.s1 UI-E-EJ1 cDNA clone UI-E-EJ1-ajj-p-12-0-UI 3', mRNA sequence /clone=UI-E-EJ1-ajj-p-12-0-UI /clone_end=3' /gb=BM684924 /gi=18994820 /ug=Hs.18514 /len=1033 | BM684924 | Hs.18514 | |
| 8675 | 0.006699 | UI-H-EI0-ayo-a-20-0-UI.s1 NCI_CGAP_EI0 cDNA clone IMAGE:5841307 3', mRNA sequence /clone=IMAGE:5841307 /clone_end=3' /gb=BQ004581 /gi=19729481 /ug=Hs.412459 /len=1095 | BQ004581 | Hs.412459 | |
| 8709 | 0.004131 | clone alpha_est218/52C1 mRNA sequence /gb=AF001542 /gi=2529714 /ug=Hs.356442 /len=2992 | AF001542 | Hs.356442 | |
| 8746 | 0.023731 | tg02e02.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:2107610 3', mRNA sequence /clone=IMAGE:2107610 /clone_end=3' /gb=AI380429 /gi=4190282 /ug=Hs.172445 /len=478 | AI380429 | Hs.172445 | |
| 8782 | 0.001703 | mitochondrion, complete genome | NC_001807 | | |
| 8796 | 0.043185 | ESTs, cDNA, 3' end /clone=UI-E-EJ0-aii-l-19-0-UI /clone_end=3' /gb=BM681301 /gi=18991197 /ug=Hs.355029 /len=591 | BM681301 | Hs.355029 | |
| 8801 | 0.006699 | cDNA, 5' end /clone=IMAGE:5185850 /clone_end=5' /gb=BI759660 /gi=15751238 /ug=Hs.250691 /len=866 | BI759660 | Hs.250691 | |
| 8803 | 0.018314 | clone alpha_est218/52C1 mRNA sequence /gb=AF001542 /gi=2529714 /ug=Hs.356442 /len=2992 | AF001542 | Hs.356442 | |
| 8808 | 0.012137 | EST(cDNA clone CS0DF021YG07 5 prime) | AL535948 | | NP_006612 |
| 8828 | 0.043185 | cDNA FLJ13443 fis, clone PLACE1002853 | AK023505 | | NP_078968 |
| 8840 | 0.038517 | No significant match | SEQ.ID.No.54 | | |
| 8856 | 0.020878 | control | | | |

| Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids | | | | | |
|--|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 8954 | 0.005723 | nj20a07.s1 NCI_CGAP_AA1 cDNA clone IMAGE:993012 3', mRNA sequence /clone=IMAGE:993012 /clone_end=3' /gb=AA570674 /gi=2344654 /ug=Hs.162392 /len=435 | AA570674 | Hs.162392 | |
| 8972 | 0.038517 | EST (ym20a08.r1 Soares infant brain 1NIB IMAGE:48353 5') | H15948 | | |
| 8990 | 0.016017 | hypothetical protein FLJ39514 (FLJ39514), mRNA /cds=(121,2040) /gb=NM_152540 /gi=22749126 /ug=Hs.48565 /len=2221 | NM_152540 | Hs.48565 | NP_689753 |
| 9088 | 0.030399 | clone IMAGE:3875308, mRNA, partial cds /cds=UNKNOWN /gb=BC013784 /gi=15489380 /ug=Hs.351379 /len=2872 | BC013784 | Hs.351379 | |
| 9162 | 0.012137 | ah98a04.s1 Soares_NFL_T_GBC_S1 cDNA clone IMAGE:1327086 3', mRNA sequence /clone=IMAGE:1327086 /clone_end=3' /gb=AA757363 /gi=2805226 /ug=Hs.105224 /len=444 | AA757363 | Hs.105224 | |
| 9192 | 0.043185 | mRNA full length insert cDNA clone EUROIMAGE 1271944 /cds=UNKNOWN /gb=AJ420453 /gi=17066317 /ug=Hs.351834 /len=1186 | AJ420453 | Hs.351834 | NP_006435 |
| 9217 | 0.030399 | EST (clone IMAGE:4719448 5') | BG570753 | | |
| 9222 | 0.010515 | EST(cDNA clone CS0DI054YF18 5 prime) | AL549795 | | NP_003109 |
| 9225 | 0.048295 | UI-H-DT0-atx-c-08-0-UI.s1 NCI_CGAP_DT0 cDNA clone IMAGE:5865535 3', mRNA sequence /clone=IMAGE:5865535 /clone_end=3' /gb=BM992885 /gi=19712274 /ug=Hs.436581 /len=1301 | BM992885 | Hs.436581 | |
| 9266 | 0.026896 | clone FLB2932 mRNA sequence /gb=AF138859 /gi=7340965 /ug=Hs.274405 /len=2990 | AF138859 | Hs.274405 | |
| 9274 | 0.002459 | mRNA; cDNA DKFZp586G2120 (from clone DKFZp586G2120); complete cds /cds=(19,2604) /gb=AL136924 /gi=12053342 /ug=Hs.62349 /len=4137 | AL136924 | Hs.62349 | NP_061866 |
| 9275 | 0.003489 | ESTs, cDNA, 5' end /clone=IMAGE:3857750 /clone_end=5' /gb=BF035134 /gi=10742846 /ug=Hs.195789 /len=847 | BF035134 | Hs.195789 | |

| Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids | | | | | |
|--|----------|---|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 9289 | 0.048295 | UI-CF-EC1-abq-b-24-0-UI.s1 UI-CF-EC1 cDNA clone UI-CF-EC1-abq-b-24-0-UI 3', mRNA sequence /clone=UI-CF-EC1-abq-b-24-0-UI /clone_end=3' /gb=BM972502 /gi=19590088 /ug=Hs.366185 /len=718 | BM972502 | Hs.366185 | |
| 9310 | 0.038517 | No significant match | SEQ.ID.No.71 | | |
| 9319 | 9.48E-04 | No significant match (ORF:+2:2~226[225]), low complexity | SEQ.ID.No.17 | | |
| 9326 | 0.034264 | UI-1-BB1p-akc-h-10-0-UI.s1 NCI_CGAP_PI6 cDNA clone UI-1-BB1p-akc-h-10-0-UI 3', mRNA sequence /clone=UI-1-BB1p-akc-h-10-0-UI /clone_end=3' /gb=BQ026175 /gi=19761454 /ug=Hs.127786 /len=1398 | BQ026175 | Hs.127786 | |
| 9447 | 0.030399 | hypothetical protein PNAS-131 (PNAS-131), mRNA /cds=(288,686) /gb=NM_031446 /gi=21361962 /ug=Hs.37883 /len=1124 | NM_031446 | Hs.37883 | NP_113634 |
| 9468 | 0.013965 | hypothetical protein MGC13159 (MGC13159), mRNA /cds=(592,1017) /gb=NM_032927 /gi=14249719 /ug=Hs.12845 /len=1759 | NM_032927 | Hs.12845 | NP_116316 |
| 9489 | 0.002935 | similar to putative (H. sapiens) (LOC129641), mRNA | XM_059369 | | |
| 9498 | 0.005723 | PFTAIRE protein kinase 1 (PFTK1), mRNA /cds=(145,1500) /gb=NM_012395 /gi=6912583 /ug=Hs.57856 /len=4957 | NM_012395 | Hs.57856 | NP_036527 |
| 9511 | 0.034264 | emopamil binding related protein, delta8-delta7 sterol isomerase related protein (EBRP), mRNA /cds=(53,673) /gb=NM_032565 /gi=14211872 /ug=Hs.433278 /len=931 | NM_032565 | Hs.433278 | NP_115954 |
| 9516 | 0.007812 | ras gene family, member E (ARHE), mRNA /cds=(141,875) /gb=NM_005168 /gi=21361257 /ug=Hs.6838 /len=2685 | NM_005168 | Hs.6838 | NP_005159 |
| 9530 | 0.030399 | hypothetical protein FLJ10856 (FLJ10856), mRNA /cds=(148,1233) /gb=NM_018247 /gi=8922719 /ug=Hs.108530 /len=3720 | NM_018247 | Hs.108530 | NP_060717 |
| 9533 | 0.023731 | hypothetical protein FLJ20303 (FLJ20303), mRNA /cds=(86,1681) /gb=NM_017755 /gi=8923284 /ug=Hs.17138 /len=2427 | NM_017755 | Hs.17138 | NP_060225 |
| 9570 | 0.034264 | ERO1-like (S. cerevisiae) (ERO1L), mRNA /cds=(227,1633) /gb=NM_014584 /gi=7657068 /ug=Hs.25740 /len=3334 | NM_014584 | Hs.25740 | NP_055399 |

| Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids | | | | | |
|--|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | D scription | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 9581 | 0.007812 | partial steerin-1 gene | AJ251973 | | |
| 9722 | 0.043185 | EST(nk66b07.s1 NCI_CGAP_Sch1 clone IMAGE:1018453) | AA578852 | | |
| 9745 | 0.020878 | hypothetical protein MGC32104 (MGC32104), mRNA /cds=(101,1651) /gb=NM_144684 /gi=21389584 /ug=Hs.147025 /len=4732 | NM_144684 | Hs.147025 | NP_653285 |
| 9762 | 0.004131 | poly(A) binding protein, cytoplasmic 5 (PABPC5), mRNA /cds=(441,1589) /gb=NM_080832 /gi=18201887 /ug=Hs.190614 /len=3521 | NM_080832 | Hs.190614 | NP_543022 |
| 9817 | 0.016017 | EST (nh05d12.s1 NCI_CGAP_Thy1 IMAGE:943415) | AA493662 | | |
| 9820 | 0.034264 | EST (nk75h03.s1 NCI_CGAP_Sch1 cDNA clone IMAGE:1019381 3') | AA551135 | | |
| 9835 | 0.043185 | armadillo repeat protein ALEX2 (ALEX2), mRNA /cds=(458,2356) /gb=NM_014782 /gi=21361239 /ug=Hs.48924 /len=2788 | NM_014782 | Hs.48924 | NP_808818 |
| 9886 | 0.013965 | mRNA, cDNA DKFZp451F1910 (from clone DKFZp451F1910) /gb=AL833265 /gi=21733898 /ug=Hs.332030 /len=5254 | AL833265 | Hs.332030 | |
| 9913 | 0.048295 | serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1 (SERPINE1), mRNA /cds=(76,1284) /gb=NM_000602 /gi=10835158 /ug=Hs.82085 /len=2876 | NM_000602 | Hs.82085 | NP_000593 |
| 9965 | 0.004872 | hypothetical protein DKFZp434K1421 (DKFZP434K1421), mRNA /cds=(29,1705) /gb=NM_032141 /gi=14149806 /ug=Hs.374609 /len=2547 | NM_032141 | Hs.374609 | NP_115517 |
| 9977 | 0.030399 | mitochondrial carrier 2 (MTCH2), nuclear gene encoding mitochondrial protein, mRNA /cds=(49,960) /gb=NM_014342 /gi=7657346 /ug=Hs.279609 /len=1104 | NM_014342 | Hs.279609 | NP_055157 |
| 9978 | 0.005723 | cerebral cavernous malformations 1 (CCM1), mRNA /cds=(26,1615) /gb=NM_004912 /gi=4758657 /ug=Hs.93810 /len=2004 | NM_004912 | Hs.93810 | NP_004903 |
| 9990 | 0.034264 | hypothetical protein FLJ23467 (FLJ23467), mRNA /cds=(103,657) /gb=NM_024575 /gi=13375749 /ug=Hs.16179 /len=1196 | NM_024575 | Hs.16179 | NP_078851 |
| 10026 | 0.002935 | dishevelled associated activator of morphogenesis 1 (DAAM1), mRNA /cds=(126,3362) /gb=NM_014992 /gi=21071076 /ug=Hs.197751 /len=4256 | NM_014992 | Hs.197751 | NP_055807 |

| Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids | | | | | |
|--|----------|---|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Prot in Accession No. |
| 10051 | 0.012137 | DNA segment on chromosome X and Y (unique) 155 expressed sequence (DXYS155E), mRNA /cds=(167,1324) /gb=NM_005088 /gi=10835221 /ug=Hs.21595 /len=3233 | NM_005088 | Hs.21595 | NP_005079 |
| 10052 | 0.048295 | casein kinase (LOC149420), mRNA /cds=(290,1315) /gb=NM_152835 /gi=22779869 /ug=Hs.29911 /len=4299 | NM_152835 | Hs.29911 | NP_690048 |
| 10053 | 0.048295 | inorganic pyrophosphatase (SID6-306), mRNA /cds=(108,932) /gb=NM_006903 /gi=13491177 /ug=Hs.5123 /len=1115 | NM_006903 | Hs.5123 | NP_789845 |
| 10077 | 0.018314 | ATPase, H transporting, lysosomal 70kDa; V1 subunit A, isoform 1 (ATP6V1A1), mRNA /cds=(67,1920) /gb=NM_001690 /gi=19913423 /ug=Hs.281866 /len=4567 | NM_001690 | Hs.281866 | NP_001681 |
| 10080 | 4.04E-04 | hypothetical protein DKFZp761N0624 (DKFZp761N0624), mRNA /cds=(113,1444) /gb=NM_032295 /gi=14150046 /ug=Hs.21893 /len=2973 | NM_032295 | Hs.21893 | NP_115671 |
| 10134 | 0.020878 | x159d02.x1 NCI_CGAP_Pan1 cDNA clone IMAGE:2678979 3', mRNA sequence /clone=IMAGE:2678979 /clone_end=3' /gb=AW190111 /gi=6464591 /ug=Hs.377837 /len=248 | AW190111 | Hs.377837 | |
| 10151 | 0.023731 | cDNA FLJ36605 fis, clone TRACH2015316, highly similar to VIMENTIN. /cds=(631,1317) /gb=AK093924 /gi=21752883 /ug=Hs.379100 /len=2665 | AK093924 | Hs.379100 | |
| 10181 | 0.016017 | UI-1-BB1p-aut-a-09-0-UI.s1 NCI_CGAP_PI6 cDNA clone UI-1-BB1p-aut-a-09-0-UI 3', mRNA sequence /clone=UI-1-BB1p-aut-a-09-0-UI /clone_end=3' /gb=BQ024447 /gi=19759726 /ug=Hs.150289 /len=1021 | BQ024447 | Hs.150289 | |
| 10183 | 0.026896 | cDNA: FLJ20924 fis, clone ADSE00928. /gb=AK024577 /gi=10436889 /ug=Hs.306692 /len=1516 | AK024577 | Hs.306692 | |
| 10189 | 0.038517 | EST(ag56f05.s1 Gessler Wilms tumor clone 1126977 3') | AA665893 | | |
| 10205 | 0.001703 | EST (ol74f05.s1 NCI_CGAP_Kid3 cDNA clone IMAGE:1535361 3') | AA919165 | | |
| 10235 | 0.043185 | UI-H-ED0-awz-e-06-0-UI.s1 NCI_CGAP_ED0 cDNA clone IMAGE:5825645 3', mRNA sequence /clone=IMAGE:5825645 /clone_end=3' /gb=BM995013 /gi=19719914 /ug=Hs.23871 /len=1235 | BM995013 | Hs.23871 | |

| Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids | | | | | |
|--|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 10240 | 0.030399 | hypothetical protein DKFZp586C1924 (DKFZp586C1924), mRNA /cds=(106,693) /gb=NM_032273 /gi=14150016 /ug=Hs.108338 /len=782 | NM_032273 | Hs.108338 | NP_115649 |
| 10247 | 0.023731 | vimentin (VIM) gene | M18895 | | |
| 10274 | 0.007812 | EST (EST97907 Thyroid cDNA 5') | AA384394 | | |
| 10323 | 0.030399 | mRNA; cDNA DKFZp434K1115 (from clone DKFZp434K1115); complete cds /cds=(97,2877) /gb=AL136764 /gi=12053044 /ug=Hs.42676 /len=4868 | AL136764 | Hs.42676 | |
| 10328 | 0.030399 | EST (CM0-UM0033-010300-257-c04 UM0033) | AW796764 | | |
| 10350 | 0.007812 | hypothetical protein FLJ90013 (FLJ90013), mRNA /cds=(15,1703) /gb=NM_153365 /gi=23503310 /ug=Hs.25119 /len=3382 | NM_153365 | Hs.25119 | NP_699196 |
| 10382 | 0.026896 | hypothetical protein DKFZp761N0624 (DKFZp761N0624), mRNA /cds=(113,1444) /gb=NM_032295 /gi=14150046 /ug=Hs.21893 /len=2973 | NM_032295 | Hs.21893 | NP_115671 |
| 10385 | 0.038517 | chondroitin sulfate GalNAcT-2 (GALNAcT-2), mRNA /cds=(336,1964) /gb=NM_018590 /gi=24429591 /ug=Hs.180758 /len=3745 | NM_018590 | Hs.180758 | NP_061060 |
| 10388 | 0.016017 | UI-CF-FN0-aes-e-05-0-UI.s1 UI-CF-FN0 cDNA clone UI-CF-FN0-aes-e-05-0-UI 3', mRNA sequence /clone=UI-CF-FN0-aes-e-05-0-UI /clone_end=3' /gb=BU607793 /gi=23272751 /ug=Hs.188375 /len=1090 | BU607793 | Hs.188375 | |
| 10443 | 0.032747 | EST(xw02a10.x1 NCI_CGAP_Brn53 cDNA clone IMAGE:2826810 3' similar to TR:Q12791 Q12791 CALCIUM-ACTIVATED POTASSIUM CHANNEL) | AW305218 | | NP_002238 |
| 10474 | 0.048295 | EST(cDNA clone IMAGE:2505486 3') | AW004819 | | NP_612487 |
| 10505 | 0.013965 | mRNA; cDNA DKFZp451B134 (from clone DKFZp451B134) /gb=AL832009 /gi=21732549 /ug=Hs.102796 /len=4843 | AL832009 | Hs.102796 | |
| 10566 | 0.034264 | actin, beta (ACTB), mRNA /cds=(74,1201) /gb=NM_001101 /gi=5016088 /ug=Hs.426930 /len=1793 | NM_001101 | Hs.426930 | NP_001092 |
| 10596 | 0.038517 | 602584296F1 NIH_MGC_76 cDNA clone IMAGE:4712302 5', mRNA sequence /clone=IMAGE:4712302 /clone_end=5' /gb=BG564611 /gi=13572263 /ug=Hs.136470 /len=896 | BG564611 | Hs.136470 | |

| Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids | | | | | |
|--|----------|--|--------------------|----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigen Accession No. | Protein Accession No. |
| 10627 | 0.016017 | 602584221F1 NIH_MGC_76 cDNA clone IMAGE:4712140 5', mRNA sequence /clone=IMAGE:4712140 /clone_end=5' /gb=BG564543 /gi=13572195 /ug=Hs.105449 /len=981 | BG564543 | Hs.105449 | |
| 10633 | 0.018314 | UI-E-CL1-afa-n-02-0-UI.r1 UI-E-CL1 cDNA clone UI-E-CL1-afa-n-02-0-UI 5', mRNA sequence /clone=UI-E-CL1-afa-n-02-0-UI /clone_end=5' /gb=BM696235 /gi=19009493 /ug=Hs.446332 /len=1366 | BM696235 | Hs.446332 | |
| 10675 | 0.006699 | cDNA FLJ11309 fis, clone PLACE1010076. /gb=AK002171 /gi=7023887 /ug=Hs.28005 /len=3232 | AK002171 | Hs.28005 | |
| 10680 | 0.013965 | cDNA, 5' end /clone=IMAGE:4513481 /clone_end=5' /gb=BG287554 /gi=13041502 /ug=Hs.374391 /len=988 | BG287554 | Hs.374391 | NP_776158 |
| 10717 | 0.004131 | No significant match | SEQ.ID.No.83 | | |
| 10771 | 0.023731 | HUM515D03B Clontech placenta polyA mRNA (#6518) cDNA clone GEN-515D03 5', mRNA sequence /clone=GEN-515D03 /clone_end=5' /gb=D58893 /gi=968527 /ug=Hs.335953 /len=365 | D58893 | Hs.335953 | |
| 10788 | 0.006699 | yg45f12.s1 Soares infant brain 1NIB cDNA clone IMAGE:35625 3', mRNA sequence /clone=IMAGE:35625 /clone_end=3' /gb=R45691 /gi=822137 /ug=Hs.268774 /len=574 | R45691 | Hs.268774 | |
| 10804 | 0.038517 | EST (yr74c11.s1 Soares fetal liver spleen 1NFLS IMAGE:211028 3') | H65780 | | |
| 10847 | 0.038517 | hypothetical protein MGC3200 (MGC3200), mRNA /cds=(108,764) /gb=NM_032305 /gi=14150063 /ug=Hs.9088 /len=1191 | NM_032305 | Hs.9088 | NP_115681 |
| 10855 | 0.016017 | EST 7h93e02.x1 NCI_CGAP_Co16 cDNA clone IMAGE:3323546 3' | BF064070 | | |
| 10869 | 0.026896 | EST DKFZp434D1916_r1 434 (synonym:htes3) cDNA clone DKFZp434D1916 5' | AL041117 | | |
| 10898 | 0.016017 | heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa) (HSPA5), mRNA /cds=(205,2169) /gb=NM_005347 /gi=21361242 /ug=Hs.75410 /len=3925 | NM_005347 | Hs.75410 | NP_005338 |
| 10901 | 0.030399 | CCR4-NOT transcription complex, subunit 7 (CNOT7), transcript variant 1, mRNA /cds=(340,1128) /gb=NM_013354 /gi=17978498 /ug=Hs.380963 /len=2653 | NM_013354 | Hs.380963 | NP_473367 |

| Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids | | | | | |
|--|----------|---|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 10940 | 0.004872 | mRNA, cDNA DKFZp686K192 (from clone DKFZp686K192) /gb=AL832209 /gi=21732754 /ug=Hs.259347 /len=6707 | AL832209 | Hs.259347 | |
| 10972 | 0.026896 | fetal liver cDNA library Human cDNA | AI132941 | | |
| 10976 | 0.034264 | in56e04.x1 HR85 islet cDNA clone IMAGE:6126055 3', mRNA sequence /clone=IMAGE:6126055 /clone_end=3' /gb=BU784825 /gi=23830229 /ug=Hs.442971 /len=548 | BU784825 | Hs.442971 | |
| 10984 | 0.034264 | ESTs, cDNA, 3' end /clone=IMAGE:2385007 /clone_end=3' /gb=AI796655 /gi=5362118 /ug=Hs.132315 /len=516 | AI796655 | Hs.132315 | |
| 10992 | 0.048295 | mRNA, cDNA DKFZp586K1922 (from clone DKFZp586K1922) /gb=AL110204 /gi=5817123 /ug=Hs.193784 /len=3561 | AL110204 | Hs.193784 | |
| 11003 | 0.026896 | cDNA FLJ14832 fis, clone OVARC1001169. /gb=AK027738 /gi=14042638 /ug=Hs.235860 /len=2350 | AK027738 | Hs.235860 | |
| 11009 | 0.034264 | EST(adult retina cDNA Danio rerio cDNA clone 4201579 3' similar to TR:Q9YH14 Q9YH14 PROGESTERONE RECEPTOR BINDING PROTEIN.) | BI880587 | | |
| 11032 | 0.009079 | nj38c05.s1 NCI_CGAP_AA1 cDNA clone IMAGE:994760 3' similar to gb:M62424 THROMBIN RECEPTOR PRECURSOR mRNA sequence /clone=IMAGE:994760 /clone_end=3' /gb=AA548630 /gi=2318912 /ug=Hs.105848 /len=555 | AA548630 | Hs.105848 | |
| 11132 | 0.048295 | UI-H-CO0-aqz-b-03-0-UI.s1 NCI_CGAP_Sub9 cDNA clone IMAGE:3105700 3', mRNA sequence /clone=IMAGE:3105700 /clone_end=3' /gb=BQ027621 /gi=19762900 /ug=Hs.442094 /len=922 | BQ027621 | Hs.442094 | |
| 11136 | 0.048295 | clone IMAGE:3138608, mRNA /cds=UNKNOWN /gb=BC007266 /gi=13938277 /ug=Hs.334566 /len=1635 | BC007266 | Hs.334566 | |
| 11141 | 0.023731 | cDNA FLJ38591 fis, clone HEART1000151. /gb=AK095910 /gi=21755261 /ug=Hs.63243 /len=2411 | AK095910 | Hs.63243 | |
| 11143 | 0.020878 | EST(NIH_MGC_75 cDNA clone IMAGE:4614964 5') | BG427835 | | |
| 11146 | 0.038517 | EST380541 MAGE resequences, MAGJ cDNA, mRNA sequence /gb=AW968465 /gi=8158306 /ug=Hs.351848 /len=658 | AW968465 | Hs.351848 | |

| Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids | | | | | |
|--|----------|---|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 11161 | 0.043185 | ESTs, cDNA /gb=AW975851 /gi=8167072 /ug=Hs.361171 /len=684 | AW975851 | Hs.361171 | |
| 11164 | 0.026896 | UI-H-CO0-arf-f-05-0-UI.s1 NCI_CGAP_Sub9 cDNA clone IMAGE:3106304 3', mRNA sequence /clone=IMAGE:3106304 /clone_end=3' /gb=BQ027925 /gi=19763204 /ug=Hs.162459 /len=968 | BQ027925 | Hs.162459 | |
| 11165 | 0.026896 | mRNA full length insert cDNA clone EUROIMAGE 73337. /gb=AL109705 /gi=5689834 /ug=Hs.9997 /len=1227 | AL109705 | Hs.9997 | |
| 11203 | 4.04E-04 | cDNA FLJ38383 fis, clone FEBRA2003726. /gb=AK095702 /gi=21755022 /ug=Hs.433517 /len=3240 | AK095702 | Hs.433517 | |
| 11243 | 0.009079 | apoA polymorphism Kringle IV gene, exons 1 and 2 | L14005 | | |
| 11321 | 0.026896 | transient receptor potential cation channel, subfamily C, member 1 (TRPC1), mRNA /cds=(138,2417) /gb=NM_003304 /gi=27545448 /ug=Hs.250687 /len=4085 | NM_003304 | Hs.250687 | NP_003295 |
| 11365 | 0.028869 | Rho-specific guanine-nucleotide exchange factor 164 kDa (P164RHOGF), mRNA /cds=(16,6207) /gb=NM_014786 /gi=21361457 /ug=Hs.45180 /len=7540 | NM_014786 | Hs.45180 | NP_055601 |
| 11376 | 0.020878 | a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 3 (ADAMTS3), mRNA /cds=(38,3655) /gb=NM_014243 /gi=21265036 /ug=Hs.27916 /len=5821 | NM_014243 | Hs.27916 | NP_055058 |
| 11380 | 0.009079 | clone IMAGE:4837455, mRNA /gb=BC045818 /gi=28279091 /ug=Hs.406481 /len=2600 | BC045818 | Hs.406481 | |
| 11402 | 0.043185 | cytochrome c, somatic (CYCS), mRNA /cds=(61,378) /gb=NM_018947 /gi=21361707 /ug=Hs.169248 /len=3990 | NM_018947 | Hs.169248 | NP_061820 |
| 11427 | 0.034264 | DKFZP586A0522 protein (DKFZP586A0522), mRNA /cds=(21,755) /gb=NM_014033 /gi=13378140 /ug=Hs.288771 /len=1705 | NM_014033 | Hs.288771 | NP_054752 |
| 11438 | 0.013965 | hypothetical protein FLJ20360 (FLJ20360), mRNA /cds=(80,2305) /gb=NM_017782 /gi=8923334 /ug=Hs.26434 /len=3041 | NM_017782 | Hs.26434 | NP_060252 |
| 11467 | 0.030399 | SMT3 suppressor of mif two 3 1 (yeast) (SMT3H1), mRNA /cds=(95,406) /gb=NM_006936 /gi=5902095 /ug=Hs.85119 /len=1733 | NM_006936 | Hs.85119 | NP_008867 |

| Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids | | | | | |
|--|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 11482 | 0.043185 | clone IMAGE:5271722, mRNA /gb=BC038786 /gi=24270905 /ug=Hs.190456 /len=1535 | BC038786 | Hs.190456 | |
| 11502 | 0.023731 | mRNA for KIAA1229 protein, partial cds /cds=UNKNOWN /gb=AB033055 /gi=6330699 /ug=Hs.71109/len=5654 | AB033055 | Hs.71109 | |
| 11546 | 0.020878 | EST(PM3-NT0011-120400-001-b03 NT0011) | AW888715 | | |
| 11584 | 0.043185 | clone IMAGE:4769230, mRNA /gb=BC022409 /gi=18490247 /ug=Hs.346398 /len=1667 | BC022409 | Hs.346398 | |
| 11593 | 0.006699 | 602634689F1 NCI_CGAP_Skn3 cDNA clone IMAGE:4779575 5', mRNA sequence /clone=IMAGE:4779575 /clone_end=5' /gb=BG743384 /gi=14054037 /ug=Hs.32345 /len=805 | BG743384 | Hs.32345 | |
| 11597 | 0.048295 | EST HUM517A08B Clontech human placenta polyA mRNA (#6572) Human sapiens cDNA clone GEN-517A08 5' | D63277 | | |
| 11615 | 0.016017 | mRNA for KIAA0261 gene, partial cds. /cds=(1,3866) /gb=D87450 /gi=1665788 /ug=Hs.154978 /len=6155 | D87450 | Hs.154978 | |
| 11617 | 0.013965 | UI-H-EI1-azc-f-09-0-UI.s1 NCI_CGAP_EI1 cDNA clone IMAGE:5846792 3', mRNA sequence /clone=IMAGE:5846792 /clone_end=3' /gb=BQ026855 /gi=19762134 /ug=Hs.446663 /len=875 | BQ026855 | Hs.446663 | |
| 11634 | 0.010515 | hypothetical protein FLJ12118 (FLJ12118), mRNA /cds=(24,1718) /gb=NM_024537 /gi=13375694 /ug=Hs.381043 /len=1843 | NM_024537 | Hs.381043 | NP_078813 |
| 11636 | 0.018314 | hypothetical protein FLJ20719 (FLJ20719), mRNA /cds=(402,2213) /gb=NM_017940 /gi=24308174 /ug=Hs.446473 /len=3745 | NM_017940 | Hs.446473 | NP_060410 |
| 11654 | 0.038517 | clone IMAGE:5260918, mRNA /gb=BC035085 /gi=23958865 /ug=Hs.250448 /len=3052 | BC035085 | Hs.250448 | |
| 11733 | 0.030399 | hypothetical protein FLJ14360 (FLJ14360), mRNA /cds=(110,2014) /gb=NM_032775 /gi=24432025 /ug=Hs.347964 /len=2602 | NM_032775 | Hs.347964 | NP_116164 |
| 11770 | 0.048295 | FLJ33160 fis, clone UTERU2000485 /cds=UNKNOWN /gb=AK057722 /gi=16553641 /ug=Hs.124733 /len=2328 | AK057722 | Hs.124733 | |
| 11851 | 0.026896 | mitochondrion, complete genome | NC_001807 | | |

| Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids | | | | | |
|--|----------|---|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 11855 | 0.013965 | vacuolar protein sorting 41 (yeast) (VPS41), transcript variant 1, mRNA /cds=(27,2591) /gb=NM_014396 /gi=18105059 /ug=Hs.180941 /len=4914 | NM_014396 | Hs.180941 | NP_542198 |
| 11870 | 0.043185 | clone 114 tumor rejection antigen mRNA, complete cds /cds=(3482,3544) /gb=AF445027 /gi=17386079 /ug=Hs.24723 /len=3648 | AF445027 | Hs.24723 | |
| 11883 | 0.048295 | nuclear receptor co-repressor 2 (NCOR2), mRNA /cds=(2,7555) /gb=NM_006312 /gi=5454073 /ug=Hs.287994 /len=8561 | NM_006312 | Hs.287994 | NP_006303 |
| 11897 | 0.016017 | hypothetical protein FLJ20701 (FLJ20701), mRNA /cds=(39,938) /gb=NM_017933 /gi=8923631 /ug=Hs.424598 /len=2284 | NM_017933 | Hs.424598 | NP_060403 |
| 11901 | 0.048295 | chromosome 14 open reading frame 103 (C14orf103), mRNA /cds=(354,2342) /gb=NM_018036 /gi=21361677 /ug=Hs.168241 /len=3361 | NM_018036 | Hs.168241 | NP_060506 |
| 11907 | 0.026896 | hypothetical gene supported by AL117650 (LOC123223), mRNA | XM_071824 | | |
| 11913 | 0.048295 | mRNA; cDNA DKFZp434H2019 (from clone DKFZp434H2019) /gb=AL137535 /gi=6808211 /ug=Hs.15806 /len=1974 | AL137535 | Hs.15806 | |
| 11946 | 0.013965 | hypothetical protein FLJ20432 (FLJ20432), mRNA /cds=(603,1361) /gb=NM_017819 /gi=8923404 /ug=Hs.57898 /len=1654 | NM_017819 | Hs.57898 | NP_060289 |
| 11947 | 0.032747 | polymerase (RNA) II (DNA directed) polypeptide H (POLR2H), mRNA /cds=(88,540) /gb=NM_006232 /gi=14589952 /ug=Hs.432574 /len=821 | NM_006232 | Hs.432574 | NP_006223 |
| 11967 | 0.020878 | TNF receptor-associated factor 5 (TRAF5), transcript variant 1, mRNA /cds=(194,1867) /gb=NM_004619 /gi=22027625 /ug=Hs.29736 /len=4132 | NM_004619 | Hs.29736 | NP_665702 |
| 11974 | 0.034264 | cDNA FLJ12280 fis, clone MAMMA1001744. /gb=AK022342 /gi=10433719 /ug=Hs.288467 /len=3189 | AK022342 | Hs.288467 | |
| 11979 | 0.046968 | chromosome 20 open reading frame 6 (C20orf6), mRNA /cds=(109,2664) /gb=NM_016649 /gi=22507381 /ug=Hs.88820 /len=3216 | NM_016649 | Hs.88820 | NP_057733 |
| 11985 | 0.030399 | protocadherin beta 16 (PCDHB16), mRNA /cds=(1156,3486) /gb=NM_020957 /gi=14195604 /ug=Hs.147674 /len=4827 | NM_020957 | Hs.147674 | NP_066008 |

| Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids | | | | | |
|--|----------|--|--------------------|----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigen Accession No. | Protein Accession No. |
| 12080 | 0.030399 | AGENCOURT_8899857 NIH_MGC_142 cDNA clone IMAGE:6451082 5', mRNA sequence /clone=IMAGE:6451082 /clone_end=5' /gb=BU595281 /gi=23247040 /ug=Hs.5250 /len=1163 | BU595281 | Hs.5250 | |
| 12085 | 0.016017 | retinoic acid induced 14 (RAI14), mRNA /cds=(112,3054) /gb=NM_015577 /gi=13470085 /ug=Hs.15165 /len=4925 | NM_015577 | Hs.15165 | NP_056392 |
| 12087 | 0.043185 | hypothetical protein FLJ21313 (FLJ21313), mRNA /cds=(199,1497) /gb=NM_023927 /gi=12965196 /ug=Hs.235445 /len=2912 | NM_023927 | Hs.235445 | NP_076416 |
| 12099 | 0.019416 | nuclear cap binding protein subunit 2, 20kDa (NCBP2), mRNA /cds=(27,497) /gb=NM_007362 /gi=19923386 /ug=Hs.240770 /len=2120 | NM_007362 | Hs.240770 | NP_031388 |
| 12103 | 0.032747 | UI-H-FH0-bce-d-09-0-UI.s1 NCI_CGAP_FH0 cDNA clone UI-H-FH0-bce-d-09-0-UI 3', mRNA sequence /clone=UI-H-FH0-bce-d-09-0-UI /clone_end=3' /gb=BQ774102 /gi=21982578 /ug=Hs.380398 /len=1094 | BQ774102 | Hs.380398 | |
| 12161 | 0.012137 | EST(hh76d05.y1 NCI_CGAP_GU1 cDNA clone IMAGE:2968713 5' similar to contains L1.t1 L1 repetitive element ; | AW663260 | | |
| 12224 | 0.030399 | gp25L2 protein (HSGP25L2G), mRNA /cds=(76,720) /gb=NM_017510 /gi=24475637 /ug=Hs.279929 /len=1420 | NM_017510 | Hs.279929 | NP_059980 |
| 12229 | 0.034264 | clone IMAGE:3924941, mRNA /gb=BC029341 /gi=20379505 /ug=Hs.391380 /len=1657 | BC029341 | Hs.391380 | |
| 12233 | 0.026896 | chemokine-like factor super family 3 (CKLFSF3), mRNA /cds=(527,1075) /gb=NM_144601 /gi=21389400 /ug=Hs.7773 /len=2318 | NM_144601 | Hs.7773 | NP_653202 |
| 12243 | 0.038517 | mRNA; cDNA DKFZp313P0434 (from clone DKFZp313P0434) /gb=AL832702 /gi=21733281 /ug=Hs.125019 /len=2995 | AL832702 | Hs.125019 | |
| 12248 | 0.021523 | EST(yd28g06.r1 Soares fetal liver spleen 1NFLS IMAGE:109594 5') | T82238 | | |
| 12257 | 0.048295 | EST390958 MAGE resequences, MAGP cDNA, mRNA sequence /gb=AW978849 /gi=8170126 /ug=Hs.124977 /len=678 | AW978849 | Hs.124977 | |
| 12267 | 0.018314 | EST (op46b10.s1 Soares_NFL_T_GBC_S1 IMAGE:1579867 3') | AA978266 | | |

| Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids | | | | | |
|--|----------|---|------------------|-----------------------|-----------------------|
| Spot | p-value | D scription | Gene Accession N | Unigene Accession No. | Protein Accession No. |
| 12355 | 0.043185 | cDNA FLJ36238 fis, clone THYMU2001422. /gb=AK093557 /gi=21752458 /ug=Hs.345588 /len=2269 | AK093557 | Hs.345588 | |
| 12389 | 0.030399 | UI-HF-BN0-afr-f-07-0-UI.r1 NIH_MGC_50 cDNA clone IMAGE:3067908 5', mRNA sequence /clone=IMAGE:3067908 /clone_end=5' /gb=BU431616 /gi=22770103 /ug=Hs.202538 /len=551 | BU431616 | Hs.202538 | |
| 12426 | 0.010515 | 602590145F1 NIH_MGC_76 cDNA clone IMAGE:4724074 5', mRNA sequence /clone=IMAGE:4724074 /clone_end=5' /gb=BG564169 /gi=13571821 /ug=Hs.444093 /len=792 | BG564169 | Hs.444093 | |
| 12429 | 0.006699 | EST(cDNA clone IMAGE:3913767 5') | BE890088 | | |
| 12440 | 0.034264 | clone IMAGE:5286019, mRNA /gb=BC042960 /gi=27693187 /ug=Hs.5724 /len=3174 | BC042960 | Hs.5724 | |
| 12470 | 0.038517 | cDNA: FLJ22930 fis, clone KAT07255. /gb=AK026583 /gi=10439467 /ug=Hs.90790 /len=1600 | AK026583 | Hs.90790 | |
| 12484 | 0.041767 | qa50a08.x1 Soares_NhHMPu_S1 cDNA clone IMAGE:1690166 3', mRNA sequence /clone=IMAGE:1690166 /clone_end=3' /gb=AI123569 /gi=3539335 /ug=Hs.117060 /len=773 | AI123569 | Hs.117060 | |
| 12540 | 0.023731 | UI-H-FE0-bbv-m-15-0-UI.s1 NCI_CGAP_FE0 cDNA clone UI-H-FE0-bbv-m-15-0-UI 3', mRNA sequence /clone=UI-H-FE0-bbv-m-15-0-UI /clone_end=3' /gb=CA416757 /gi=24779408 /ug=Hs.399730 /len=759 | CA416757 | Hs.399730 | |
| 12541 | 9.48E-04 | yb61c11.s1 Stratagene ovary (#937217) cDNA clone IMAGE:75668 3', mRNA sequence /clone=IMAGE:75668 /clone_end=3' /gb=T58438 /gi=660275 /ug=Hs.189678 /len=506 | T58438 | Hs.189678 | |
| 12562 | 0.023731 | C14379 Clontech aorta polyA mRNA (#6572) cDNA clone GEN-051F07 3', mRNA sequence /clone=GEN-051F07 /clone_end=3' /gb=C14379 /gi=1569086 /ug=Hs.439346 /len=417 | C14379 | Hs.439346 | |
| 12574 | 0.043185 | UI-H-ED0-awx-b-15-0-UI.s1 NCI_CGAP_ED0 cDNA clone IMAGE:5824814 3', mRNA sequence /clone=IMAGE:5824814 /clone_end=3' /gb=BQ020068 /gi=19755345 /ug=Hs.396278 /len=1351 | BQ020068 | Hs.396278 | |
| 12604 | 0.001703 | EST(IL3-HT0618-120500-138-D11 HT0618 cDNA, MRNA sequence) | BE179957 | | |

| Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids | | | | | |
|--|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 12664 | 0.016017 | hypothetical protein FLJ12888 (FLJ12888), mRNA /cds=(333,2210) /gb=NM_024945 /gi=13376426 /ug=Hs.284137 /len=3413 | NM_024945 | Hs.284137 | NP_079221 |
| 12685 | 0.013965 | EST (th94c08.x1Soares_NSF_F8_9W_OT_P A_P_S1 cDNA clone IMAGE:2126318 3' | AI435422 | | |
| 12695 | 0.038517 | mitochondrion, complete genome | NC_001807 | | |
| 12725 | 0.043185 | EST(CM3-BN0151-130400-146-f01_1 BN0151) | BE008220 | | |
| 12732 | 0.006699 | mitochondrion, complete genome | NC_001807 | | |
| 12734 | 1.21E-05 | mRNA for FLJ00201 protein. /cds=(1,2119) /gb=AK074129. /gi=18676605 /ug=Hs.353001 /len=4443 | AK074129 | Hs.353001 | |
| 12739 | 0.043185 | xn86b03.x1 Soares_NFL_T_GBC_S1 cDNA clone IMAGE:2701325 3', mRNA sequence /clone=IMAGE:2701325 /clone_end=3' /gb=AW195867 /gi=6475097 /ug=Hs.370978 /len=571 | AW195867 | Hs.370978 | |
| 12836 | 0.002935 | BX090814 Soares_fetal_liver_spleen_1NFLS_S1 cDNA clone IMAGp998J084249 ; IMAGE:1673959, mRNA sequence /clone=IMAGp998J084249_ ; IMAGE:1673959 /gb=BX090814 /gi=27824521 /ug=Hs.125457 /len=471 | BX090814 | Hs.125457 | |
| 12850 | 0.043185 | mitogen-activated protein kinase kinase 2 (MAP3K2), mRNA /cds=(102,1964) /gb=NM_006609 /gi=21735555 /ug=Hs.28827 /len=3336 | NM_006609 | Hs.28827 | NP_006600 |
| 12851 | 0.012137 | FLJ11311 fis, clone PLACE1010102/cds=UNKNOWN /gb=AK002173 /gi=7023889 /ug=Hs.5518 /len=1839 | AK002173 | Hs.5518 | NP_689971 |
| 12892 | 0.012137 | ESTs, cDNA, 5' end /clone=IMAGE:1554245 /clone_end=5' /gb=AI792925 /gi=5340641 /ug=Hs.137097 /len=585 | AI792925 | Hs.137097 | |
| 12944 | 0.043162 | QV0-CT0181-041199-048-h11 CT0181, cDNA, mRNA sequence /gb=AW752027 /gi=7667063 /ug=Hs.293346 /len=634 | AW752027 | Hs.293346 | |
| 12970 | 0.038517 | EST(yy21h08.s1 Soares melanocyte 2NbHM H.sapiens cDNA clone IMAGE:271935 3') | N35259 | | NP_079229 |
| 12983 | 0.048295 | EST(cDNA clone IMAGE:2771386 3') | AW269219 | | NP_689632 |

| Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids | | | | | |
|--|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 13006 | 0.043185 | BX109725 Soares retina N2b4HR cDNA clone IMAGp998H04439, mRNA sequence /clone=IMAGp998H04439;_IMAGE:221235 /gb=BX109725 /gi=27877852 /ug=Hs.16886 /len=720 | BX109725 | Hs.16886 | |
| 13007 | 0.009079 | EST(cDNA clone GKCAHD03 5') | AV696986 | | NP_072179 |
| 13015 | 0.00412 | hypothetical protein FLJ31131 (FLJ31131), mRNA /cds=(20,421) /gb=NM_152535 /gi=22749108 /ug=Hs.23853 /len=1970 | NM_152535 | Hs.23853 | |
| 13021 | 0.00412 | EST(cDNA clone GLCAOE01 3') | AV646538 | | |
| 13065 | 0.026896 | control | | | |
| 13073 | 0.025373 | UI-H-BI4-aqa-c-02-0-UI.s1 NCI_CGAP_Sub8 cDNA clone IMAGE:3089258 3', mRNA sequence /clone=IMAGE:3089258 /clone_end=3' /gb=BF508251 /gi=11591549 /ug=Hs.197875 /len=1237 | BF508251 | Hs.197875 | |
| 13106 | 0.013965 | growth arrest and DNA-damage-inducible, beta (GADD45B), mRNA /cds=(101,586) /gb=NM_015675 /gi=9945331 /ug=Hs.110571 /len=1121 | NM_015675 | Hs.110571 | NP_056490 |
| 13140 | 0.012137 | epithelial V-like antigen 1 (EVA1), transcript variant 1, mRNA /cds=(142,789) /gb=NM_005797 /gi=21536270 /ug=Hs.116651 /len=2634 | NM_005797 | Hs.116651 | NP_658911 |
| 13148 | 0.030399 | likely ortholog of mouse nervous system polycomb 1 (NSPC1), mRNA /cds=(28,771) /gb=NM_032673 /gi=14249239 /ug=Hs.316750 /len=904 | NM_032673 | Hs.316750 | NP_116062 |
| 13161 | 0.023731 | hypothetical protein FLJ10035 (FLJ10035), mRNA /cds=(251,1132) /gb=NM_030803 /gi=24475809 /ug=Hs.16390 /len=2404 | NM_030803 | Hs.16390 | NP_110430 |
| 13202 | 0.023731 | hypothetical protein FLJ12806 (FLJ12806), mRNA /cds=(158,1078) /gb=NM_022831 /gi=12383075 /ug=Hs.107637 /len=2485 | NM_022831 | Hs.107637 | NP_073742 |
| 13210 | 0.048295 | hypothetical protein FLJ13188 (FLJ13188), mRNA /cds=(247,948) /gb=NM_022063 /gi=11545770 /ug=Hs.11859 /len=2746 | NM_022063 | Hs.11859 | NP_071346 |
| 13237 | 0.048295 | KIAA0635 gene product (KIAA0635), mRNA /cds=(833,3373) /gb=NM_014645 /gi=7662215 /ug=Hs.185091 /len=5138 | NM_014645 | Hs.185091 | NP_055460 |

| Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids | | | | | |
|--|----------|--|-------------------------|-----------------------------|-----------------------------|
| Spot | p-value | Description | Gen Accession No. | Unigene Accession No. | Protein Accession No. |
| 13319 | 0.043185 | cDNA FLJ33540 fis, clone BRAMY2007613. /gb=AK090859 /gi=21749098 /ug=Hs.21213 /len=2030 | AK090859 | Hs.21213 | |
| 13335 | 0.013965 | hypothetical protein FLJ12118 (FLJ12118), mRNA /cds=(24,1718) /gb=NM_024537 /gi=13375694 /ug=Hs.381043 /len=1843 | NM_024537 | Hs.381043 | NP_078813 |
| 13339 | 0.013965 | mRNA for KIAA1133 protein, partial cds. /cds=(1,2676) /gb=AB051436 /gi=13195720 /ug=Hs.318584 /len=6542 | AB051436 | Hs.318584 | |
| 13385 | 0.043185 | membrane-bound transcription factor protease, site 1 (MBTPS1), mRNA /cds=(497,3655) /gb=NM_003791 /gi=4506774 /ug=Hs.75890 /len=4338 | NM_003791 | Hs.75890 | NP_003782 |
| 13459 | 0.006699 | N-ethylmaleimide-sensitive factor (NSF), mRNA /cds=(61,2295) /gb=NM_006178 /gi=11079227 /ug=Hs.108802 /len=3960 | NM_006178 | Hs.108802 | NP_006169 |
| 13514 | 0.023731 | cDNA FLJ39478 fis, clone PROST2013605. /gb=AK096797 /gi=21756367 /ug=Hs.372680 /len=2507 | AK096797 | Hs.372680 | |
| 13522 | 0.020878 | mRNA; cDNA DKFZp451O1818 (from clone DKFZp451O1818) /gb=AL832650 /gi=21733226 /ug=Hs.12396 /len=4870 | AL832650 | Hs.12396 | |
| 13528 | 0.018314 | AGENCOURT_6428635 NIH_MGC_85 cDNA clone IMAGE:5505112 5', mRNA sequence /clone=IMAGE:5505112 /clone_end=5' /gb=BM464974 /gi=18514016 /ug=Hs.446428 /len=1097 | BM464974 | Hs.446428 | |
| 13529 | 0.038517 | mRNA; cDNA DKFZp313K2018 (from clone DKFZp313K2018) /gb=AL832067 /gi=21732608 /ug=Hs.194603 /len=7379 | AL832067 | Hs.194603 | |
| 13530 | 0.012137 | synaptic nuclei expressed gene 1 (SYNE- 1), transcript variant beta, mRNA /cds=(121,10086) /gb=NM_015293 /gi=19526752 /ug=Hs.192102 /len=10742 | NM_015293 | Hs.192102 | NP_598411 |
| 13559 | 7.73E-04 | EST(7f95d03.x1 NCI_CGAP_Brn23 cDNA clone IMAGE:3304709 3') | BE858787 | | NP_115872 |
| 13581 | 0.048295 | dishevelled 1 (homologous to Drosophila dsh) (DVL1), mRNA | XM_001589 | | |
| 13601 | 0.013965 | similar to rat myomegalin (LOC64182), mRNA /cds=(336,1268) /gb=NM_022359 /gi=21314705 /ug=Hs.333512 /len=1717 | NM_022359 | Hs.333512 | NP_071754 |
| 13615 | 0.002051 | mRNA full length insert cDNA clone EUROIMAGE 1476475 /gb=AJ420560 /gi=17066424 /ug=Hs.93231 /len=1346 | AJ420560 | Hs.93231 | |

| Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids | | | | | |
|--|----------|---|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 13664 | 0.005723 | prothymosin, alpha (gene sequence 28) (PTMA), mRNA /cds=(182,514) /gb=NM_002823 /gi=21359859 /ug=Hs.250655 /len=1233 | NM_002823 | Hs.250655 | NP_002814 |
| 13678 | 0.020878 | toll-like receptor 3 (TLR3), mRNA /cds=(102,2816) /gb=NM_003265 /gi=19718735 /ug=Hs.29499 /len=3057 | NM_003265 | Hs.29499 | NP_003256 |
| 13708 | 0.013965 | CUG triplet repeat RNA-binding protein 1 (CUGBP1), mRNA /cds=(137,1585) /gb=NM_006560 /gi=5729793 /ug=Hs.81248 /len=2113 | NM_006560 | Hs.81248 | NP_006551 |
| 13717 | 0.032747 | HRAS-like suppressor 3 (HRASLS3), mRNA /cds=(408,896) /gb=NM_007069 /gi=5901975 /ug=Hs.37189 /len=1070 | NM_007069 | Hs.37189 | NP_009000 |
| 13755 | 0.043185 | cyclin H (CCNH), mRNA /cds=(233,1204) /gb=NM_001239 /gi=17738313 /ug=Hs.514 /len=1398 | NM_001239 | Hs.514 | NP_001230 |
| 13766 | 0.005723 | zinc finger protein 363 (ZNF363), mRNA /cds=(27,812) /gb=NM_015436 /gi=24308060 /ug=Hs.48297 /len=1543 | NM_015436 | Hs.48297 | NP_056251 |
| 13786 | 0.038517 | mitochondrion, complete genome | NC_001807 | | |
| 13817 | 0.030399 | MAD, mothers against decapentaplegic 7 (Drosophila) (MADH7), mRNA /cds=(296,1576) /gb=NM_005904 /gi=5174516 /ug=Hs.100602 /len=3111 | NM_005904 | Hs.100602 | NP_005895 |
| 13830 | 0.041767 | ATPase, H transporting, lysosomal 9kDa, V0 subunit e (ATP6V0E), mRNA /cds=(76,321) /gb=NM_003945 /gi=19913435 /ug=Hs.415629 /len=849 | NM_003945 | Hs.415629 | NP_003936 |
| 13837 | 0.020878 | mRNA; cDNA DKFZp434A0225 (from clone DKFZp434A0225) /cds=(1,1628) /gb=AL137349 /gi=6807861 /ug=Hs.83293 /len=4087 | AL137349 | Hs.83293 | |
| 13843 | 0.048295 | ankyrin repeat domain 10 (ANKRD10), mRNA /cds=(136,1398) /gb=NM_017664 /gi=8923103 /ug=Hs.172572 /len=2509 | NM_017664 | Hs.172572 | NP_060134 |
| 13891 | 0.023731 | cDNA FLJ38641 fis, clone HHDP2003983. /gb=AK095960 /gi=21755328 /ug=Hs.24831 /len=2685 | AK095960 | Hs.24831 | |
| 13896 | 0.032747 | UI-H-FL1-bfx-j-06-0-UI.s1 NCI_CGAP_FL1 cDNA clone UI-H-FL1-bfx-j-06-0-UI 3', mRNA sequence /clone=UI-H-FL1-bfx-j-06-0-UI /clone_end=3' /gb=BU620821 /gi=23287036 /ug=Hs.12420 /len=1123 | BU620821 | Hs.12420 | |
| 13961 | 0.034264 | Novel | SEQ.ID.No.90 | | |

| Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids | | | | | |
|--|----------|---|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 13972 | 0.020878 | zo15e02.s1 Stratagene colon (#937204) cDNA clone IMAGE:586970 3' similar to contains Alu repetitive element;contains element PTR5 repetitive element ;, mRNA sequence /clone=IMAGE:586970 /clone_end=3' /gb=AA130992 /gi=1692483 /ug=Hs.426360 /len=489 | AA130992 | Hs.426360 | |
| 13985 | 0.030399 | EST (wd75h02.x1 NCI_CGAP_Lu24 cDNA clone IMAGE:2337459 3') | AI914259 | | |
| 13995 | 0.048295 | p10-binding protein (BITE), mRNA /cds=(149,1942) /gb=NM_024491 /gi=13346499 /ug=Hs.42315 /len=2628 | NM_024491 | Hs.42315 | NP_077817 |
| 14059 | 0.043185 | EST (cDNA clone IMAGE:2490676 3') | AI972954 | | NP_000996 |
| 14070 | 0.020878 | EST wr69a08.x1 NCI_CGAP_Ut1 cDNA clone IMAGE:2492918 3' similar to contains Alu repetitive element;contains element MSR1 repetitive element ; | AI978999 | | |
| 14111 | 0.010515 | hypothetical protein MGC3121 (MGC3121), mRNA /cds=(179,1936) /gb=NM_024031 /gi=13128979 /ug=Hs.293629 /len=2063 | NM_024031 | Hs.293629 | NP_076936 |
| 14122 | 0.006699 | 602152950F1 NIH_MGC_81 cDNA clone IMAGE:4293853 5', mRNA sequence /clone=IMAGE:4293853 /clone_end=5' /gb=BF673050 /gi=11946945 /ug=Hs.208558 /len=830 | BF673050 | Hs.208558 | |
| 14129 | 0.043185 | zu07g05.s1 Soares_testis_NHT cDNA clone IMAGE:731192 3' similar to P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR. ;, mRNA sequence /clone=IMAGE:731192 /clone_end=3' /gb=AA417352 /gi=2077434 /ug=Hs.445851 /len=519 | AA417352 | Hs.445851 | |
| 14135 | 0.030399 | mitochondrion, complete genome | NC_001807 | | |
| 14163 | 0.043185 | EST(AV657608 GLC cDNA clone GLCFDF10 3') | AV657608 | | |
| 14185 | 0.026896 | EST (CM0-UM0041-240200-241-h10 UM0041 cDNA) | AW797721 | | |
| 14248 | 0.004872 | UI-H-BI1-adn-h-11-0-UI.s1 NCI_CGAP_Sub3 cDNA clone IMAGE:2717445 3', mRNA sequence /clone=IMAGE:2717445 /clone_end=3' /gb=AW136054 /gi=6140187 /ug=Hs.437432 /len=820 | AW136054 | Hs.437432 | |
| 14286 | 0.012137 | mRNA; cDNA DKFZp434J214 (from clone DKFZp434J214); partial cds /cds=(1,1082) /gb=AL080156 /gi=5262614 /ug=Hs.12813 /len=2749 | AL080156 | Hs.12813 | NP_056323 |

| Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids | | | | | |
|--|----------|---|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 14289 | 0.012678 | clone DJ0798C17, complete sequence | AC004889 | | |
| 14375 | 5.04E-04 | ESTs, cDNA, 3' end /clone=IMAGE:2402646 /clone_end=3' /gb=AI768858 /gi=5235367 /ug=Hs.157149 /len=562 | AI768858 | Hs.157149 | NP_066012 |
| 14387 | 0.018314 | likely ortholog of rat V-1 protein (V-1), mRNA /cds=(229,585) /gb=NM_145808 /gi=21956644 /ug=Hs.21321 /len=3770 | NM_145808 | Hs.21321 | NP_665807 |
| 14415 | 0.002935 | ESTs, cDNA, 5' end /clone=IMAGE:4515481 /clone_end=5' /gb=BG292389 /gi=13051140 /ug=Hs.374490 /len=887 | BG292389 | Hs.374490 | |
| 14418 | 0.048295 | cDNA: FLJ22844 fis, clone KAIA5181. /gb=AK026497 /gi=10439371 /ug=Hs.296322 /len=2381 | AK026497 | Hs.296322 | |
| 14485 | 0.026896 | No significant match, ORF-1(2~259), +3(120~344) | SEQ.ID.No.5 | | |
| 14603 | 0.038517 | cDNA, 5' end /clone=IMAGE:4475610 /clone_end=5' /gb=BG256145 /gi=12765961 /ug=Hs.5905 /len=949 | BG256145 | Hs.5905 | NP_002031 |
| 14617 | 0.013965 | hypothetical protein FLJ20719 (FLJ20719), mRNA /cds=(402,2213) /gb=NM_017940 /gi=24308174 /ug=Hs.446473 /len=3745 | NM_017940 | Hs.446473 | NP_060410 |
| 14623 | 0.028869 | hypothetical protein FLJ35779 (FLJ35779), mRNA /cds=(42,1694) /gb=NM_152408 /gi=22748864 /ug=Hs.432726 /len=1698 | NM_152408 | Hs.432726 | NP_689621 |
| 14631 | 0.018314 | EST(12h2 retina cDNA randomly primed sublibrary) | W26795 | | |
| 14637 | 0.034264 | hypothetical protein PRO1331 (PRO1331), mRNA /cds=(423,617) /gb=NM_030778 /gi=13562115 /ug=Hs.301824 /len=1634 | NM_030778 | Hs.301824 | NP_110405 |
| 14671 | 0.016017 | UI-H-EI0-aye-c-17-0-UI.s1 NCI_CGAP_EI0 cDNA clone UI-H-EI0-aye-c-17-0-UI 3', mRNA sequence /clone=UI-H-EI0-aye-c-17-0-UI /clone_end=3' /gb=CA447385 /gi=24811805 /ug=Hs.420740 /len=812 | CA447385 | Hs.420740 | |
| 14676 | 0.020878 | EST(QV0-CT0225-101299-071-b01 CT0225) | AW377614 | | NP_842565 |
| 14766 | 0.038517 | cDNA FLJ30301 fis, clone BRACE2003217. /gb=AK054863 /gi=16549482 /ug=Hs.285728 /len=2186 | AK054863 | Hs.285728 | |
| 14828 | 0.030399 | ESTs, cDNA, 3' end /clone=IMAGE:2342469 /clone_end=3' /gb=AI871745 /gi=5545717 /ug=Hs.117777 /len=542 | AI871745 | Hs.117777 | |

| Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids | | | | | |
|--|----------|---|--------------------|----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unig n Accession No. | Protein Accession No. |
| 14831 | 0.026896 | clone IMAGE:4183899, mRNA /cds=UNKNOWN /gb=BC008625 /gi=14250384 /ug=Hs.55336 /len=1413 | BC008625 | Hs.55336 | |
| 14871 | 0.048295 | EST, cDNA, 3' end /clone=IMAGE:2488402 /clone_end=3' /gb=AI970954 /gi=5767780 /ug=Hs.311478 /len=509 | AI970954 | Hs.311478 | |
| 14896 | 0.012137 | mitochondrion, complete genome | NC_001807 | | |
| 14942 | 0.048295 | EST, cDNA /gb=AW360966 /gi=6865616 /ug=Hs.6653 /len=661 | AW360966 | Hs.6653 | NP_055942 |
| 14951 | 0.023731 | clone IMAGE:4820928, mRNA /gb=BC033530 /gi=23272327 /ug=Hs.324359 /len=2018 | BC033530 | Hs.324359 | |

| TABLE 3E | | | | | |
|--|----------|---|--------------------|-----------------------|-----------------------|
| Genes Corresponding T Differentially Expressed Genes in Figure 12 - Hypertension | | | | | |
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 22 | 0.039765 | 54TmP (54tm) (=S83365 RAB5-interaction protein) | AF004876 | | NP_065203 |
| 59 | 0.017681 | spectrin, alpha, non-erythrocytic 1 (alpha-fodrin) (SPTAN1), mRNA /cds=(103,7521) /gb=NM_003127 /gi=4507190 /ug=Hs.77196 /len=7787 | NM_003127 | Hs.77196 | NP_003118 |
| 115 | 0.018081 | laminin receptor 1 (ribosomal protein SA, 67kDa) (LAMR1), mRNA /cds=(86,973) /gb=NM_002295 /gi=9845501 /ug=Hs.181357 /len=1039 | NM_002295 | Hs.181357 | NP_002286 |
| 144 | 0.018081 | KIAA0961 protein | NM_014898 | | NP_055713 |
| 154 | 0.032959 | hypothetical protein DJ328E19.C1.1 (DJ328E19.C1.1), mRNA /cds=(18,2783) /gb=NM_015383 /gi=7657016 /ug=Hs.218329 /len=3689 | NM_015383 | Hs.218329 | NP_056198 |
| 169 | 0.031117 | nuclear protein double minute 1 (MDM1), mRNA /cds=(93,2237) /gb=NM_017440 /gi=24586654 /ug=Hs.12871 /len=2942 | NM_017440 | Hs.12871 | NP_064513 |
| 170 | 0.036914 | Duffy blood group (FY), mRNA /cds=(495,1511) /gb=NM_002036 /gi=4503818 /ug=Hs.183 /len=1559 | NM_002036 | Hs.183 | NP_002027 |
| 207 | 9.44E-04 | putative p150 | AAC51271 | | |
| 214 | 0.008722 | neuronal thread protein AD7c-NTP | NP_055301 | | |
| 224 | 0.005674 | ubiquitin specific protease 7 (herpes virus-associated) (USP7), mRNA /cds=(200,3508) /gb=NM_003470 /gi=4507856 /ug=Hs.78683 /len=4022 | NM_003470 | Hs.78683 | NP_003461 |
| 288 | 0.01072 | phosphodiesterase 8B (PDE8B), mRNA /cds=(46,2703) /gb=NM_003719 /gi=26006850 /ug=Hs.78106 /len=3567 | NM_003719 | Hs.78106 | NP_003710 |
| 290 | 0.032959 | Niemann-Pick disease, type C2 (NPC2), mRNA /cds=(116,571) /gb=NM_006432 /gi=20149580 /ug=Hs.433222 /len=929 | NM_006432 | Hs.433222 | NP_006423 |
| 298 | 0.024584 | KIAA0429 gene product (KIAA0429), mRNA /cds=(2374,3444) /gb=NM_014751 /gi=7662113 /ug=Hs.77694 /len=5645 | NM_014751 | Hs.77694 | NP_055566 |
| 323 | 0.032959 | associated molecule with the SH3 domain of STAM (AMSH), mRNA /cds=(188,1462) /gb=NM_006463 /gi=17738303 /ug=Hs.12479 /len=2107 | NM_006463 | Hs.12479 | NP_006454 |
| 325 | 0.007886 | thyroid autoantigen 70kDa (Ku antigen) (G22P1), mRNA /cds=(656,2485) /gb=NM_001469 /gi=20070134 /ug=Hs.197345 /len=2743 | NM_001469 | Hs.197345 | NP_001460 |

| Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension | | | | | |
|---|----------|---|--------------------|----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigen Accession No. | Protein Accession No. |
| 326 | 0.024587 | proteasome (prosome, macropain) 26S subunit, ATPase, 5 (PSMC5), mRNA /cds=(42,1262) /gb=NM_002805 /gi=24497434 /ug=Hs.79387 /len=1332 | NM_002805 | Hs.79387 | NP_002796 |
| 332 | 0.041254 | similar to rat nuclear ubiquitous casein kinase 2 (NUCKS), mRNA /cds=(67,558) /gb=NM_022731 /gi=12232386 /ug=Hs.118064 /len=1811 | NM_022731 | Hs.118064 | NP_073568 |
| 342 | 0.013102 | cytochrome c oxidase subunit VIc (COX6C), nuclear gene encoding mitochondrial protein, mRNA /cds=(61,288) /gb=NM_004374 /gi=17999531 /ug=Hs.351875 /len=444 | NM_004374 | Hs.351875 | NP_004365 |
| 344 | 0.03489 | tumor necrosis factor, alpha-induced protein 6 (TNFAIP6), mRNA /cds=(77,910) /gb=NM_007115 /gi=26051242 /ug=Hs.29352 /len=1440 | NM_007115 | Hs.29352 | NP_009046 |
| 357 | 0.016974 | deleted in pancreatic carcinoma (DPC4) gene, exon 3 | AF045440 | | |
| 366 | 0.0261 | voltage-dependent anion channel 1 (VDAC1), mRNA /cds=(100,951) /gb=NM_003374 /gi=4507878 /ug=Hs.149155 /len=1806 | NM_003374 | Hs.149155 | NP_003365 |
| 367 | 0.048543 | RNA (guanine-7-) methyltransferase (RNMT), mRNA /cds=(197,1627) /gb=NM_003799 /gi=4506566 /ug=Hs.8086 /len=6203 | NM_003799 | Hs.8086 | NP_003790 |
| 371 | 0.011469 | ecotropic viral integration site 2A (EVI2A), mRNA /cds=(220,918) /gb=NM_014210 /gi=7657074 /ug=Hs.70499 /len=1563 | NM_014210 | Hs.70499 | NP_055025 |
| 378 | 0.023148 | vanilloid receptor; CARKL and CTNS; TIP1; P2X5b and P2X5a; HUMINAE | AF168787 | | |
| 383 | 0.001232 | zinc finger protein 223 (ZNF223), mRNA /cds=(239,1687) /gb=NM_013361 /gi=7019588 /ug=Hs.279782 /len=2033 | NM_013361 | Hs.279782 | NP_037493 |
| 384 | 0.009349 | ADP-ribosylation factor-like 6 interacting protein (ARL6IP), mRNA /cds=(70,681) /gb=NM_015161 /gi=24308006 /ug=Hs.75249 /len=2280 | NM_015161 | Hs.75249 | NP_055976 |
| 396 | 0.01072 | hypothetical protein FLJ20445 (FLJ20445), mRNA /cds=(293,1129) /gb=NM_017824 /gi=19923500 /ug=Hs.343748 /len=3896 | NM_017824 | Hs.343748 | NP_060294 |
| 430 | 0.048543 | hypothetical protein MGC13061 (MGC13061), mRNA /cds=(52,684) /gb=NM_032322 /gi=14150095 /ug=Hs.29874 /len=1947 | NM_032322 | Hs.29874 | NP_115698 |

| Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension | | | | | |
|---|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 434 | 0.00242 | phosphoglycerate kinase 1 (PGK1), mRNA /cds=(70,1323) /gb=NM_000291 /gi=22095338 /ug=Hs.78771 /len=2338 | NM_000291 | Hs.78771 | NP_000282 |
| 436 | 0.041254 | golgi phosphoprotein 4 (GOLPH4), mRNA /cds=(14,2104) /gb=NM_014498 /gi=7657137 /ug=Hs.143600 /len=2506 | NM_014498 | Hs.143600 | NP_055313 |
| 441 | 0.004203 | ATP binding protein associated with cell differentiation (APACD), mRNA /cds=(130,810) /gb=NM_005783 /gi=18104958 /ug=Hs.153884 /len=1494 | NM_005783 | Hs.153884 | NP_005774 |
| 444 | 0.024587 | HSPC019 protein (HSPC019), mRNA /cds=(58,444) /gb=NM_014028 /gi=7661737 /ug=Hs.163724 /len=2411 | NM_014028 | Hs.163724 | NP_054747 |
| 448 | 0.001232 | laminin receptor 1 (ribosomal protein SA, 67kDa) (LAMR1), mRNA /cds=(86,973) /gb=NM_002295 /gi=9845501 /ug=Hs.181357 /len=1039 | NM_002295 | Hs.181357 | NP_002286 |
| 450 | 0.0261 | nuclear factor NF-IL6 | X52560 | | |
| 453 | 0.007056 | WD repeat domain 1 (WDR1), transcript variant 1, mRNA /cds=(203,2023) /gb=NM_017491 /gi=17105397 /ug=Hs.85100 /len=3079 | NM_017491 | Hs.85100 | NP_059830 |
| 476 | 0.008722 | KIAA1116 protein (KIAA1116), mRNA /cds=(186,4001) /gb=NM_014892 /gi=7662491 /ug=Hs.227602 /len=4664 | NM_014892 | Hs.227602 | NP_055707 |
| 512 | 0.010015 | myosin IXB (MYO9B), mRNA /cds=(1,6069) /gb=NM_004145 /gi=4758749 /ug=Hs.159629 /len=6069 | NM_004145 | Hs.159629 | NP_004136 |
| 565 | 0.009763 | topoisomerase (DNA) III alpha (TOP3A), mRNA /cds=(230,3235) /gb=NM_004618 /gi=20143947 /ug=Hs.91175 /len=3807 | NM_004618 | Hs.91175 | NP_004609 |
| 575 | 0.007634 | tenascin XB (TNXB), transcript variant XB, mRNA /cds=(205,13074) /gb=NM_019105 /gi=20544188 /ug=Hs.169886 /len=13268 | NM_019105 | Hs.169886 | NP_115859 |
| 595 | 0.038337 | NS1-associated protein 1 (NSAP1), mRNA /cds=(526,2397) /gb=NM_006372 /gi=23397426 /ug=Hs.373499 /len=2932 | NM_006372 | Hs.373499 | NP_006363 |
| 598 | 0.025888 | glutamyl-tRNA synthetase (QARS), mRNA /cds=(6,2333) /gb=NM_005051 /gi=4826959 /ug=Hs.79322 /len=2437 | NM_005051 | Hs.79322 | NP_005042 |
| 599 | 0.01747 | hypothetical protein similar to RNA-binding protein lark (MGC10871), mRNA /cds=(54,1133) /gb=NM_031492 /gi=13899353 /ug=Hs.49994 /len=1821 | NM_031492 | Hs.49994 | NP_113680 |

| Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension | | | | | |
|---|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 607 | 0.043544 | ribosomal protein S27a (RPS27A), mRNA /cds=(39,509) /gb=NM_002954 /gi=27436941 /ug=Hs.311640 /len=541 | NM_002954 | Hs.311640 | NP_002945 |
| 634 | 0.039267 | mitofusin 1 (MFN1), transcript variant 1, mRNA /cds=(84,2309) /gb=NM_033540 /gi=16117784 /ug=Hs.197877 /len=3275 | NM_033540 | Hs.197877 | NP_284941 |
| 671 | 0.047349 | KIAA0471 gene product (KIAA0471), mRNA /cds=(413,1525) /gb=NM_014857 /gi=7662143 /ug=Hs.242271 /len=6834 | NM_014857 | Hs.242271 | NP_055672 |
| 678 | 0.048238 | clone alpha_est218/52C1 mRNA sequence /gb=AF001542 /gi=2529714 /ug=Hs.356442 /len=2992 | AF001542 | Hs.356442 | |
| 679 | 0.014931 | hypothetical protein LOC51255 (LOC51255), mRNA /cds=(31,492) /gb=NM_016494 /gi=24475978 /ug=Hs.11156 /len=601 | NM_016494 | Hs.11156 | NP_057578 |
| 703 | 0.00223 | cytochrome b-245, beta polypeptide (chronic granulomatous disease) (CYBB), mRNA /cds=(15,1727) /gb=NM_000397 /gi=6996020 /ug=Hs.88974 /len=4266 | NM_000397 | Hs.88974 | NP_000388 |
| 726 | 0.041254 | tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide (YWHAG), mRNA /cds=(192,935) /gb=NM_012479 /gi=21464100 /ug=Hs.25001 /len=3747 | NM_012479 | Hs.25001 | NP_036611 |
| 776 | 0.031156 | GW128 protein (GW128), mRNA /cds=(699,890) /gb=NM_014052 /gi=7661715 /ug=Hs.182238 /len=2011 | NM_014052 | Hs.182238 | |
| 787 | 0.039034 | cargo selection protein (mannose 6 phosphate receptor binding protein) (TIP47), mRNA /cds=(67,1371) /gb=NM_005817 /gi=20127485 /ug=Hs.140452 /len=2239 | NM_005817 | Hs.140452 | NP_005808 |
| 794 | 0.005674 | zn87g06.x5 Stratagene lung carcinoma 937218 cDNA clone IMAGE:565210 3' similar to contains Alu repetitive element; contains element MER22 repetitive element ; mRNA sequence /clone=IMAGE:565210 /clone_end=3' /gb=AI732466 /gi=5053579 /ug=Hs.193133 /len=526 | AI732466 | Hs.193133 | |
| 802 | 0.011469 | striated muscle contraction regulatory protein (Id2B) mRNA, complete cds. /cds=(110,220) /gb=M96843 /gi=397775 /ug=Hs.296811 /len=1167 | M96843 | Hs.296811 | |

| Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension | | | | | |
|---|----------|---|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 805 | 0.048543 | ribosomal protein S17 (RPS17), mRNA /cds=(26,433) /gb=NM_001021 /gi=14591913 /ug=Hs.5174 /len=515 | NM_001021 | Hs.5174 | NP_001012 |
| 810 | 0.039034 | KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3 (KDEL3), transcript variant 1, mRNA /cds=(157,801) /gb=NM_006855 /gi=8051612 /ug=Hs.250696 /len=1705 | NM_006855 | Hs.250696 | NP_057839 |
| 835 | 0.00489 | likely ortholog of mouse tumor differentially expressed 1, like (TDE1L), mRNA /cds=(76,1437) /gb=NM_020755 /gi=24308212 /ug=Hs.146668 /len=3149 | NM_020755 | Hs.146668 | NP_065806 |
| 844 | 0.021781 | sorting nexin 2 (SNX2), mRNA /cds=(50,1609) /gb=NM_003100 /gi=23111037 /ug=Hs.11183 /len=2091 | NM_003100 | Hs.11183 | NP_003091 |
| 851 | 0.005674 | of89c05.s1 NCI_CGAP_Li5 cDNA clone. IMAGE:1437512 3' similar to contains Alu repetitive element, mRNA sequence /clone=IMAGE:1437512 /clone_end=3' /gb=AA894384 /gi=3030785 /ug=Hs.432123 /len=296 | AA894384 | Hs.432123 | |
| 865 | 0.043576 | mitochondrion, complete genome | NC_001807 | | |
| 866 | 7.88E-04 | polycystic kidney disease 2 (autosomal dominant) (PKD2), mRNA /cds=(67,2973) /gb=NM_000297 /gi=4505834 /ug=Hs.82001 /len=5057 | NM_000297 | Hs.82001 | NP_000288 |
| 868 | 0.048543 | hypothetical protein LOC123803 (LOC123803), mRNA /cds=(15,947) /gb=NM_173474 /gi=27735048 /ug=Hs.351573 /len=1146 | NM_173474 | Hs.351573 | NP_775745 |
| 870 | 0.00527 | KIAA0062 mRNA, partial cds /cds=(1,1598) /gb=D31887 /gi=505101 /ug=Hs.89868 /len=4573 | D31887 | Hs.89868 | |
| 882 | 0.015924 | hypothetical protein H41 (H41), mRNA /cds=(324,1100) /gb=NM_017548 /gi=24475997 /ug=Hs.283690 /len=3346 | NM_017548 | Hs.283690 | NP_060018 |
| 917 | 0.023148 | mRNA for integrin, alpha subunit /gb=X68742 /gi=33949 /ug=Hs.116774 /len=3453 | X68742 | Hs.116774 | |
| 923 | 0.023148 | eukaryotic translation initiation factor 3, subunit 3 gamma, 40kDa (EIF3S3), mRNA /cds=(6,1064) /gb=NM_003756 /gi=4503514 /ug=Hs.58189 /len=1280 | NM_003756 | Hs.58189 | NP_003747 |
| 939 | 0.016974 | protein phosphatase 1, regulatory (inhibitor) subunit 8 (PPP1R8), transcript variant 2, mRNA /cds=(836,1465) /gb=NM_138558 /gi=20336238 /ug=Hs.356590 /len=2691 | NM_138558 | Hs.356590 | NP_612568 |

| Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension | | | | | |
|---|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | D scription | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 943 | 0.011469 | XIST, coding sequence "a" mRNA (locus DXS399E). /gb=X56199 /gi=37987 /ug=Hs.352403 /len=1614 | X56199 | Hs.352403 | |
| 944 | 0.043576 | neuronal protein | X79682 | | |
| 953 | 2.73E-04 | mRNA for KIAA0592 protein, partial cds. /cds=(1,4062) /gb=AB011164 /gi=3043707 /ug=Hs.439367 /len=4623 | AB011164 | Hs.439367 | |
| 954 | 0.015924 | cell cycle progression 8 protein (CPR8), mRNA /cds=(13,1140) /gb=NM_004748 /gi=4758047 /ug=Hs.82506 /len=1856 | NM_004748 | Hs.82506 | NP_004739 |
| 965 | 0.031117 | testis enhanced gene transcript (TEGT), mRNA /cds=(41,754) /gb=NM_003217 /gi=4507432 /ug=Hs.74637 /len=2600 | NM_003217 | Hs.74637 | NP_003208 |
| 976 | 0.020482 | engulfment and cell motility 1 (ced-12 C. elegans) (ELMO1), transcript variant 1, mRNA /cds=(253,2436) /gb=NM_014800 /gi=18765699 /ug=Hs.31463 /len=3657 | NM_014800 | Hs.31463 | NP_569709 |
| 978 | 0.031117 | cyclin D binding myb-like transcription factor 1 (DMTF1), mRNA /cds=(276,2558) /gb=NM_021145 /gi=10863946 /ug=Hs.5671 /len=3767 | NM_021145 | Hs.5671 | NP_066968 |
| 985 | 0.012262 | PABP-interacting protein 2 (PAIP2), mRNA /cds=(150,533) /gb=NM_016480 /gi=19923458 /ug=Hs.396644 /len=1514 | NM_016480 | Hs.396644 | NP_057564 |
| 986 | 0.031117 | diazepam binding inhibitor (GABA receptor modulator, acyl-Coenzyme A binding protein) (DBI), mRNA /cds=(20,334) /gb=NM_020548 /gi=24475624 /ug=Hs.78888 /len=556 | NM_020548 | Hs.78888 | NP_065438 |
| 987 | 0.024587 | brain protein 44-like (BRP44L), mRNA /cds=(123,452) /gb=NM_016098 /gi=7706368 /ug=Hs.108725 /len=988 | NM_016098 | Hs.108725 | NP_057182 |
| 989 | 0.009349 | 5.8S ribosomal RNA | J01866 | | |
| 992 | 0.01925 | chemokine (C-X-C motif) ligand 3 (CXCL3), mRNA /cds=(78,398) /gb=NM_002090 /gi=4504156 /ug=Hs.89690 /len=1064 | NM_002090 | Hs.89690 | NP_002081 |
| 998 | 0.024587 | down-regulator of transcription 1, TBP-binding (negative cofactor 2) (DR1), mRNA /cds=(548,1078) /gb=NM_001938 /gi=4503380 /ug=Hs.16697 /len=1375 | NM_001938 | Hs.16697 | NP_001929 |
| 1008 | 0.024587 | Alg5, S. cerevisiae, of (ALG5), mRNA /cds=(28,1002) /gb=NM_013338 /gi=9665250 /ug=Hs.227933 /len=1125 | NM_013338 | Hs.227933 | NP_037470 |

| Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension | | | | | |
|---|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 1011 | 0.001737 | v-raf-1 murine leukemia viral oncogene 1 (RAF1), mRNA /cds=(130,2076) /gb=NM_002880 /gi=4506400 /ug=Hs.349650 /len=2977 | NM_002880 | Hs.349650 | NP_002871 |
| 1014 | 0.041254 | likely ortholog of rat vacuole membrane protein 1 (VMP1), mRNA /cds=(114,1334) /gb=NM_030938 /gi=20070348 /ug=Hs.166254 /len=2530 | NM_030938 | Hs.166254 | NP_112200 |
| 1015 | 0.013102 | actinin, alpha 1 (ACTN1), mRNA /cds=(184,2862) /gb=NM_001102 /gi=12025669 /ug=Hs.119000 /len=3398 | NM_001102 | Hs.119000 | NP_001093 |
| 1026 | 0.010015 | methionine adenosyltransferase II, beta (MAT2B), mRNA /cds=(73,1077) /gb=NM_013283 /gi=20127525 /ug=Hs.54642 /len=2054 | NM_013283 | Hs.54642 | NP_037415 |
| 1028 | 7.18E-04 | ATP synthase, H transporting, mitochondrial F1 complex, epsilon subunit (ATP5E), nuclear gene encoding mitochondrial protein, mRNA /cds=(95,250) /gb=NM_006886 /gi=21327678 /ug=Hs.177530 /len=417 | NM_006886 | Hs.177530 | NP_008817 |
| 1031 | 0.023148 | decorin (DCN), transcript variant A1, mRNA /cds=(200,1279) /gb=NM_001920 /gi=19743844 /ug=Hs.433989 /len=1751 | NM_001920 | Hs.433989 | NP_598014 |
| 1048 | 0.041254 | tetraspan 2 (TSPAN-2), mRNA /cds=(33,698) /gb=NM_005725 /gi=21264579 /ug=Hs.234863 /len=3179 | NM_005725 | Hs.234863 | NP_005716 |
| 1057 | 0.013102 | mRNA for KIAA1609 protein, partial cds. /cds=(1,1423) /gb=AB046829 /gi=15425661 /ug=Hs.14449 /len=4683 | AB046829 | Hs.14449 | |
| 1060 | 0.009349 | NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4, 15kDa (NDUFB4), mRNA /cds=(9,398) /gb=NM_004547 /gi=6041668 /ug=Hs.227750 /len=464 | NM_004547 | Hs.227750 | NP_004538 |
| 1063 | 0.015924 | superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1 (adult)) (SOD1), mRNA /cds=(1,465) /gb=NM_000454 /gi=4507148 /ug=Hs.75428 /len=560 | NM_000454 | Hs.75428 | NP_000445 |
| 1080 | 0.015924 | Similar to RIKEN cDNA 4833424O15 gene, clone IMAGE:4793707, mRNA /gb=BC040174 /gi=25777829 /ug=Hs.312481 /len=3745 | BC040174 | Hs.312481 | |
| 1082 | 0.012262 | KIAA0349 gene | AB002347 | | NP_056070 |

| Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension | | | | | |
|---|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unig ne Accession No. | Protein Accession No. |
| 1087 | 0.015924 | heat shock 70kDa protein 9B (mortalin-2) (HSPA9B), nuclear gene encoding mitochondrial protein, mRNA /cds=(94,2133) /gb=NM_004134 /gi=24234687 /ug=Hs.3069 /len=2852 | NM_004134 | Hs.3069 | NP_004125 |
| 1099 | 0.004328 | DKFZP586O0120 protein (DKFZP586O0120), mRNA /cds=(21,359) /gb=NM_014077 /gi=7661695 /ug=Hs.4766 /len=1465 | NM_014077 | Hs.4766 | NP_054796 |
| 1102 | 0.027691 | basic leucine zipper and W2 domains 1 (BZW1), mRNA /cds=(81,1340) /gb=NM_014670 /gi=7661849 /ug=Hs.155291 /len=2998 | NM_014670 | Hs.155291 | NP_055485 |
| 1107 | 0.018081 | similar to RIKEN cDNA 2610030J16 gene (MGC2541), mRNA /cds=(738,1712) /gb=NM_080670 /gi=18087848 /ug=Hs.173103 /len=2685 | NM_080670 | Hs.173103 | NP_542401 |
| 1108 | 0.041254 | frizzled 9 (Drosophila) (FZD9), mRNA /cds=(26,1801) /gb=NM_003508 /gi=4503834 /ug=Hs.158335 /len=2184 | NM_003508 | Hs.158335 | NP_003499 |
| 1110 | 0.011469 | ribosomal protein L41 (RPL41), mRNA /cds=(84,161) /gb=NM_021104 /gi=10863874 /ug=Hs.356795 /len=478 | NM_021104 | Hs.356795 | NP_066927 |
| 1111 | 0.021781 | hypothetical protein (HSPC016), mRNA /cds=(39,233) /gb=NM_015933 /gi=7705430 /ug=Hs.397853 /len=384 | NM_015933 | Hs.397853 | NP_057017 |
| 1113 | 0.00527 | nischarin (NISCH), mRNA /cds=(27,4541) /gb=NM_007184 /gi=6005787 /ug=Hs.26285 /len=5132 | NM_007184 | Hs.26285 | NP_009115 |
| 1114 | 0.014931 | stromal antigen 2 (STAG2), mRNA /cds=(405,3893) /gb=NM_006603 /gi=27552767 /ug=Hs.8217 /len=4197 | NM_006603 | Hs.8217 | NP_006594 |
| 1118 | 0.007056 | hypothetical protein FLJ12584 (FLJ12584), mRNA /cds=(97,1623) /gb=NM_025139 /gi=13376722 /ug=Hs.288897 /len=1744 | NM_025139 | Hs.288897 | NP_079415 |
| 1119 | 0.013991 | pp9974 mRNA, complete cds /cds=(2009,2350) /gb=AF318382 /gi=18027855 /ug=Hs.251664 /len=2630 | AF318382 | Hs.251664 | |
| 1120 | 0.001033 | clone 25032 mRNA sequence /cds=UNKNOWN /gb=AF131764 /gi=4406586 /ug=Hs.13399 /len=1798 | AF131764 | Hs.13399 | NP_071919 |
| 1121 | 0.007056 | cDNA FLJ31399 fis, clone NT2NE1000181. /gb=AK055961 /gi=16550820 /ug=Hs.179833 /len=2159 | AK055961 | Hs.179833 | |
| 1122 | 0.032959 | RAB1B, member RAS oncogene family (RAB1B), mRNA /cds=(48,653) /gb=NM_030981 /gi=13569961 /ug=Hs.300816 /len=1985 | NM_030981 | Hs.300816 | NP_112243 |

| Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension | | | | | |
|---|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 1125 | 0.015924 | hypothetical protein BC006130 (LOC93622), mRNA /cds=(110,469) /gb=NM_138699 /gi=20162561 /ug=Hs.6815 /len=1961 | NM_138699 | Hs.6815 | NP_619644 |
| 1138 | 0.043576 | brain and nasopharyngeal carcinoma susceptibility protein (NSG-X), mRNA /cds=(186,518) /gb=NM_014411 /gi=14149650 /ug=Hs.26937 /len=1897 | NM_014411 | Hs.26937 | NP_055226 |
| 1144 | 0.023148 | mRNA; cDNA DKFZp761M0223 (from clone DKFZp761M0223) /gb=AL137938 /gi=6851002 /ug=Hs.77646 /len=3764 | AL137938 | Hs.77646 | |
| 1145 | 0.046005 | hypothetical protein FLJ22843 (FLJ22843), mRNA /cds=(532,1287) /gb=NM_025184 /gi=13376775 /ug=Hs.301143 /len=2291 | NM_025184 | Hs.301143 | NP_079460 |
| 1151 | 0.004203 | RAD21 (S. pombe) (RAD21), mRNA /cds=(185,2080) /gb=NM_006265 /gi=5453993 /ug=Hs.81848 /len=3647 | NM_006265 | Hs.81848 | NP_006256 |
| 1163 | 0.007578 | reticulon 4 (RTN4), mRNA /cds=(245,3823) /gb=NM_020532 /gi=24638438 /ug=Hs.65450 /len=4166 | NM_020532 | Hs.65450 | NP_722550 |
| 1170 | 0.015924 | myosin, light polypeptide 6, alkali, smooth muscle and non-muscle (MYL6), transcript variant 3, mRNA /cds=(41,514) /gb=NM_079425 /gi=17986263 /ug=Hs.77385 /len=717 | NM_079425 | Hs.77385 | NP_524149 |
| 1172 | 0.009349 | hypothetical protein FLJ23445 (FLJ23445), mRNA /cds=(44,658) /gb=NM_025075 /gi=13376622 /ug=Hs.288151 /len=963 | NM_025075 | Hs.288151 | NP_079351 |
| 1179 | 0.032959 | ribosomal protein, large, P0 (RPLP0), transcript variant 2, mRNA /cds=(111,1064) /gb=NM_053275 /gi=16933545 /ug=Hs.406511 /len=1148 | NM_053275 | Hs.406511 | NP_444505 |
| 1187 | 0.015924 | serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 (SERPINA1), mRNA /cds=(233,1489) /gb=NM_000295 /gi=21361197 /ug=Hs.297681 /len=1584 | NM_000295 | Hs.297681 | NP_000286 |
| 1198 | 0.003332 | hypothetical protein FLJ20729 (FLJ20729), mRNA /cds=(135,1547) /gb=NM_017953 /gi=20149642 /ug=Hs.5111 /len=2821 | NM_017953 | Hs.5111 | NP_060423 |
| 1199 | 0.029363 | unnamed protein product | BAB15362 | | |
| 1200 | 0.024587 | hypothetical gene supported by XM_000590 (LOC59176) | XM_000590 | | |
| 1208 | 0.023027 | mitochondrion, complete genome | NC_001807 | | |

| Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension | | | | | |
|---|----------|--|-------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gen Accession No. | Unigene Accession No. | Protein Accession No. |
| 1224 | 0.046005 | CASP8 and FADD-like apoptosis regulator (CFLAR), mRNA /cds=(482,1924) /gb=NM_003879 /gi=21361768 /ug=Hs.195175 /len=2243 | NM_003879 | Hs.195175 | NP_003870 |
| 1229 | 3.02E-04 | mRNA for KIAA0642 protein, partial cds. /cds=(200,4189) /gb=AB014542 /gi=20521116 /ug=Hs.323317 /len=5937 | AB014542 | Hs.323317 | |
| 1231 | 0.01072 | alpha-2 macroglobulin family protein VIP (VIP), mRNA /cds=(18,5675) /gb=NM_015692 /gi=23510326 /ug=Hs.375610 /len=5852 | NM_015692 | Hs.375610 | NP_056507 |
| 1235 | 0.015924 | mRNA, cDNA DKFZp564A026 (from clone DKFZp564A026) /gb=AL050367 /gi=4914600 /ug=Hs.66762 /len=3958 | AL050367 | Hs.66762 | |
| 1236 | 0.004536 | matrix metalloproteinase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV collagenase) (MMP9), mRNA /cds=(20,2143) /gb=NM_004994 /gi=4826835 /ug=Hs.151738 /len=2334 | NM_004994 | Hs.151738 | NP_004985 |
| 1240 | 0.01925 | HSPC273 (=KIAA1192) | AF161391 | | NP_060555 |
| 1242 | 0.024587 | programmed cell death 4 (neoplastic transformation inhibitor) (PDCD4), transcript variant 2, mRNA /cds=(361,1737) /gb=NM_145341 /gi=21735597 /ug=Hs.326248 /len=2403 | NM_145341 | Hs.326248 | NP_663314 |
| 1243 | 0.004677 | MAD, mothers against decapentaplegic 7 (Drosophila) (MADH7), mRNA /cds=(296,1576) /gb=NM_005904 /gi=5174516 /ug=Hs.100602 /len=3111 | NM_005904 | Hs.100602 | NP_005895 |
| 1247 | 0.016974 | NICE-5 protein (HSA243666), mRNA /cds=(7,660) /gb=NM_017582 /gi=21361606 /ug=Hs.337078 /len=2523 | NM_017582 | Hs.337078 | NP_060052 |
| 1253 | 0.003603 | helicase with zinc finger domain (HELZ), mRNA /cds=(146,5974) /gb=NM_014877 /gi=7661883 /ug=Hs.3085 /len=6274 | NM_014877 | Hs.3085 | NP_055692 |
| 1257 | 0.003603 | isovaleryl-CoA dehydrogenase (IVD) gene, exon 12 and partial cds | AF038318 | | |
| 1264 | 0.048543 | mRNA for KIAA1143 protein, partial cds. /cds=(1,351) /gb=AB032969 /gi=6329965 /ug=Hs.173042 /len=4946 | AB032969 | Hs.173042 | |
| 1266 | 2.73E-04 | ATP-binding cassette, sub-family A (ABC1), member 5 (ABCA5), transcript variant 1, mRNA /cds=(1219,6147) /gb=NM_018672 /gi=27262623 /ug=Hs.180513 /len=7044 | NM_018672 | Hs.180513 | NP_758424 |

| G n s Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension | | | | | |
|---|----------|--|-------------------------|-----------------------------|-----------------------------|
| Spot | p-value | Description | Gen Acc ssion No. | Unigene Accession No. | Prot in Acc ssion No. |
| 1272 | 0.00527 | collagen, type XII, alpha-1 (COL12A1), transcript variant long, mRNA /cds=(114,9305) /gb=NM_004370 /gi=18201922 /ug=Hs.101302 /len=11554 | NM_004370 | Hs.101302 | NP_542376 |
| 1274 | 0.023148 | HSJ1a (HSJ1) mRNA, complete cds; alternatively spliced. /cds=(26,859) /gb=S37375 /gi=250081 /ug=Hs.433237 /len=1760 | S37375 | Hs.433237 | |
| 1275 | 0.008722 | gp25L2 protein (HSGP25L2G), mRNA /cds=(76,720) /gb=NM_017510 /gi=24475637 /ug=Hs.279929 /len=1420 | NM_017510 | Hs.279929 | NP_059980 |
| 1282 | 0.037092 | hypothetical protein MDS025 (MDS025), mRNA /cds=(363,1127) /gb=NM_021825 /gi=21361605 /ug=Hs.154938 /len=1585 | NM_021825 | Hs.154938 | NP_068597 |
| 1286 | 0.003332 | FLJ22781 fis, clone KAIA1958 /cds=UNKNOWN /gb=AK026434 /gi=10439298 /ug=Hs.213236 /len=2599 | AK026434 | Hs.213236 | |
| 1291 | 0.032959 | Similar to adducin 1 (alpha), clone MGC:44427 IMAGE:5297337, mRNA, complete cds /cds=(869,2857) /gb=BC042998 /gi=28175763 /ug=Hs.183706 /len=4761 | BC042998 | Hs.183706 | NP_789771 |
| 1297 | 0.031195 | hypothetical protein MGC3232 (MGC3232), mRNA /cds=(85,2181) /gb=NM_032313 /gi=14150077 /ug=Hs.8715 /len=2316 | NM_032313 | Hs.8715 | NP_115689 |
| 1300 | 0.046432 | laminin, gamma 1 (formerly LAMB2) (LAMC1), mRNA /cds=(300,5129) /gb=NM_002293 /gi=9845497 /ug=Hs.432855 /len=7923 | NM_002293 | Hs.432855 | NP_002284 |
| 1302 | 0.024587 | hypothetical protein FLJ11286 (FLJ11286), mRNA /cds=(96,971) /gb=NM_018381 /gi=8922978 /ug=Hs.12151 /len=1911 | NM_018381 | Hs.12151 | NP_060851 |
| 1304 | 0.002054 | eukaryotic translation elongation factor 1 beta 2 (EEF1B2), transcript variant 1, mRNA /cds=(236,913) /gb=NM_001959 /gi=16519564 /ug=Hs.421608 /len=961 | NM_001959 | Hs.421608 | NP_066944 |
| 1305 | 1.63E-04 | cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA /cds=(90,281) /gb=NM_001867 /gi=18105039 /ug=Hs.430075 /len=448 | NM_001867 | Hs.430075 | NP_001858 |
| 1306 | 0.020748 | poly(A) binding protein, cytoplasmic 1 (PABPC1), mRNA /cds=(503,2404) /gb=NM_002568 /gi=4505574 /ug=Hs.172182 /len=2848 | NM_002568 | Hs.172182 | NP_002559 |

| Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension | | | | | |
|---|----------|---|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 1312 | 0.012262 | endothelial zinc finger protein 2 (EZF-2), mRNA /cds=(234,1214) /gb=NM_018337 /gi=8922893 /ug=Hs.24545 /len=1907 | NM_018337 | Hs.24545 | NP_060807 |
| 1313 | 0.041547 | Similar to LYRIC, clone MGC:41931 IMAGE:5298467, mRNA, complete cds /cds=(329,2077) /gb=BC045642 /gi=28277146 /ug=Hs.243901 /len=3729 | BC045642 | Hs.243901 | |
| 1316 | 0.007886 | ubiquitin-like 5 (UBL5), mRNA /cds=(66,287) /gb=NM_024292 /gi=13236509 /ug=Hs.13836 /len=413 | NM_024292 | Hs.13836 | NP_077268 |
| 1318 | 0.003152 | SH3-domain binding protein 5 (BTK-associated) (SH3BP5), mRNA /cds=(64,1341) /gb=NM_004844 /gi=4759057 /ug=Hs.109150 /len=2570 | NM_004844 | Hs.109150 | NP_004835 |
| 1321 | 0.012262 | general transcription factor IIIC, polypeptide 5, 63kDa (GTF3C5), mRNA /cds=(293,1852) /gb=NM_012087 /gi=6912401 /ug=Hs.286088 /len=2385 | NM_012087 | Hs.286088 | NP_036219 |
| 1322 | 0.005674 | high-mobility group 20B (HMG20B), mRNA /cds=(19,1044) /gb=NM_006339 /gi=5454079 /ug=Hs.32317 /len=1232 | NM_006339 | Hs.32317 | NP_006330 |
| 1323 | 0.012262 | KIAA1630 protein (KIAA1630), mRNA /cds=(72,2831) /gb=NM_018706 /gi=18375677 /ug=Hs.271586 /len=3180 | NM_018706 | Hs.271586 | NP_061176 |
| 1343 | 0.036914 | hypothetical protein FLJ12438 (FLJ12438), mRNA /cds=(174,1340) /gb=NM_021933 /gi=11345471 /ug=Hs.8595 /len=1575 | NM_021933 | Hs.8595 | NP_068752 |
| 1349 | 0.01286 | mRNA; cDNA DKFZp313D2314 (from clone DKFZp313D2314) /gb=AL832057 /gi=21732598 /ug=Hs.3685 /len=3141 | AL832057 | Hs.3685 | |
| 1369 | 2.05E-04 | peroxiredoxin 2 (PRDX2), mRNA /cds=(90,686) /gb=NM_005809 /gi=5902725 /ug=Hs.432121 /len=937 | NM_005809 | Hs.432121 | NP_005800 |
| 1370 | 0.010212 | solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6 (SLC25A6), nuclear gene encoding mitochondrial protein, mRNA /cds=(93,989) /gb=NM_001636 /gi=27764862 /ug=Hs.407372 /len=1455 | NM_001636 | Hs.407372 | NP_001627 |
| 1374 | 0.00527 | likely ortholog of rat p47 (p47), mRNA /cds=(86,1198) /gb=NM_016143 /gi=20149634 /ug=Hs.12865 /len=1450 | NM_016143 | Hs.12865 | |
| 1376 | 0.036914 | chaperonin containing TCP1, subunit 5 (epsilon) (CCT5), mRNA /cds=(92,1717) /gb=NM_012073 /gi=24307938 /ug=Hs.1600 /len=1961 | NM_012073 | Hs.1600 | NP_036205 |

| Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension | | | | | |
|---|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 1377 | 0.006106 | procollagen (type III) N-endopeptidase (PCOLN3), mRNA /cds=(41,997) /gb=NM_002768 /gi=4506138 /ug=Hs.183138 /len=2474 | NM_002768 | Hs.183138 | NP_002759 |
| 1386 | 0.00633 | AGENCOURT_6424254 NIH_MGC_67 cDNA clone IMAGE:5491531 5', mRNA sequence /clone=IMAGE:5491531 /clone_end=5' /gb=BM479954 /gi=18528996 /ug=Hs.381243 /len=1112 | BM479954 | Hs.381243 | |
| 1389 | 7.18E-04 | heparan sulfate proteoglycan (HSPG2) mRNA, complete cds | M85289 | | NP_005520 |
| 1401 | 0.009763 | prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy) (PSAP), mRNA /cds=(39,1613) /gb=NM_002778 /gi=11386146 /ug=Hs.406455 /len=2767 | NM_002778 | Hs.406455 | NP_002769 |
| 1420 | 0.00527 | ribosomal protein L36a-like (RPL36AL), mRNA /cds=(95,415) /gb=NM_001001 /gi=16306559 /ug=Hs.419465 /len=537 | NM_001001 | Hs.419465 | NP_000992 |
| 1421 | 0.036914 | mRNA; cDNA DKFZp434K052 (from clone DKFZp434K052) /gb=AL137398 /gi=6807944 /ug=Hs.169639 /len=1921 | AL137398 | Hs.169639 | |
| 1423 | 0.048543 | cytochrome c oxidase subunit VIIa polypeptide 2 (liver) (COX7A2), nuclear gene encoding mitochondrial protein, mRNA /cds=(76,327) /gb=NM_001865 /gi=18105035 /ug=Hs.70312 /len=470 | NM_001865 | Hs.70312 | NP_001856 |
| 1424 | 0.003893 | RAP1A, member of RAS oncogene family (RAP1A), mRNA /cds=(313,867) /gb=NM_002884 /gi=4506412 /ug=Hs.865 /len=1579 | NM_002884 | Hs.865 | NP_002875 |
| 1433 | 0.043576 | PAI-1 gene, PAI-1-HindIII-2 allele, 3' sequence | AF110527 | | |
| 1447 | 0.027691 | Hypothetical protein(KIAA0993) | AB023210 | | NP_848700 |
| 1454 | 0.015924 | Dmx-like 1 (DMXL1), mRNA /cds=(81,9164) /gb=NM_005509 /gi=21536473 /ug=Hs.181042 /len=11072 | NM_005509 | Hs.181042 | NP_005500 |
| 1477 | 0.041547 | zinc finger protein 302 (ZNF302), mRNA /cds=(337,1773) /gb=NM_018675 /gi=11034834 /ug=Hs.125287 /len=2978 | NM_018675 | Hs.125287 | NP_061145 |
| 1485 | 0.048543 | SRY (sex determining region Y)-box 5 (SOX5), transcript variant B, mRNA /cds=(373,2625) /gb=NM_152989 /gi=23308714 /ug=Hs.87224 /len=4492 | NM_152989 | Hs.87224 | NP_821078 |
| 1489 | 0.016974 | mRNA for KIAA1432 protein, partial cds. /cds=(1,2391) /gb=AB037853 /gi=20521915 /ug=Hs.279556 /len=4961 | AB037853 | Hs.279556 | |

| Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension | | | | | |
|---|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Acc'ssion No. | Unigene Accession No. | Protein Accession No. |
| 1494 | 0.011469 | basic leucine zipper and W2 domains 2 (BZW2), mRNA /cds=(163,1422) /gb=NM_014038 /gi=7661743 /ug=Hs.5216 /len=1869 | NM_014038 | Hs.5216 | NP_054757 |
| 1501 | 0.003893 | tropomyosin 4 | Y00169 | | |
| 1503 | 0.003079 | retrovirus-related leucine zipper protein p40 - human retrotransposon L1.1 | I38587 | | |
| 1514 | 0.015924 | defender against cell death 1 (DAD1), mRNA /cds=(67,408) /gb=NM_001344 /gi=4503252 /ug=Hs.82890 /len=699 | NM_001344 | Hs.82890 | NP_001335 |
| 1518 | 0.009349 | KIAA0466 protein | AB007935 | | NP_001533 |
| 1521 | 0.020482 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1), mRNA /cds=(289,2511) /gb=NM_004939 /gi=4826685 /ug=Hs.78580 /len=2706 | NM_004939 | Hs.78580 | NP_004930 |
| 1522 | 0.001465 | G protein-coupled receptor 64 (GPR64), mRNA /cds=(73,3117) /gb=NM_005756 /gi=5031732 /ug=Hs.184942 /len=4665 | NM_005756 | Hs.184942 | NP_005747 |
| 1529 | 0.011469 | ubiquinol-cytochrome c reductase binding protein (UQCRB), mRNA /cds=(54,389) /gb=NM_006294 /gi=20070231 /ug=Hs.131255 /len=965 | NM_006294 | Hs.131255 | NP_006285 |
| 1535 | 0.014701 | mRNA for KIAA0752 protein, partial cds. /cds=(1,1006) /gb=AB018295 /gi=3882224 /ug=Hs.126779 /len=4332 | AB018295 | Hs.126779 | NP_775934 |
| 1543 | 0.023148 | actin, alpha 2, smooth muscle, aorta (ACTA2), mRNA /cds=(48,1181) /gb=NM_001613 /gi=4501882 /ug=Hs.195851 /len=1330 | NM_001613 | Hs.195851 | NP_001604 |
| 1549 | 0.001465 | BRCA1, Rho7 and vat1 genes, complete cds, and ipf35 gene, partial cds | L78833 | | |
| 1552 | 0.006566 | RNA-binding region (RNP1, RRM) containing 2 (RNPC2), mRNA /cds=(150,1724) /gb=NM_004902 /gi=4757925 /ug=Hs.145696 /len=2595 | NM_004902 | Hs.145696 | NP_004893 |
| 1553 | 0.039034 | lymphocyte cytosolic protein 1 (L-plastin) (LCP1), mRNA /cds=(174,2057) /gb=NM_002298 /gi=7382490 /ug=Hs.381099 /len=3723 | NM_002298 | Hs.381099 | NP_002289 |
| 1555 | 0.03489 | KIAA1573 mRNA protein | AB046793 | | |
| 1572 | 0.015924 | ribosomal protein L27a (RPL27A), mRNA /cds=(23,469) /gb=NM_000990 /gi=14141189 /ug=Hs.76064 /len=514 | NM_000990 | Hs.76064 | NP_000981 |
| 1577 | 0.021781 | POM121 membrane glycoprotein (rat) (POM121), mRNA /cds=(978,3932) /gb=NM_172020 /gi=26051277 /ug=Hs.295112 /len=6014 | NM_172020 | Hs.295112 | NP_742017 |

| Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension | | | | | |
|---|----------|---|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 1580 | 0.0261 | profilin 1 (PFN1), mRNA /cds=(137,559) /gb=NM_005022 /gi=16753213 /ug=Hs.408943 /len=847 | NM_005022 | Hs.408943 | NP_005013 |
| 1587 | 0.03489 | PTD012 protein (PTD012), mRNA /cds=(200,997) /gb=NM_014039 /gi=21361494 /ug=Hs.8360 /len=2403 | NM_014039 | Hs.8360 | NP_054758 |
| 1592 | 0.041547 | KIAA0071 gene, partial cds /cds=UNKNOWN /gb=D31888 /gi=506340 /ug=Hs.78398 /len=5241 | D31888 | Hs.78398 | NP_055971 |
| 1593 | 0.032959 | hypothetical protein BC018068 (LOC221044), mRNA /cds=(231,695) /gb=NM_145314 /gi=21687122 /ug=Hs.112998 /len=840 | NM_145314 | Hs.112998 | NP_660357 |
| 1598 | 0.029363 | troponin I, skeletal, slow (TNNI1), mRNA /cds=(74,637) /gb=NM_003281 /gi=21361554 /ug=Hs.84673 /len=1108 | NM_003281 | Hs.84673 | NP_003272 |
| 1607 | 0.0261 | sulfatase SULF1 precursor, mRNA, complete cds /cds=(707,3322) /gb=AF545571 /gi=28191289 /ug=Hs.70823 /len=5699 | AF545571 | Hs.70823 | NP_055985 |
| 1630 | 2.73E-04 | calpain 2, (mII) large subunit (CAPN2), mRNA /cds=(143,2245) /gb=NM_001748 /gi=12408645 /ug=Hs.76288 /len=3419 | NM_001748 | Hs.76288 | NP_001739 |
| 1652 | 0.031117 | procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD), mRNA /cds=(201,2384) /gb=NM_000302 /gi=4557836 /ug=Hs.75093 /len=3115 | NM_000302 | Hs.75093 | NP_000293 |
| 1654 | 0.016974 | DKFZp434M092 (from clone DKFZp434M092) | AL137412 | | NP_057479 |
| 1659 | 0.041254 | likely ortholog of mouse elongation protein 3 (S. cerevisiae) (ELP3), mRNA /cds=(7,1650) /gb=NM_018091 /gi=23510282 /ug=Hs.267905 /len=3095 | NM_018091 | Hs.267905 | NP_060561 |
| 1661 | 0.006106 | cofactor required for Sp1 transcriptional activation, subunit 3, 130kDa (CRSP3), mRNA /cds=(120,4226) /gb=NM_004830 /gi=7019352 /ug=Hs.29679 /len=5176 | NM_004830 | Hs.29679 | NP_057063 |
| 1662 | 0.020482 | NS1-binding protein (NS1-BP), mRNA /cds=(556,2484) /gb=NM_006469 /gi=24475846 /ug=Hs.197298 /len=4137 | NM_006469 | Hs.197298 | NP_006460 |
| 1663 | 0.015924 | sarcolipin (SLN), mRNA /cds=(169,264) /gb=NM_003063 /gi=4507062 /ug=Hs.334629 /len=716 | NM_003063 | Hs.334629 | NP_003054 |

| Genes Corrsponding To Differentially Express d Genes in Figure 12 - Hypertension | | | | | |
|--|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 1665 | 0.008133 | eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA /cds=(63,1451) /gb=NM_001402 /gi=25453469 /ug=Hs.422118 /len=1837 | NM_001402 | Hs.422118 | NP_001393 |
| 1666 | 0.003079 | interleukin 1 receptor accessory protein (IL1RAP), transcript variant 1, mRNA /cds=(207,1919) /gb=NM_002182 /gi=24430220 /ug=Hs.173880 /len=4726 | NM_002182 | Hs.173880 | NP_608273 |
| 1667 | 0.032959 | interleukin 1 receptor, type I (IL1R1), mRNA /cds=(83,1792) /gb=NM_000877 /gi=27894331 /ug=Hs.82112 /len=4909 | NM_000877 | Hs.82112 | NP_000868 |
| 1674 | 0.027691 | calreticulin (CALR), mRNA /cds=(69,1322) /gb=NM_004343 /gi=5921996 /ug=Hs.353170 /len=1899 | NM_004343 | Hs.353170 | NP_004334 |
| 1675 | 0.004536 | coagulation factor XIII, A1 polypeptide (F13A1), mRNA /cds=(102,2300) /gb=NM_000129 /gi=9961355 /ug=Hs.80424 /len=3833 | NM_000129 | Hs.80424 | NP_000120 |
| 1676 | 0.032959 | muscle specific gene (M9), mRNA /cds=(172,828) /gb=NM_013234 /gi=10801344 /ug=Hs.283781 /len=911 | NM_013234 | Hs.283781 | NP_037366 |
| 1682 | 0.007056 | mRNA; cDNA DKFZp586A061 (from clone DKFZp586A061) /gb=AL080232 /gi=5262725 /ug=Hs.220696 /len=3052 | AL080232 | Hs.220696 | |
| 1687 | 0.002625 | diazepam binding inhibitor (GABA receptor modulator, acyl-Coenzyme A binding protein) (DBI), mRNA /cds=(20,334) /gb=NM_020548 /gi=24475624 /ug=Hs.78888 /len=556 | NM_020548 | Hs.78888 | NP_065438 |
| 1703 | 7.88E-04 | cDNA FLJ35517 fis, clone SPLEN2000698. /gb=AK092836 /gi=21751529 /ug=Hs.291804 /len=2536 | AK092836 | Hs.291804 | |
| 1710 | 0.016974 | RNA binding motif, single stranded interacting protein (RBMS3), mRNA /cds=(175,1410) /gb=NM_014483 /gi=7657505 /ug=Hs.158446 /len=1461 | NM_014483 | Hs.158446 | NP_055298 |
| 1712 | 0.013991 | TNFAIP3 interacting protein 2 (TNIP2), mRNA /cds=(376,1344) /gb=NM_024309 /gi=13236543 /ug=Hs.288991 /len=1960 | NM_024309 | Hs.288991 | NP_077285 |
| 1730 | 0.043576 | mitochondrion, complete genome | NC_001807 | | |
| 1731 | 0.027656 | hypothetical protein dJ122O8.2 (DJ122O8.2), mRNA /cds=(34,300) /gb=NM_020466 /gi=20070310 /ug=Hs.268115 /len=902 | NM_020466 | Hs.268115 | NP_065199 |
| 1742 | 0.01925 | KIAA0998 protein (KIAA0998), mRNA /cds=(71,2524) /gb=NM_015072 /gi=19923419 /ug=Hs.131525 /len=3122 | NM_015072 | Hs.131525 | NP_055887 |

| Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension | | | | | |
|---|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 1759 | 0.00527 | MEP50 protein (MEP50), mRNA /cds=(40,1068) /gb=NM_024102 /gi=20127622 /ug=Hs.11039 /len=2428 | NM_024102 | Hs.11039 | NP_077007 |
| 1760 | 0.027691 | FLJ32238 fis, clone PLACE6004993 /cds=UNKNOWN /gb=AK056800 /gi=16552307 /ug=Hs.183161 /len=2204 | AK056800 | Hs.183161 | NP_036595 |
| 1769 | 0.003603 | ribosomal protein L10 (RPL10), mRNA /cds=(42,686) /gb=NM_006013 /gi=15718685 /ug=Hs.412900 /len=2188 | NM_006013 | Hs.412900 | NP_006004 |
| 1773 | 0.003893 | ribosomal protein, large, P1 (RPLP1), mRNA /cds=(130,474) /gb=NM_001003 /gi=16905511 /ug=Hs.424299 /len=512 | NM_001003 | Hs.424299 | NP_000994 |
| 1795 | 0.01925 | serine/threonine kinase 16 (STK16), mRNA /cds=(119,1051) /gb=NM_003691 /gi=4505836 /ug=Hs.153003 /len=1382 | NM_003691 | Hs.153003 | NP_003682 |
| 1797 | 0.006566 | cDNA FLJ14066 fis, clone HEMBB1001197. /gb=AK024128 /gi=10436433 /ug=Hs.306665 /len=2086 | AK024128 | Hs.306665 | |
| 1798 | 0.021781 | NADH dehydrogenase (ubiquinone) flavoprotein 1, 51kDa (NDUFV1), mRNA /cds=(70,1464) /gb=NM_007103 /gi=20149567 /ug=Hs.7744 /len=1566 | NM_007103 | Hs.7744 | NP_009034 |
| 1809 | 0.015924 | clone IMAGE:3907313, mRNA /gb=BC041424 /gi=27370744 /ug=Hs.434753 /len=1700 | BC041424 | Hs.434753 | |
| 1832 | 0.032959 | ubiquitin protein ligase (UBE3B), mRNA /cds=(585,3791) /gb=NM_130466 /gi=26080339 /ug=Hs.17639 /len=5731 | NM_130466 | Hs.17639 | NP_569733 |
| 1836 | 0.001596 | hypothetical protein FLJ23445 (FLJ23445), mRNA /cds=(44,658) /gb=NM_025075 /gi=13376622 /ug=Hs.288151 /len=963 | NM_025075 | Hs.288151 | NP_079351 |
| 1844 | 0.001033 | cDNA FLJ32247 fis, clone PROST1000120. /gb=AK056809 /gi=16552317 /ug=Hs.293663 /len=3019 | AK056809 | Hs.293663 | |
| 1854 | 0.001737 | clone IMAGE:3611719, mRNA, partial cds /cds=(1,2592) /gb=BC003542 /gi=13097656 /ug=Hs.244482 /len=3234 | BC003542 | Hs.244482 | |
| 1858 | 0.00448 | cDNA FLJ41000 fis, clone UTERU2016761, highly similar to ES/130 mRNA. /gb=AK098319 /gi=21758311 /ug=Hs.356310 /len=2196 | AK098319 | Hs.356310 | |
| 1860 | 0.0261 | hypothetical protein FLJ20559 (FLJ20559), mRNA /cds=(211,810) /gb=NM_017881 /gi=8923529 /ug=Hs.98135 /len=1172 | NM_017881 | Hs.98135 | NP_060351 |

| Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension | | | | | |
|---|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 1861 | 0.031117 | hypothetical protein FLJ21841 (FLJ21841), mRNA /cds=(184,1476) /gb=NM_024609 /gi=13375818 /ug=Hs.29076 /len=2327 | NM_024609 | Hs.29076 | NP_078885 |
| 1872 | 0.027691 | suppressor of Ty 16 (S. cerevisiae) (SUPT16H), mRNA /cds=(340,3483) /gb=NM_007192 /gi=19924176 /ug=Hs.14963 /len=4696 | NM_007192 | Hs.14963 | NP_009123 |
| 1873 | 0.015924 | Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed (fox derived); ribosomal protein S30 (FAU), mRNA /cds=(106,507) /gb=NM_001997 /gi=17981709 /ug=Hs.177415 /len=574 | NM_001997 | Hs.177415 | NP_001988 |
| 1882 | 0.005674 | HSPC023 protein (HSPC023), mRNA /cds=(10,309) /gb=NM_014047 /gi=7661741 /ug=Hs.420065 /len=616 | NM_014047 | Hs.420065 | NP_054766 |
| 1896 | 0.039034 | ATP synthase, H transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 2 (ATP5G2), mRNA /cds=(60,485) /gb=NM_005176 /gi=6671590 /ug=Hs.89399 /len=746 | NM_005176 | Hs.89399 | NP_005167 |
| 1897 | 0.024587 | Csa-19 | U12404 | | NP_009035 |
| 1918 | 0.001465 | voltage-dependent anion channel 3 (VDAC3), mRNA /cds=(100,951) /gb=NM_005662 /gi=25188178 /ug=Hs.7381 /len=1414 | NM_005662 | Hs.7381 | NP_005653 |
| 1926 | 0.011469 | KIAA0738 gene product (KIAA0738), mRNA /cds=(134,2899) /gb=NM_014719 /gi=7662275 /ug=Hs.406492 /len=4076 | NM_014719 | Hs.406492 | NP_055534 |
| 1932 | 0.041254 | SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 2 (SMARCD2), mRNA /cds=(423,1850) /gb=NM_003077 /gi=21264350 /ug=Hs.250581 /len=2704 | NM_003077 | Hs.250581 | NP_003068 |
| 1970 | 0.00223 | Yeast centromere vector pRS315 with LEU2 marker, complete sequence | U03441 | | |
| 1976 | 0.016974 | likely ortholog of mouse exocyst component protein 70 kDa (S. cerevisiae) Exo70: exocyst component protein 70 kDa (S. cerevisiae) (EXO70), mRNA /cds=(4,1965) /gb=NM_015219 /gi=24308034 /ug=Hs.325530 /len=4596 | NM_015219 | Hs.325530 | NP_056034 |
| 1987 | 0.008133 | hypothetical protein MGC8721 (MGC8721), mRNA /cds=(17,1036) /gb=NM_016127 /gi=18252054 /ug=Hs.279921 /len=1840 | NM_016127 | Hs.279921 | NP_057211 |

| Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension | | | | | |
|---|----------|---|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 2005 | 4.48E-04 | class I histone deacetylase (HDAC8) | AF230097 | | NP_060956 |
| 2012 | 0.008722 | polyhomeotic-like 2 (Drosophila) (PHC2), mRNA /cds=(9,1310) /gb=NM_004427 /gi=4758241 /ug=Hs.165263 /len=2555 | NM_004427 | Hs.165263 | NP_004418 |
| 2033 | 0.003079 | calmodulin 1 (phosphorylase kinase, delta) (CALM1), mRNA /cds=(200,649) /gb=NM_006888 /gi=5901911 /ug=Hs.282410 /len=1526 | NM_006888 | Hs.282410 | NP_008819 |
| 2041 | 0.008722 | ribosomal protein L32 (RPL32), mRNA /cds=(51,458) /gb=NM_000994 /gi=15812220 /ug=Hs.169793 /len=521 | NM_000994 | Hs.169793 | NP_000985 |
| 2044 | 0.03489 | CGI-31 protein (CGI-31), mRNA /cds=(50,940) /gb=NM_015959 /gi=7705725 /ug=Hs.279861 /len=1669 | NM_015959 | Hs.279861 | NP_057043 |
| 2047 | 0.010015 | p8 protein (candidate of metastasis 1) (P8), mRNA /cds=(103,351) /gb=NM_012385 /gi=6912569 /ug=Hs.424279 /len=719 | NM_012385 | Hs.424279 | NP_036517 |
| 2048 | 0.009349 | mRNA for KIAA0701 protein, partial cds. /cds=(1,4065) /gb=AB014601 /gi=20521136 /ug=Hs.153293 /len=4625 | AB014601 | Hs.153293 | |
| 2054 | 0.006566 | mRNA; cDNA DKFZp586J1922 (from clone DKFZp586J1922) /gb=AL110203 /gi=5817122 /ug=Hs.138411 /len=2060 | AL110203 | Hs.138411 | |
| 2070 | 0.029363 | myotubular myopathy 1 (MTM1), mRNA /cds=(55,1866) /gb=NM_000252 /gi=4557895 /ug=Hs.75302 /len=3411 | NM_000252 | Hs.75302 | NP_000243 |
| 2071 | 0.048543 | mRNA for KIAA0194 gene, partial cds. /cds=(1,4310) /gb=D83778 /gi=1228038 /ug=Hs.216958 /len=5245 | D83778 | Hs.216958 | |
| 2077 | 0.002054 | musculus exoribonuclease 1 (Xrn1) | NM_011916 | | NP_036046 |
| 2083 | 0.018081 | major histocompatibility complex, class I, B (HLA-B), mRNA /cds=(11,1099) /gb=NM_005514 /gi=21327676 /ug=Hs.77961 /len=1310 | NM_005514 | Hs.77961 | NP_005505 |
| 2088 | 0.003079 | hypothetical protein LOC51257 (LOC51257), mRNA /cds=(352,1092) /gb=NM_016496 /gi=24475980 /ug=Hs.132744 /len=1614 | NM_016496 | Hs.132744 | NP_057580 |
| 2128 | 0.021781 | vacuolar protein sorting 35 (yeast) (VPS35), mRNA /cds=(48,2438) /gb=NM_018206 /gi=17999540 /ug=Hs.264190 /len=2707 | NM_018206 | Hs.264190 | NP_060676 |
| 2151 | 0.003079 | retinoblastoma-like 2 (p130) (RBL2), mRNA /cds=(70,3489) /gb=NM_005611 /gi=21361291 /ug=Hs.79362 /len=4853 | NM_005611 | Hs.79362 | NP_005602 |

| Genes C responding To Differentially Expressed Genes in Figure 12 - Hyp rtension | | | | | |
|--|----------|---|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 2163 | 0.012262 | eukaryotic translation initiation factor 3, subunit 6 interacting protein (EIF3S6IP), mRNA /cds=(34,1728) /gb=NM_016091 /gi=7705432 /ug=Hs.119503 /len=1901 | NM_016091 | Hs.119503 | NP_057175 |
| 2164 | 0.002054 | KIAA1074 protein (KIAA1074); mRNA /cds=(151,5280) /gb=NM_014915 /gi=7662473 /ug=Hs.129218 /len=5360 | NM_014915 | Hs.129218 | NP_055730 |
| 2166 | 0.010015 | nephroblastoma overexpressed gene (NOV), mRNA /cds=(73,1146) /gb=NM_002514 /gi=19923725 /ug=Hs.235935 /len=2389 | NM_002514 | Hs.235935 | NP_002505 |
| 2168 | 0.003079 | LOC119392 (LOC119392), mRNA /cds=(53,751) /gb=NM_145247 /gi=21687029 /ug=Hs.93667 /len=1460 | NM_145247 | Hs.93667 | NP_660290 |
| 2175 | 0.041254 | clone IMAGE:4799018, mRNA /gb=BC045722 /gi=28277129 /ug=Hs.153527 /len=2587 | BC045722 | Hs.153527 | |
| 2178 | 0.043576 | crystallin, zeta (quinone reductase)-like 1 (CRYZL1), transcript variant 3, mRNA /cds=(86,682) /gb=NM_145858 /gi=22202615 /ug=Hs.330208 /len=2099 | NM_145858 | Hs.330208 | NP_665857 |
| 2191 | 0.009349 | cDNA FLJ34376 fis, clone FEBRA2017780, weakly similar to RNA binding motif protein 9. /gb=AK091695 /gi=21750125 /ug=Hs.376650 /len=2397 | AK091695 | Hs.376650 | |
| 2192 | 0.013102 | hypothetical protein KIAA0473 gene product | NM_014787 | | NP_055602 |
| 2197 | 0.007578 | COX11 cytochrome c oxidase assembly protein (yeast) (COX11), nuclear gene encoding mitochondrial protein, mRNA /cds=(48,878) /gb=NM_004375 /gi=17921983 /ug=Hs.241515 /len=2717 | NM_004375 | Hs.241515 | NP_004366 |
| 2199 | 0.043576 | DnaJ (Hsp40) subfamily C, member 8 (DNAJC8), mRNA /cds=(8,802) /gb=NM_014280 /gi=7657610 /ug=Hs.433540 /len=1525 | NM_014280 | Hs.433540 | NP_055095 |
| 2211 | 6.55E-04 | L-isoaspartyl/D-aspartyl O-methyltransferase (PCMT1) gene, exon 1, | U49740 | | |
| 2221 | 0.0261 | clone MGC:43950 IMAGE:5276217, mRNA, complete cds /cds=(351,392) /gb=BC037901 /gi=23138800 /ug=Hs.262716 /len=2214 | BC037901 | Hs.262716 | |
| 2239 | 0.03489 | hypothetical protein (KIAA1162) | AB032988 | | NP_066979 |
| 2256 | 0.03489 | splicing factor 3a, subunit 3, 60kDa (SF3A3), mRNA /cds=(9,1514) /gb=NM_006802 /gi=5803166 /ug=Hs.77897 /len=2733 | NM_006802 | Hs.77897 | NP_006793 |
| 2269 | 0.003603 | PRO2822 | AAF69654 | | |

| Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension | | | | | |
|---|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 2271 | 0.001596 | transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein; A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel a> | AF196779 | | |
| 2289 | 0.003332 | SPARC-like 1 (mast9, hev1) (SPARCL1), mRNA /cds=(323,2317) /gb=NM_004684 /gi=21359870 /ug=Hs.75445 /len=2808 | NM_004684 | Hs.75445 | NP_004675 |
| 2295 | 0.016974 | non-metastatic cells 1, protein (NM23A) expressed in (NME1), mRNA /cds=(85,543) /gb=NM_000269 /gi=4557796 /ug=Hs.118638 /len=732 | NM_000269 | Hs.118638 | NP_000260 |
| 2297 | 0.003332 | zinc finger protein 2 (A1-5) (ZNF2), mRNA /cds=(855,1733) /gb=NM_021088 /gi=20304090 /ug=Hs.192285 /len=2630 | NM_021088 | Hs.192285 | NP_066574 |
| 2303 | 0.023148 | cDNA FLJ13446 fis, clone PLACE1002968. /gb=AK023508 /gi=10435460 /ug=Hs.201925 /len=1712 | AK023508 | Hs.201925 | |
| 2305 | 0.021781 | KIAA0970 protein (KIAA0970), mRNA /cds=(335,2668) /gb=NM_014923 /gi=7662419 /ug=Hs.103329 /len=4863 | NM_014923 | Hs.103329 | |
| 2306 | 0.036914 | S100 calcium binding protein A4 (calcium protein, calvasculin, metastasin, murine placental (S100A4), transcript variant 1, mRNA /cds=(70,375) /gb=NM_002961 /gi=9845514 /ug=Hs.81256 /len=512 | NM_002961 | Hs.81256 | NP_062427 |
| 2307 | 0.01925 | matrilin 3 (MATN3) precursor, mRNA /cds=(64,1524) /gb=NM_002381 /gi=13518040 /ug=Hs.278461 /len=2599 | NM_002381 | Hs.278461 | NP_002372 |
| 2317 | 0.012262 | mRNA for KIAA0570 protein, partial cds. /cds=(480,10718) /gb=AB011142 /gi=20521084 /ug=Hs.180948 /len=11269 | AB011142 | Hs.180948 | |
| 2324 | 0.018081 | hypothetical protein KIAA0883 | AB020690 | | NP_009188 |
| 2341 | 0.011469 | eukaryotic translation initiation factor 3, subunit 5 epsilon, 47kDa (EIF3S5), mRNA /cds=(7,1080) /gb=NM_003754 /gi=4503518 /ug=Hs.7811 /len=1231 | NM_003754 | Hs.7811 | NP_003745 |
| 2348 | 0.031117 | neuropilin-2 (a5) | AF022861 | | |
| 2414 | 0.007578 | metaxin 1 (MTX1), mRNA /cds=(1,954) /gb=NM_002455 /gi=4505280 /ug=Hs.247551 /len=1065 | NM_002455 | Hs.247551 | NP_002446 |

| Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension | | | | | |
|---|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Prot in Accession No. |
| 2445 | 0.014931 | matrilin 1, cartilage matrix protein (MATN1), mRNA /cds=(490,1980) /gb=NM_002379 /gi=13518035 /ug=Hs.150366 /len=2414 | NM_002379 | Hs.150366 | NP_002370 |
| 2457 | 0.029362 | ATPase, Na /K transporting, alpha 2 () polypeptide (ATP1A2), mRNA /cds=(105,3167) /gb=NM_000702 /gi=4502270 /ug=Hs.34114 /len=5511 | NM_000702 | Hs.34114 | NP_000693 |
| 2475 | 0.00189 | aldehyde dehydrogenase 5 family, member A1 (succinate-semialdehyde dehydrogenase) (ALDH5A1), transcript variant 1, nuclear gene encoding mitochondrial protein, mRNA /cds=(29,1675) /gb=NM_170740 /gi=25777720 /ug=Hs.5299 /len=5170 | NM_170740 | Hs.5299 | NP_733936 |
| 2491 | 0.003332 | clone IMAGE:5265791, mRNA /gb=BC035170 /gi=23958673 /ug=Hs.385807 /len=3000 | BC035170 | Hs.385807 | |
| 2510 | 0.046005 | EST (xm35g05.x1 NCI_CGAP_GC6 cDNA clone IMAGE:2686232 3') | AW196683 | | NP_004958 |
| 2511 | 0.015924 | ribosomal protein L35a (RPL35A), mRNA /cds=(74,406) /gb=NM_000996 /gi=16117790 /ug=Hs.288544 /len=511 | NM_000996 | Hs.288544 | NP_000987 |
| 2525 | 0.032959 | eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA /cds=(63,1451) /gb=NM_001402 /gi=25453469 /ug=Hs.422118 /len=1837 | NM_001402 | Hs.422118 | NP_001393 |
| 2539 | 1.18E-04 | Similar to hypothetical protein DKFZp5471224, clone IMAGE:5271326, mRNA /gb=BC039372 /gi=25058800 /ug=Hs.439358 /len=2494 | BC039372 | Hs.439358 | |
| 2542 | 0.004203 | leucyl-tRNA synthetase (LARS), mRNA /cds=(73,3603) /gb=NM_020117 /gi=24496788 /ug=Hs.6762 /len=4248 | NM_020117 | Hs.6762 | NP_064502 |
| 2590 | 0.046131 | enabled (Drosophila) (ENAH), mRNA /cds=(77,646) /gb=NM_018212 /gi=8922657 /ug=Hs.14838 /len=2943 | NM_018212 | Hs.14838 | NP_060682 |
| 2607 | 0.014931 | mitochondrion, complete genome | NC_001807 | | |
| 2609 | 0.036914 | cDNA FLJ14643 fis, clone NT2RP2001597, weakly similar to RYANODINE RECEPTOR, CARDIAC MUSCLE. /gb=AK027549 /gi=14042305 /ug=Hs.181161 /len=3586 | AK027549 | Hs.181161 | |
| 2625 | 0.001128 | hypothetical protein (KIAA0714) | AB018257 | | |
| 2626 | 0.048543 | general transcription factor IIB (GTF2B), mRNA /cds=(39,989) /gb=NM_001514 /gi=13435384 /ug=Hs.258561 /len=1268 | NM_001514 | Hs.258561 | NP_001505 |

| Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension | | | | | |
|---|----------|--|--------------------------|-----------------------------|-----------------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 2633 | 0.036914 | qb78b04.x1 Soares_fetal_heart_NbHH19W cDNA clone IMAGE:1706191 3', mRNA sequence /clone=IMAGE:1706191 /clone_end=3' /gb=AI144533 /gi=3666342 /ug=Hs.368824 /len=461 | AI144533 | Hs.368824 | |
| 2645 | 0.013102 | cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA /cds=(90,281) /gb=NM_001867 /gi=18105039 /ug=Hs.430075 /len=448 | NM_001867 | Hs.430075 | NP_001858 |
| 2678 | 0.015924 | protein-L-isoaspartate (D-aspartate) O- methyltransferase (PCMT1), mRNA /cds=(74,757) /gb=NM_005389 /gi=4885538 /ug=Hs.79137 /len=1599 | NM_005389 | Hs.79137 | NP_005380 |
| 2679 | 7.18E-04 | goliath protein (GP), mRNA /cds=(428,1258) /gb=NM_018434 /gi=20127393 /ug=Hs.155718 /len=1445 | NM_018434 | Hs.155718 | NP_060904 |
| 2684 | 6.55E-04 | squalene epoxidase (SQLE), mRNA /cds=(215,1939) /gb=NM_003129 /gi=6806899 /ug=Hs.71465 /len=2277 | NM_003129 | Hs.71465 | NP_003120 |
| 2696 | 0.032959 | cartilage linking protein 1 (CRTL1), mRNA /cds=(316,1380) /gb=NM_001884 /gi=4503052 /ug=Hs.2799 /len=1492 | NM_001884 | Hs.2799 | NP_001875 |
| 2708 | 0.020482 | mRNA for KIAA1338 protein, partial cds. /cds=(1,4488) /gb=AB037759 /gi=7243056 /ug=Hs.261587 /len=4994 | AB037759 | Hs.261587 | |
| 2713 | 0.003332 | caveolin-1/-2 locus, Contig1, D7S522, genes CAV2 CAV1 | AJ133269 | | |
| 2718 | 0.048543 | 17-beta-hydroxysteroid dehydrogenase type VII isoform mRNA, complete cds. /cds=(79,414) /gb=AF165514 /gi=9294734 /ug=Hs.380900 /len=1272 | AF165514 | Hs.380900 | NP_057455 |
| 2721 | 0.002625 | NRF1 protein (NRF1)= non-functional folate binding protein | L24123 | | |
| 2723 | 0.006106 | hypothetical protein FLJ12552 (FLJ12552), mRNA /cds=(6,1106) /gb=NM_022832 /gi=12383077 /ug=Hs.109268 /len=2483 | NM_022832 | Hs.109268 | NP_073743 |
| 2732 | 0.006566 | Similar to RIKEN cDNA 4921510P06 gene, clone MGC:9752 IMAGE:3855177, mRNA, complete cds | BC009053 | | NP_055494 |
| 2736 | 0.020482 | Down syndrome critical region gene 3 (DSCR3), mRNA /cds=(240,1133) /gb=NM_006052 /gi=5174424 /ug=Hs.26146 /len=3252 | NM_006052 | Hs.26146 | NP_006043 |

| Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension | | | | | |
|---|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 2743 | 0.012262 | clone MGC:9947 IMAGE:3876105, mRNA, complete cds /cds=(51,2216) /gb=BC013590 /gi=15488925 /ug=Hs.2437 /len=2651 | BC013590 | Hs.2437 | |
| 2745 | 0.006106 | calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced | AF223391 | | |
| 2751 | 0.015924 | transmembrane 4 superfamily member tetraspan NET-2 (NET-2), mRNA /cds=(66,983) /gb=NM_012338 /gi=21264567 /ug=Hs.16529 /len=2267 | NM_012338 | Hs.16529 | NP_036470 |
| 2778 | 0.032959 | SET translocation (myeloid leukemia-associated) (SET), mRNA /cds=(4,837) /gb=NM_003011 /gi=4506890 /ug=Hs.145279 /len=2577 | NM_003011 | Hs.145279 | NP_003002 |
| 2810 | 0.007578 | ATP synthase, H transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3 (ATP5G3), mRNA /cds=(255,683) /gb=NM_001689 /gi=4502300 /ug=Hs.429 /len=826 | NM_001689 | Hs.429 | NP_001680 |
| 2815 | 0.015924 | proteasome (prosome, macropain) subunit, alpha type, 6 (PSMA6), mRNA /cds=(110,850) /gb=NM_002791 /gi=23110943 /ug=Hs.410276 /len=1035 | NM_002791 | Hs.410276 | NP_002782 |
| 2816 | 0.039034 | CD109 (CD109), mRNA /cds=(113,4450) /gb=NM_133493 /gi=19424129 /ug=Hs.55964 /len=5883 | NM_133493 | Hs.55964 | NP_598000 |
| 2821 | 8.48E-05 | transcription factor forkhead-like 7 (FKHL7) gene, complete cds | AF048693 | | |
| 2822 | 0.011469 | Rho-related BTB domain containing 3 (RHOBTB3), mRNA /cds=(336,2171) /gb=NM_014899 /gi=7662355 /ug=Hs.10432 /len=4099 | NM_014899 | Hs.10432 | NP_055714 |
| 2840 | 0.013991 | KIAA0040 gene product (KIAA0040), mRNA /cds=(921,1382) /gb=NM_014656 /gi=7657258 /ug=Hs.158282 /len=4564 | NM_014656 | Hs.158282 | NP_055471 |
| 2843 | 0.048543 | UI-E-EJ0-ahj-n-19-0-UI.r1 UI-E-EJ0 cDNA clone UI-E-EJ0-ahj-n-19-0-UI 5', mRNA sequence /clone=UI-E-EJ0-ahj-n-19-0-UI /clone_end=5' /gb=BM701108 /gi=19014366 /ug=Hs.401941 /len=1923 | BM701108 | Hs.401941 | |
| 2848 | 0.008133 | BJ-HCC-24 tumor antigen mRNA, complete cds /cds=(2,1240) /gb=AY121805 /gi=22002585 /ug=Hs.433489 /len=1488 | AY121805 | Hs.433489 | |
| 2850 | 0.00223 | helicase II (RAD54L) mRNA, complete cds. /cds=(54,4979) /gb=U09820 /gi=606832 /ug=Hs.96264 /len=6115 | U09820 | Hs.96264 | NP_612115 |

| Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension | | | | | |
|---|----------|---|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 2856 | 0.013991 | proteasome (prosome, macropain) subunit, alpha type, 5 (PSMA5), mRNA /cds=(86,811) /gb=NM_002790 /gi=23110941 /ug=Hs.76913 /len=1023 | NM_002790 | Hs.76913 | NP_002781 |
| 2867 | 0.001465 | mitogen-activated protein kinase kinase 1 interacting protein 1 (MAP2K1IP1), mRNA /cds=(250,624) /gb=NM_021970 /gi=21614526 /ug=Hs.6361 /len=1416 | NM_021970 | Hs.6361 | NP_068805 |
| 2883 | 0.020482 | thymosin, beta 10 (TMSB10), mRNA /cds=(66,200) /gb=NM_021103 /gi=10863894 /ug=Hs.76293 /len=453 | NM_021103 | Hs.76293 | NP_066926 |
| 2885 | 0.021781 | chromosome 1 specific transCRipt KIAA0491 | AB007960 | | NP_057093 |
| 2887 | 0.031117 | RNA binding motif protein 12 (RBM12), transcript variant 1, mRNA /cds=(275,3073) /gb=NM_006047 /gi=23510460 /ug=Hs.180895 /len=6650 | NM_006047 | Hs.180895 | NP_690051 |
| 2891 | 0.023148 | patched related protein translocated in renal cancer (TRC8), mRNA /cds=(215,2209) /gb=NM_007218 /gi=21314653 /ug=Hs.28285 /len=2481 | NM_007218 | Hs.28285 | NP_009149 |
| 2894 | 0.039034 | ab23g04.x5 Stratagene lung (#937210) cDNA clone IMAGE:841686 3' similar to Q04609 PROSTATE-SPECIFIC MEMBRANE ANTIGEN ;, mRNA sequence /clone=IMAGE:841686 /clone_end=3' /gb=AI791154 /gi=5338870 /ug=Hs.445939 /len=440 | AI791154 | Hs.445939 | |
| 2901 | 0.03489 | A kinase (PRKA) anchor protein (yotiao) 9 (AKAP9), transcript variant 4, mRNA /cds=(223,5190) /gb=NM_147166 /gi=22538388 /ug=Hs.58103 /len=6058 | NM_147166 | Hs.58103 | NP_671714 |
| 2912 | 0.01072 | KIAA0690 protein (KIAA0690), mRNA /cds=(87,3980) /gb=NM_015179 /gi=15987120 /ug=Hs.60103 /len=4396 | NM_015179 | Hs.60103 | NP_055994 |
| 2913 | 0.006106 | mortality factor 4 like 1 (MORF4L1), mRNA /cds=(132,1103) /gb=NM_006791 /gi=5803101 /ug=Hs.6353 /len=1766 | NM_006791 | Hs.6353 | NP_006782 |
| 2928 | 0.004536 | ligase IV, DNA, ATP-dependent (LIG4), mRNA /cds=(274,3009) /gb=NM_002312 /gi=23199992 /ug=Hs.166091 /len=3325 | NM_002312 | Hs.166091 | NP_002303 |
| 2932 | 0.041254 | cyclin D binding myb-like transcription factor 1 (DMTF1), mRNA /cds=(276,2558) /gb=NM_021145 /gi=10863946 /ug=Hs.5671 /len=3767 | NM_021145 | Hs.5671 | NP_066968 |

| Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension | | | | | |
|---|----------|---|--------------------|----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigen Accession No. | Protein Accession No. |
| 2938 | 0.006106 | ribosomal protein L7a (RPL7A), mRNA /cds=(31,831) /gb=NM_000972 /gi=18390348 /ug=Hs.99858 /len=890 | NM_000972 | Hs.99858 | NP_000963 |
| 2946 | 0.007578 | CD164 antigen, sialomucin (CD164), mRNA /cds=(94,687) /gb=NM_006016 /gi=21361273 /ug=Hs.43910 /len=3038 | NM_006016 | Hs.43910 | NP_006007 |
| 2947 | 0.001596 | hemoglobin, alpha 2 (HBA2), mRNA /cds=(38,466) /gb=NM_000517 /gi=14043068 /ug=Hs.347939 /len=575 | NM_000517 | Hs.347939 | NP_000508 |
| 2948 | 0.041254 | endothelial differentiation-related factor 1 (EDF1), transcript variant alpha, mRNA /cds=(29,475) /gb=NM_003792 /gi=24497592 /ug=Hs.174050 /len=658 | NM_003792 | Hs.174050 | NP_694880 |
| 2950 | 6.55E-04 | cytochrome c oxidase subunit IV isoform 1 (COX4I1), nuclear gene encoding mitochondrial protein, mRNA /cds=(165,674) /gb=NM_001861 /gi=17017985 /ug=Hs.433419 /len=802 | NM_001861 | Hs.433419 | NP_001852 |
| 2954 | 0.023148 | muscleblind-like (Drosophila) (MBNL), mRNA /cds=(1415,2527) /gb=NM_021038 /gi=10518339 /ug=Hs.28578 /len=5940 | NM_021038 | Hs.28578 | NP_066368 |
| 2961 | 0.013102 | line-1 protein ORF2 (=p150) | B28096 | | |
| 2962 | 0.007578 | ORF2 contains a reverse transcriptase domain | AAB59368 | | |
| 2963 | 0.001232 | cDNA FLJ40109 fis, clone TESTI2007685. /gb=AK097428 /gi=21757181 /ug=Hs.377146 /len=2007 | AK097428 | Hs.377146 | |
| 2975 | 0.0261 | actin related protein 2/3 complex, subunit 3, 21kDa (ARPC3), mRNA /cds=(94,630) /gb=NM_005719 /gi=23397667 /ug=Hs.293750 /len=912 | NM_005719 | Hs.293750 | NP_005710 |
| 2976 | 0.008133 | myosin, light polypeptide 6, alkali, smooth muscle and non-muscle (MYL6), transcript variant 3, mRNA /cds=(41,514) /gb=NM_079425 /gi=17986263 /ug=Hs.77385 /len=717 | NM_079425 | Hs.77385 | NP_524149 |
| 2984 | 0.043576 | hypothetical protein FLJ10290 (FLJ10290), mRNA /cds=(78,1340) /gb=NM_018047 /gi=8922327 /ug=Hs.25516 /len=2297 | NM_018047 | Hs.25516 | NP_060517 |
| 2985 | 0.006106 | eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein) (EEF1D), transcript variant 1, mRNA /cds=(198,2141) /gb=NM_032378 /gi=25453473 /ug=Hs.334798 /len=2216 | NM_032378 | Hs.334798 | NP_115754 |

| Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension | | | | | |
|---|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 2988 | 0.016974 | cDNA: FLJ22636 fis, clone HSI06658, highly similar to HSAJ4162 mRNA for putative lipoic acid synthetase. /gb=AK026289 /gi=10439102 /ug=Hs.9280 /len=1732 | AK026289 | Hs.9280 | NP_006850 |
| 2989 | 4.06E-04 | hypothetical protein DKFZp434B195 (DKFZP434B195), mRNA /cds=(514,1290) /gb=NM_031284 /gi=21361960 /ug=Hs.10748 /len=2262 | NM_031284 | Hs.10748 | NP_112574 |
| 2991 | 0.009349 | prothymosin, alpha (gene sequence 28) (PTMA), mRNA /cds=(182,514) /gb=NM_002823 /gi=21359859 /ug=Hs.250655 /len=1233 | NM_002823 | Hs.250655 | NP_002814 |
| 2993 | 0.001596 | integrin beta 4 binding protein (ITGB4BP), mRNA /cds=(71,808) /gb=NM_002212 /gi=4504770 /ug=Hs.406444 /len=1112 | NM_002212 | Hs.406444 | NP_002203 |
| 2996 | 0.048543 | ribosomal protein. L12 (RPL12), mRNA /cds=(89,586) /gb=NM_000976 /gi=15431291 /ug=Hs.405042 /len=632 | NM_000976 | Hs.405042 | NP_000967 |
| 3002 | 7.18E-04 | high-mobility group phosphoprotein (HMGI-C) gene; exons 1-3, complete cds | L41044 | | |
| 3011 | 0.007578 | mitochondrion, complete genome | NC_001807 | | |
| 3020 | 0.046005 | hypothetical protein DJ667H12.2 (DJ667H12.2), mRNA /cds=(180,1250) /gb=NM_019605 /gi=19923818 /ug=Hs.21068 /len=2038 | NM_019605 | Hs.21068 | NP_062551 |
| 3025 | 0.018081 | FLJ30708 fis, clone FCBBF2001238 /cds=UNKNOWN /gb=AK055270 /gi=16549967 /ug=Hs.94812 /len=1965 | AK055270 | Hs.94812 | |
| 3026 | 0.002844 | calmodulin 2 (phosphorylase kinase, delta) (CALM2), mRNA /cds=(69,518) /gb=NM_001743 /gi=20428653 /ug=Hs.425808 /len=1128 | NM_001743 | Hs.425808 | NP_001734 |
| 3032 | 0.007578 | golgi-specific brefeldin A resistance factor 1 (GBF1), mRNA /cds=(241,5820) /gb=NM_004193 /gi=4758415 /ug=Hs.155499 /len=6376 | NM_004193 | Hs.155499 | NP_004184 |
| 3034 | 0.00223 | serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 6 (SERPINB6), mRNA /cds=(75,1205) /gb=NM_004568 /gi=28077084 /ug=Hs.41072 /len=1361 | NM_004568 | Hs.41072 | NP_004559 |
| 3040 | 5.42E-04 | DKFZp434F1011 (from clone DKFZp434F1011) /cds=UNKNOWN /gb=AL157490 /gi=7018535 /ug=Hs.274589 /len=6634 | AL157490 | Hs.274589 | |

| Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension | | | | | |
|---|----------|---|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 3044 | 0.002054 | hypothetical protein LOC51321 (LOC51321), mRNA /cds=(635,1195) /gb=NM_016627 /gi=7706167 /ug=Hs.268122 /len=1304 | NM_016627 | Hs.268122 | NP_057711 |
| 3046 | 0.004536 | kinesin family member 3B (KIF3B), mRNA /cds=(168,2411) /gb=NM_004798 /gi=4758645 /ug=Hs.301206 /len=4724 | NM_004798 | Hs.301206 | NP_004789 |
| 3049 | 0.03489 | retinol dehydrogenase 14 (all-trans and 9-cis) (RDH14), mRNA /cds=(64,1074) /gb=NM_020905 /gi=10190745 /ug=Hs.288880 /len=1538 | NM_020905 | Hs.288880 | NP_065956 |
| 3057 | 0.041254 | ferredoxin 1 (FDX1), nuclear gene encoding mitochondrial protein, mRNA /cds=(134,688) /gb=NM_004109 /gi=13677224 /ug=Hs.744 /len=1468 | NM_004109 | Hs.744 | NP_004100 |
| 3059 | 0.029363 | DKFZp434O071 (from clone DKFZp434O071) | AL080184 | | NP_057217 |
| 3061 | 0.007578 | mRNA; cDNA DKFZp586F1418 (from clone DKFZp586F1418) /gb=AL833819 /gi=21739144 /ug=Hs.296356 /len=4355 | AL833819 | Hs.296356 | |
| 3062 | 0.00489 | myosin, light polypeptide, regulatory, non-sarcomeric (20kD) (MLCB), mRNA /cds=(115,630) /gb=NM_006471 /gi=5453739 /ug=Hs.180224 /len=944 | NM_006471 | Hs.180224 | NP_006462 |
| 3065 | 0.006566 | KIAA0433 protein (KIAA0433), mRNA /cds=(510,4241) /gb=NM_015216 /gi=7662117 /ug=Hs.26179 /len=5814 | NM_015216 | Hs.26179 | NP_056031 |
| 3070 | 0.001737 | signal sequence receptor, beta (translocon-associated protein beta) (SSR2), mRNA /cds=(51,602) /gb=NM_003145 /gi=6552341 /ug=Hs.74564 /len=1093 | NM_003145 | Hs.74564 | NP_003136 |
| 3071 | 2.73E-04 | endothelin receptor type A (EDNRA), mRNA /cds=(485,1768) /gb=NM_001957 /gi=4503464 /ug=Hs.76252 /len=4105 | NM_001957 | Hs.76252 | NP_001948 |
| 3072 | 0.036914 | trichorhinophalangeal syndrome I (TRPS1), mRNA /cds=(639,4484) /gb=NM_014112 /gi=7657658 /ug=Hs.26102 /len=10011 | NM_014112 | Hs.26102 | NP_054831 |
| 3077 | 0.01072 | mRNA; cDNA DKFZp586E1120 (from clone DKFZp586E1120) /gb=AL049437 /gi=4500220 /ug=Hs.351178 /len=2141 | AL049437 | Hs.351178 | |

| Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension | | | | | |
|---|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 3079 | 2.73E-04 | ATP synthase, H transporting, mitochondrial F1 complex, epsilon subunit (ATP5E), nuclear gene encoding mitochondrial protein, mRNA /cds=(95,250) /gb=NM_006886 /gi=21327678 /ug=Hs.177530 /len=417 | NM_006886 | Hs.177530 | NP_008817 |
| 3080 | 0.021781 | extracellular link domain containing 1 (XLKD1), mRNA /cds=(91,1059) /gb=NM_006691 /gi=5729910 /ug=Hs.17917 /len=2313 | NM_006691 | Hs.17917 | NP_006682 |
| 3085 | 0.002844 | PEF protein with a long N-terminal hydrophobic domain (peflin) (PEF), mRNA /cds=(13,867) /gb=NM_012392 /gi=6912581 /ug=Hs.241531 /len=1641 | NM_012392 | Hs.241531 | NP_036524 |
| 3090 | 0.003893 | Similar to kinesin family member C1, clone MGC:1202 IMAGE:3506669, mRNA, complete cds /cds=(168,2189) /gb=BC000712 /gi=12653842 /ug=Hs.20830 /len=2400 | BC000712 | Hs.20830 | NP_002254 |
| 3094 | 0.029363 | SON DNA binding protein (SON), transcript variant e, mRNA /cds=(50,6376) /gb=NM_058183 /gi=21040317 /ug=Hs.92909 /len=8482 | NM_058183 | Hs.92909 | NP_620305 |
| 3102 | 0.013991 | deoxyribonuclease I-like 3 (DNASE1L3), mRNA /cds=(71,988) /gb=NM_004944 /gi=4826697 /ug=Hs.88646 /len=1079 | NM_004944 | Hs.88646 | NP_004935 |
| 3107 | 0.039034 | a disintegrin-like and metalloprotease (reprolysin type)-with thrombospondin type 1 motif, 5 (aggrecanase-2) (ADAMTS5), mRNA /cds=(123,2915) /gb=NM_007038 /gi=5901887 /ug=Hs.58324 /len=5533 | NM_007038 | Hs.58324 | NP_008969 |
| 3108 | 0.002625 | glycogen synthase 1 (muscle) (GYS1), mRNA /cds=(161,2374) /gb=NM_002103 /gi=4504232 /ug=Hs.772 /len=3531 | NM_002103 | Hs.772 | NP_002094 |
| 3117 | 4.93E-04 | mRNA for Sec24 protein (Sec24A isoform), partial /cds=(1,3237) /gb=AJ131244 /gi=3947687 /ug=Hs.211612 /len=5967 | AJ131244 | Hs.211612 | |
| 3124 | 0.010015 | hypothetical protein LOC51315 (LOC51315), mRNA /cds=(395,1174) /gb=NM_016618 /gi=7706155 /ug=Hs.5721 /len=1774 | NM_016618 | Hs.5721 | NP_057702 |
| 3131 | 0.016974 | putative translation initiation factor (SUI1), mRNA /cds=(148,489) /gb=NM_005801 /gi=20070210 /ug=Hs.150580 /len=1324 | NM_005801 | Hs.150580 | NP_005792 |

| Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension | | | | | |
|---|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 3136 | 0.001232 | splicing factor, arginine/serine-rich 5 (SFRS5), mRNA /cds=(219,542) /gb=NM_006925 /gi=5902077 /ug=Hs.166975 /len=1865 | NM_006925 | Hs.166975 | NP_008856 |
| 3137 | 0.002844 | yp24c06.s1 Soares breast 3NbHBst cDNA clone IMAGE:188362 3' similar to gb:M10942_cds1 metallothionein-le gene mRNA sequence /clone=IMAGE:188362 /clone_end=3' /gb=H43642 /gi=919694 /ug=Hs.418241 /len=452 | H43642 | Hs.418241 | |
| 3138 | 0.012262 | NCAG1 (NCAG1), mRNA /cds=(1477,5145) /gb=NM_032160 /gi=23943786 /ug=Hs.124673 /len=9528 | NM_032160 | Hs.124673 | NP_115536 |
| 3142 | 0.008133 | single-stranded DNA binding protein (SSBP1), mRNA /cds=(79,525) /gb=NM_003143 /gi=4507230 /ug=Hs.923 /len=628 | NM_003143 | Hs.923 | NP_003134 |
| 3149 | 0.012262 | thioredoxin domain-containing (TXNDC), mRNA /cds=(118,960) /gb=NM_030755 /gi=13559515 /ug=Hs.24766 /len=1112 | NM_030755 | Hs.24766 | NP_110382 |
| 3151 | 2.47E-04 | hypothetical protein FLJ37440 (FLJ37440), mRNA /cds=(272,1591) /gb=NM_153214 /gi=23397470 /ug=Hs.355577 /len=2299 | NM_153214 | Hs.355577 | NP_694946 |
| 3156 | 0.004203 | golgi autoantigen, golgin subfamily b, macrogolgin (with transmembrane signal), 1 (GOLGB1), mRNA /cds=(127,9906) /gb=NM_004487 /gi=4758453 /ug=Hs.7844 /len=10300 | NM_004487 | Hs.7844 | NP_004478 |
| 3162 | 0.01047 | hypothetical protein FLJ22875 (FLJ22875), mRNA /cds=(152,634) /gb=NM_032231 /gi=15638951 /ug=Hs.406548 /len=1019 | NM_032231 | Hs.406548 | NP_115607 |
| 3166 | 8.63E-04 | hypothetical protein FLJ13855 (FLJ13855), mRNA /cds=(328,1068) /gb=NM_023079 /gi=20149671 /ug=Hs.168232 /len=3053 | NM_023079 | Hs.168232 | NP_075567 |
| 3172 | 6.55E-04 | myocyte-specific enhancer factor 2A (MEF2A) gene, last coding exon, and complete cds | U49020 | | |
| 3173 | 0.004536 | hypothetical protein FLJ11730 (FLJ11730), mRNA /cds=(33,608) /gb=NM_022756 /gi=20149668 /ug=Hs.17118 /len=1558 | NM_022756 | Hs.17118 | NP_073593 |
| 3174 | 0.023148 | lectin, galactoside-binding, soluble, 1 (galectin 1) (LGALS1), mRNA /cds=(69,476) /gb=NM_002305 /gi=6006015 /ug=Hs.382367 /len=526 | NM_002305 | Hs.382367 | NP_002296 |

| Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hyp rtension | | | | | |
|---|----------|---|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 3189 | 0.001465 | melanoma adhesion molecule (MCAM), mRNA /cds=(27,1967) /gb=NM_006500 /gi=5729917 /ug=Hs.211579 /len=3583 | NM_006500 | Hs.211579 | NP_006491 |
| 3193 | 0.015924 | phosphorylase, glycogen; brain (PYGB), nuclear gene encoding mitochondrial protein, mRNA /cds=(97,2628) /gb=NM_002862 /gi=21361369 /ug=Hs.75658 /len=4166 | NM_002862 | Hs.75658 | NP_002853 |
| 3194 | 0.001033 | ornithine decarboxylase antizyme 1 (OAZ1), mRNA /gb=NM_004152 /gi=9845504 /ug=Hs.281960 /len=986 | NM_004152 | Hs.281960 | NP_004143 |
| 3196 | 0.048543 | DKFZp586E0524 (from clone DKFZp586E0524) | AL110153 | | NP_000974 |
| 3197 | 4.06E-04 | NDRG family member 2 (NDRG2), mRNA /cds=(97,1170) /gb=NM_016250 /gi=10280619 /ug=Hs.243960 /len=2024 | NM_016250 | Hs.243960 | NP_057334 |
| 3198 | 0.011469 | cDNA: FLJ21691 fis, clone COL09555. /gb=AK025344 /gi=10437842 /ug=Hs.141003 /len=1824 | AK025344 | Hs.141003 | |
| 3201 | 0.012262 | protein kinase C substrate 80K-H (PRKCSH), mRNA /cds=(137,1720) /gb=NM_002743 /gi=4506076 /ug=Hs.1432 /len=2056 | NM_002743 | Hs.1432 | NP_002734 |
| 3204 | 0.01925 | clone IMAGE:5263531, mRNA /gb=BC037740 /gi=22902216 /ug=Hs.18016 /len=5036 | BC037740 | Hs.18016 | |
| 3245 | 0.002625 | procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide (protein disulfide isomerase; thyroid hormone binding protein p55) (P4HB), mRNA /cds=(45,1571) /gb=NM_000918 /gi=20070124 /ug=Hs.410578 /len=2438 | NM_000918 | Hs.410578 | NP_000909 |
| 3275 | 0.046005 | KIAA0141 gene product (KIAA0141), mRNA /cds=(81,1628) /gb=NM_014773 /gi=7661939 /ug=Hs.63510 /len=3020 | NM_014773 | Hs.63510 | NP_055588 |
| 3282 | 0.018081 | YME1-like 1 (S. cerevisiae) (YME1L1), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA /cds=(183,2504) /gb=NM_139312 /gi=21327684 /ug=Hs.206521 /len=4036 | NM_139312 | Hs.206521 | NP_647474 |
| 3294 | 0.048543 | NCK adaptor protein 1 (NCK1), mRNA /cds=(117,1250) /gb=NM_006153 /gi=20070226 /ug=Hs.54589 /len=1947 | NM_006153 | Hs.54589 | NP_006144 |
| 3316 | 0.036914 | glutathione S-transferase M3 (brain) (GSTM3), mRNA /cds=(311,988) /gb=NM_000849 /gi=23065551 /ug=Hs.2006 /len=1572 | NM_000849 | Hs.2006 | NP_000840 |

| Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension | | | | | |
|---|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 3367 | 0.031117 | nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor) (NR3C1), mRNA /cds=(133,2466) /gb=NM_000176 /gi=4504132 /ug=Hs.75772 /len=4788 | NM_000176 | Hs.75772 | NP_000167 |
| 3377 | 0.043576 | cDNA: FLJ23538 fis, clone LNG08010, highly similar to BETA2 MEN1 region clone epsilon/beta mRNA. /gb=AK027191 /gi=10440260 /ug=Hs.240443 /len=1746 | AK027191 | Hs.240443 | |
| 3397 | 0.027691 | chromosome 20 open reading frame 6 (C20orf6), mRNA /cds=(109,2664) /gb=NM_016649 /gi=22507381 /ug=Hs.88820 /len=3216 | NM_016649 | Hs.88820 | NP_057733 |
| 3400 | 0.041254 | KH domain containing, RNA binding, signal transduction associated 1 (KHDRBS1), mRNA /cds=(107,1438) /gb=NM_006559 /gi=5730026 /ug=Hs.119537 /len=2685 | NM_006559 | Hs.119537 | NP_006550 |
| 3402 | 0.029363 | basic transcription factor 3 (BTF3), mRNA /cds=(240,728) /gb=NM_001207 /gi=20070129 /ug=Hs.101025 /len=952 | NM_001207 | Hs.101025 | NP_001198 |
| 3407 | 0.023148 | BCL2/adenovirus E1B 19kD-interacting protein 3-like (BNIP3L) | XM_048077 | | |
| 3413 | 0.046005 | myoglobin (MB), mRNA /cds=(71,535) /gb=NM_005368 /gi=4885476 /ug=Hs.118836 /len=1066 | NM_005368 | Hs.118836 | NP_005359 |
| 3431 | 0.020482 | spermine synthase gene | AJ009633 | | |
| 3440 | 0.03489 | TERF1 (TRF1)-interacting nuclear factor 2 (TINF2), mRNA /cds=(263,1327) /gb=NM_012461 /gi=6912715 /ug=Hs.7797 /len=2095 | NM_012461 | Hs.7797 | NP_036593 |
| 3441 | 0.024587 | translocase of inner mitochondrial membrane 8 B (yeast) (TIMM8B), mRNA /cds=(13,264) /gb=NM_012459 /gi=6912711 /ug=Hs.279915 /len=423 | NM_012459 | Hs.279915 | NP_036591 |
| 3443 | 0.007578 | guanylate kinase 1 (GUK1), mRNA /cds=(225,818) /gb=NM_000858 /gi=20127414 /ug=Hs.3764 /len=1082 | NM_000858 | Hs.3764 | NP_000849 |
| 3444 | 0.006566 | laminin receptor 1 (ribosomal protein SA, 67kDa) (LAMR1), mRNA /cds=(86,973) /gb=NM_002295 /gi=9845501 /ug=Hs.181357 /len=1039 | NM_002295 | Hs.181357 | NP_002286 |
| 3456 | 2.47E-04 | ionized calcium binding adapter molecule 2 (IBA2), mRNA /cds=(89,541) /gb=NM_031426 /gi=13899240 /ug=Hs.4944 /len=3381 | NM_031426 | Hs.4944 | NP_113614 |

| Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension | | | | | |
|---|----------|---|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 3461 | 0.01072 | ribosomal protein S3 (RPS3), mRNA /cds=(19,750) /gb=NM_001005 /gi=15718686 /ug=Hs.414990 /len=843 | NM_001005 | Hs.414990 | NP_000996 |
| 3463 | 0.023148 | mastermind-like 1 (Drosophila) (MAML1), mRNA /cds=(264,3314) /gb=NM_014757 /gi=13376996 /ug=Hs.76986 /len=5717 | NM_014757 | Hs.76986 | NP_055572 |
| 3464 | 0.012262 | matrilin 3 (MATN3) precursor, mRNA /cds=(64,1524) /gb=NM_002381 /gi=13518040 /ug=Hs.278461 /len=2599 | NM_002381 | Hs.278461 | NP_002372 |
| 3470 | 0.039034 | hypothetical protein FLJ10300 (FLJ10300), mRNA /cds=(1710,3359) /gb=NM_018051 /gi=21361686 /ug=Hs.42233 /len=3785 | NM_018051 | Hs.42233 | NP_060521 |
| 3472 | 0.01925 | eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA /cds=(63,1451) /gb=NM_001402 /gi=25453469 /ug=Hs.422118 /len=1837 | NM_001402 | Hs.422118 | NP_001393 |
| 3477 | 0.046005 | vacuolar protein sorting 16 (yeast) (VPS16), transcript variant 1, mRNA /cds=(49,2568) /gb=NM_022575 /gi=17978478 /ug=Hs.302441 /len=2769 | NM_022575 | Hs.302441 | NP_536339 |
| 3483 | 0.048543 | signal sequence receptor, beta (translocon-associated protein beta) (SSR2), mRNA /cds=(51,602) /gb=NM_003145 /gi=6552341 /ug=Hs.74564 /len=1093 | NM_003145 | Hs.74564 | NP_003136 |
| 3492 | 0.00527 | UI-H-BI2-ags-a-03-0-UI.s1 NCI_CGAP_Sub4 cDNA clone IMAGE:2725156 3', mRNA sequence /clone=IMAGE:2725156 /clone_end=3' /gb=AW292521 /gi=6699157 /ug=Hs.227074 /len=685 | AW292521 | Hs.227074 | |
| 3500 | 0.004536 | ASC-1 complex subunit P100 (FLJ21588), mRNA /cds=(115,2388) /gb=NM_032204 /gi=20270252 /ug=Hs.334686 /len=2808 | NM_032204 | Hs.334686 | NP_115580 |
| 3511 | 0.001033 | xf26f10.x1 NCI_CGAP_Ut1 cDNA clone IMAGE:2619211 3', mRNA sequence /clone=IMAGE:2619211 /clone_end=3' /gb=AW130007 /gi=6131612 /ug=Hs.389726 /len=423 | AW130007 | Hs.389726 | |
| 3513 | 0.041254 | chromosome 1 open reading frame 29 (C1orf29), mRNA /cds=(242,1483) /gb=NM_006820 /gi=5803026 /ug=Hs.75470 /len=2058 | NM_006820 | Hs.75470 | NP_006811 |

| Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension | | | | | |
|---|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 3521 | 0.039034 | ubiquitin-like, containing PHD and RING finger domains 2 (URF2), transcript variant 1, mRNA /cds=(341,1852) /gb=NM_152306 /gi=23312361 /ug=Hs.348602 /len=3720 | NM_152306 | Hs.348602 | NP_690856 |
| 3533 | 0.046005 | nascent-polypeptide-associated complex alpha polypeptide (NACA), mRNA /cds=(26,673) /gb=NM_005594 /gi=5031930 /ug=Hs.32916 /len=797 | NM_005594 | Hs.32916 | NP_005585 |
| 3538 | 0.027691 | insulin-like growth factor binding protein 6 (IGFBP6), mRNA /cds=(54,776) /gb=NM_002178 /gi=11321592 /ug=Hs.274313 /len=952 | NM_002178 | Hs.274313 | NP_002169 |
| 3539 | 0.007578 | ubiquitin C (UBC), mRNA /cds=(136,2193) /gb=NM_021009 /gi=20149305 /ug=Hs.183704 /len=2309 | NM_021009 | Hs.183704 | NP_066289 |
| 3540 | 0.001232 | nucleoporin 155kDa (NUP155), transcript variant 1, mRNA /cds=(119,4294) /gb=NM_153485 /gi=24430148 /ug=Hs.23255 /len=4355 | NM_153485 | Hs.23255 | NP_705618 |
| 3551 | 0.00527 | RAB9A, member RAS oncogene family (RAB9A), mRNA /cds=(192,797) /gb=NM_004251 /gi=20070189 /ug=Hs.330994 /len=1106 | NM_004251 | Hs.330994 | NP_004242 |
| 3576 | 0.007056 | osteoglycin (osteoinductive factor, mimecan) (OGN), transcript variant 1, mRNA /cds=(422,1318) /gb=NM_033014 /gi=14916497 /ug=Hs.109439 /len=2976 | NM_033014 | Hs.109439 | NP_148935 |
| 3606 | 0.018081 | nucleolar protein family A, member 3 (H/ACA small nucleolar RNPs) (NOLA3), mRNA /cds=(98,292) /gb=NM_018648 /gi=15011920 /ug=Hs.14317 /len=556 | NM_018648 | Hs.14317 | NP_061118 |
| 3613 | 0.041254 | ataxin 2 related protein (A2LP), transcript variant A, mRNA /cds=(169,3396) /gb=NM_007245 /gi=27262646 /ug=Hs.43509 /len=4386 | NM_007245 | Hs.43509 | NP_680782 |
| 3619 | 6.03E-05 | cytochrome c oxidase subunit IV isoform 1 (COX4I1), nuclear gene encoding mitochondrial protein, mRNA /cds=(165,674) /gb=NM_001861 /gi=17017985 /ug=Hs.433419 /len=802 | NM_001861 | Hs.433419 | NP_001852 |
| 3623 | 0.016974 | cDNA FLJ14089 fis, clone MAMMA1000257. /gb=AK024151 /gi=10436462 /ug=Hs.306668 /len=1730 | AK024151 | Hs.306668 | |

| Genes Corrsponding To Differentially Expressed Genes in Figure 12 - Hypertension | | | | | |
|--|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 3625 | 0.015924 | UI-E-CQ1-aev-g-12-0-UI.s1 UI-E-CQ1 cDNA clone UI-E-CQ1-aev-g-12-0-UI 3', mRNA sequence /clone=UI-E-CQ1-aev-g-12-0-UI /clone_end=3' /gb=BM666437 /gi=18974127 /ug=Hs.279806 /len=1103 | BM666437 | Hs.279806 | |
| 3640 | 0.012262 | PTD015 protein (PTD015), mRNA /cds=(148,504) /gb=NM_014040 /gi=7662642 /ug=Hs.95870 /len=620 | NM_014040 | Hs.95870 | NP_054759 |
| 3641 | 0.006106 | hypothetical protein CL25084 (CL25084), mRNA /cds=(132,1583) /gb=NM_015701 /gi=20070263 /ug=Hs.7100 /len=2412 | NM_015701 | Hs.7100 | NP_056516 |
| 3642 | 0.002625 | chromosome 1 open reading frame 22 (C1orf22), mRNA /cds=(54,2723) /gb=NM_025191 /gi=19923618 /ug=Hs.279951 /len=6298 | NM_025191 | Hs.279951 | NP_079467 |
| 3645 | 0.0261 | hypothetical protein MGC14697 (MGC14697), mRNA /cds=(264,440) /gb=NM_032747 /gi=14249375 /ug=Hs.171625 /len=581 | NM_032747 | Hs.171625 | NP_116136 |
| 3652 | 0.001128 | cDNA: FLJ22636 fis, clone HSI06658, highly similar to HSAJ4162 mRNA for putative lipoic acid synthetase. /gb=AK026289 /gi=10439102 /ug=Hs.9280 /len=1732 | AK026289 | Hs.9280 | NP_006850 |
| 3662 | 0.01925 | hypothetical protein FLJ10700 (FLJ10700), mRNA /cds=(184,1872) /gb=NM_018182 /gi=8922595 /ug=Hs.295909 /len=3434 | NM_018182 | Hs.295909 | NP_060652 |
| 3666 | 0.023148 | DAZ associated protein 2 (DAZAP2), mRNA /cds=(70,576) /gb=NM_014764 /gi=7661885 /ug=Hs.75416 /len=1897 | NM_014764 | Hs.75416 | NP_055579 |
| 3677 | 0.023148 | major histocompatibility complex, class I, B (HLA-B), mRNA /cds=(11,1099) /gb=NM_005514 /gi=21327676 /ug=Hs.77961 /len=1310 | NM_005514 | Hs.77961 | NP_005505 |
| 3683 | 0.007578 | thioredoxin reductase TR2 mRNA, partial cds /cds=(1,1740) /gb=AF171055 /gi=5764542 /ug=Hs.20030 /len=2593 | AF171055 | Hs.20030 | |
| 3685 | 0.018081 | SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1 (SMARCE1), mRNA /cds=(122,1357) /gb=NM_003079 /gi=21264354 /ug=Hs.332848 /len=1576 | NM_003079 | Hs.332848 | NP_003070 |

| Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension | | | | | |
|---|----------|---|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 3690 | 0.006566 | IK cytokine, down-regulator of HLA II (IK), mRNA /cds=(112,1785) /gb=NM_006083 /gi=11038650 /ug=Hs.8024 /len=1785 | NM_006083 | Hs.8024 | NP_006074 |
| 3705 | 0.00527 | hypothetical protein FLJ10856 (FLJ10856), mRNA /cds=(148,1233) /gb=NM_018247 /gi=8922719 /ug=Hs.108530 /len=3720 | NM_018247 | Hs.108530 | NP_060717 |
| 3708 | 0.046005 | mRNA; cDNA DKFZp667D095 (from clone DKFZp667D095) /gb=AL512749 /gi=12224966 /ug=Hs.432978 /len=1396 | AL512749 | Hs.432978 | |
| 3716 | 0.0261 | FLJ21563 fis, clone COL06445 (AK025216.1). | AK025216 | Hs.24341 | NP_056287 |
| 3730 | 0.023148 | folistatin (FST), transcript variant FST317, mRNA /cds=(28,981) /gb=NM_006350 /gi=7242223 /ug=Hs.9914 /len=1386 | NM_006350 | Hs.9914 | NP_037541 |
| 3733 | 0.041254 | MAGEF1 protein (MAGEF1), mRNA /cds=(177,1103) /gb=NM_022149 /gi=11545891 /ug=Hs.306123 /len=1615 | NM_022149 | Hs.306123 | NP_071432 |
| 3756 | 0.036914 | Ste20-related serine/threonine kinase (SLK), mRNA /cds=(512,3970) /gb=NM_014720 /gi=7661993 /ug=Hs.105751 /len=5988 | NM_014720 | Hs.105751 | NP_055535 |
| 3762 | 0.036914 | heat shock 70kDa protein 8 (HSPA8), transcript variant 1, mRNA /cds=(79,2019) /gb=NM_006597 /gi=24234684 /ug=Hs.180414 /len=2276 | NM_006597 | Hs.180414 | NP_694881 |
| 3768 | 0.005674 | Mov10, Moloney leukemia virus 10, (mouse) (MOV10), mRNA /cds=(71,3082) /gb=NM_020963 /gi=14211539 /ug=Hs.20725 /len=3328 | NM_020963 | Hs.20725 | NP_066014 |
| 3769 | 4.06E-04 | signal transducer and activator of transcription 3 (acute-phase response factor) (STAT3), transcript variant 1, mRNA /cds=(241,2553) /gb=NM_139276 /gi=21618339 /ug=Hs.321677 /len=3455 | NM_139276 | Hs.321677 | NP_644805 |
| 3783 | 0.016974 | Tat-SF1 | U76992 | | NP_055315 |
| 3794 | 0.03489 | coatamer protein complex, subunit alpha (COPA), mRNA /cds=(467,4141) /gb=NM_004371 /gi=6996002 /ug=Hs.75887 /len=5064 | NM_004371 | Hs.75887 | NP_004362 |
| 3796 | 5.42E-04 | immunoglobulin light chain | D87000 | | |
| 3798 | 0.020482 | chromodomain helicase DNA binding protein 4 (CHD4), mRNA /cds=(90,5828) /gb=NM_001273 /gi=4557452 /ug=Hs.74441 /len=6417 | NM_001273 | Hs.74441 | NP_001264 |

| Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension | | | | | |
|---|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 3800 | 0.016974 | ribosomal protein, large, P0 (RPLP0), transcript variant 2, mRNA /cds=(111,1064) /gb=NM_053275 /gi=16933545 /ug=Hs.406511 /len=1148 | NM_053275 | Hs.406511 | NP_444505 |
| 3801 | 0.003893 | ribosomal protein S7 (RPS7), mRNA /cds=(91,675) /gb=NM_001011 /gi=15431308 /ug=Hs.301547 /len=729 | NM_001011 | Hs.301547 | NP_001002 |
| 3802 | 0.001033 | cartilage associated protein (CRTAP), mRNA /cds=(12,1217) /gb=NM_006371 /gi=21536278 /ug=Hs.155481 /len=2307 | NM_006371 | Hs.155481 | NP_006362 |
| 3806 | 0.036914 | period 1 (Drosophila) (PER1), mRNA /cds=(188,4060) /gb=NM_002616 /gi=4505712 /ug=Hs.68398 /len=4656 | NM_002616 | Hs.68398 | NP_002607 |
| 3808 | 0.039034 | MN/CA9 | Z54349 | | |
| 3826 | 0.036914 | gene for neural cell adhesion molecule 3' region exon f; used in NCAM-140 6.7 kb and NCAM-180 7.4 kb transcripts | X07200 | | |
| 3827 | 0.00527 | helicase C-terminal domain- and SNF2 N-terminal domain-containing protein (CHD6-pending), mRNA /cds=(185,8326) /gb=NM_032221 /gi=21362041 /ug=Hs.45207 /len=8326 | NM_032221 | Hs.45207 | NP_115597 |
| 3830 | 0.046005 | eukaryotic translation elongation factor 1 beta 2 (EEF1B2), transcript variant 1, mRNA /cds=(236,913) /gb=NM_001959 /gi=16519564 /ug=Hs.421608 /len=961 | NM_001959 | Hs.421608 | NP_066944 |
| 3845 | 0.003893 | nuclear distribution gene C (A. nidulans) (NUDC), mRNA /cds=(91,1086) /gb=NM_006600 /gi=5729952 /ug=Hs.263812 /len=1333 | NM_006600 | Hs.263812 | NP_006591 |
| 3848 | 0.03489 | PRP4 pre-mRNA processing factor 4 (yeast) (PRPF4), mRNA /cds=(60,1628) /gb=NM_004697 /gi=24431949 /ug=Hs.374973 /len=2765 | NM_004697 | Hs.374973 | NP_004688 |
| 3849 | 0.020482 | enigma (LIM domain protein) (ENIGMA), mRNA /cds=(67,1440) /gb=NM_005451 /gi=11496884 /ug=Hs.102948 /len=1706 | NM_005451 | Hs.102948 | NP_005442 |
| 3866 | 0.016974 | protocadherin gamma subfamily C, 5 (PCDHGC5), transcript variant 1, mRNA /cds=(1,2835) /gb=NM_018929 /gi=14277683 /ug=Hs.335001 /len=4641 | NM_018929 | Hs.335001 | NP_115783 |
| 3872 | 0.001465 | 6-phosphogluconolactonase (PGLS), mRNA /cds=(18,794) /gb=NM_012088 /gi=6912585 /ug=Hs.100071 /len=1010 | NM_012088 | Hs.100071 | NP_036220 |
| 3873 | 0.046005 | proteasome (prosome, macropain) 26S subunit, ATPase, 1 (PSMC1), mRNA /cds=(49,1371) /gb=NM_002802 /gi=24430150 /ug=Hs.4745 /len=1586 | NM_002802 | Hs.4745 | NP_002793 |

| Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension | | | | | |
|---|----------|---|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 3903 | 0.043934 | carbohydrate (keratan sulfate Gal-6) sulfotransferase 1 (CHST1), mRNA /cds=(367,1602) /gb=NM_003654 /gi=4502840 /ug=Hs.104576 /len=2415 | NM_003654 | Hs.104576 | NP_003645 |
| 3907 | 0.041254 | Ig superfamily protein (Z39IG), mRNA /cds=(46,1245) /gb=NM_007268 /gi=6005957 /ug=Hs.8904 /len=1787 | NM_007268 | Hs.8904 | NP_009199 |
| 3913 | 0.012262 | hairy and enhancer of split 1, (Drosophila) (HES1), mRNA /cds=(237,1079) /gb=NM_005524 /gi=8400709 /ug=Hs.250666 /len=1471 | NM_005524 | Hs.250666 | NP_005515 |
| 3916 | 0.013991 | integral inner nuclear membrane protein (MAN1), mRNA /cds=(7,2742) /gb=NM_014319 /gi=7706606 /ug=Hs.7256 /len=4703 | NM_014319 | Hs.7256 | NP_055134 |
| 3925 | 0.001033 | similar to RIKEN cDNA 1110059E24, clone IMAGE:5218126, mRNA /gb=BC028019 /gi=20380167 /ug=Hs.112993 /len=3343 | BC028019 | Hs.112993 | |
| 3933 | 0.006106 | cDNA FLJ10266 fis, clone HEMBB1001024. /gb=AK001128 /gi=7022194 /ug=Hs.210297 /len=1244 | AK001128 | Hs.210297 | |
| 3938 | 0.039034 | mitochondrion, complete genome | NC_001807 | | |
| 3942 | 0.039034 | spectrin, alpha, non-erythrocytic 1 (alpha-fodrin) (SPTAN1), mRNA /cds=(103,7521) /gb=NM_003127 /gi=4507190 /ug=Hs.77196 /len=7787 | NM_003127 | Hs.77196 | NP_003118 |
| 3954 | 0.007056 | esophageal cancer related gene 4 protein (ECRG4), mRNA /cds=(109,555) /gb=NM_032411 /gi=14165275 /ug=Hs.43125 /len=772 | NM_032411 | Hs.43125 | NP_115787 |
| 3968 | 0.005674 | protein tyrosine phosphatase type IVA, member 2 (PTP4A2), transcript variant 1, mRNA /cds=(1011,1514) /gb=NM_003479 /gi=18104974 /ug=Hs.82911 /len=3925 | NM_003479 | Hs.82911 | NP_536317 |
| 3969 | 0.003893 | likely ortholog of mouse phosducin-like 2 (PDCL2), mRNA /cds=(101,820) /gb=NM_024065 /gi=13129043 /ug=Hs.94576 /len=1044 | NM_024065 | Hs.94576 | NP_076970 |
| 3970 | 0.011469 | HSPC182 protein (HSPC182), mRNA /cds=(66,650) /gb=NM_014188 /gi=7661831 /ug=Hs.30026 /len=1059 | NM_014188 | Hs.30026 | NP_054907 |
| 4012 | 0.03489 | transcription termination factor, RNA polymerase I (TTF1), mRNA /cds=(45,2705) /gb=NM_007344 /gi=6678454 /ug=Hs.54780 /len=2847 | NM_007344 | Hs.54780 | NP_031370 |

| Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension | | | | | |
|---|----------|---|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 4018 | 0.046005 | major histocompatibility complex, class I, C (HLA-C), mRNA /cds=(16,1116) /gb=NM_002117 /gi=19557676 /ug=Hs.277477 /len=1549 | NM_002117 | Hs.277477 | NP_002108 |
| 4019 | 0.014931 | BCG-induced gene in monocytes, clone 103 (BIGM103), mRNA /cds=(478,1860) /gb=NM_022154 /gi=24586664 /ug=Hs.284205 /len=3246 | NM_022154 | Hs.284205 | NP_071437 |
| 4023 | 0.036914 | transforming growth factor, beta receptor III (betaglycan, 300kDa) (TGFB3), mRNA /cds=(349,2898) /gb=NM_003243 /gi=4507470 /ug=Hs.342874 /len=4208 | NM_003243 | Hs.342874 | NP_003234 |
| 4026 | 0.041254 | ribosomal protein L38 (RPL38), mRNA /cds=(107,319) /gb=NM_000999 /gi=16306562 /ug=Hs.425668 /len=368 | NM_000999 | Hs.425668 | NP_000990 |
| 4074 | 0.024587 | KIAA1018 protein, (KIAA1018), mRNA /cds=(242,3295) /gb=NM_014967 /gi=7662449 /ug=Hs.5400 /len=4839 | NM_014967 | Hs.5400 | NP_055782 |
| 4078 | 0.029363 | retinoblastoma binding protein 8 (RBBP8), mRNA /cds=(299,2992) /gb=NM_002894 /gi=4506440 /ug=Hs.29287 /len=3246 | NM_002894 | Hs.29287 | NP_002885 |
| 4092 | 0.036914 | NADH dehydrogenase (ubiquinone) Fe-S protein 3, 30kDa (NADH-coenzyme Q reductase) (NDUFS3), mRNA /cds=(13,807) /gb=NM_004551 /gi=4758787 /ug=Hs.429506 /len=899 | NM_004551 | Hs.429506 | NP_004542 |
| 4093 | 0.013991 | coated vesicle membrane protein (RNP24), mRNA /cds=(24,629) /gb=NM_006815 /gi=21314646 /ug=Hs.75914 /len=2060 | NM_006815 | Hs.75914 | NP_006806 |
| 4117 | 0.012262 | RNA-directed DNA polymerase (EC | S21976 | | |
| 4119 | 6.55E-04 | reverse transcriptase homolog - human retrotransposon L1 | I38588 | | |
| 4124 | 0.046005 | prothrombin (F2) gene (Alu and KpnI repeats) | M17262 | | |
| 4130 | 0.027691 | CGI-130 protein (CGI-130), mRNA /cds=(64,576) /gb=NM_016063 /gi=7705623 /ug=Hs.32826 /len=1372 | NM_016063 | Hs.32826 | NP_057147 |
| 4133 | 0.005674 | vimentin (VIM), mRNA /cds=(123,1523) /gb=NM_003380 /gi=4507894 /ug=Hs.297753 /len=1851 | NM_003380 | Hs.297753 | NP_000995 |
| 4142 | 0.029363 | chromosome 14 open reading frame 92 (C14orf92), mRNA /cds=(33,1898) /gb=NM_014828 /gi=7662273 /ug=Hs.194035 /len=4174 | NM_014828 | Hs.194035 | NP_055643 |

| Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension | | | | | |
|---|----------|---|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 4146 | 0.043576 | serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 6 (SERPINB6), mRNA /cds=(75,1205) /gb=NM_004568 /gi=28077084 /ug=Hs.41072 /len=1361 | NM_004568 | Hs.41072 | NP_004559 |
| 4169 | 0.008722 | ribosomal protein S16 | M60854 | | NP_001011 |
| 4170 | 0.003893 | selenophosphate synthetase 2 (SPS2), mRNA /cds=(177,1523) /gb=NM_012248 /gi=24797146 /ug=Hs.118725 /len=2291 | NM_012248 | Hs.118725 | NP_036380 |
| 4174 | 0.008133 | soluble 29kDa NSF attachment protein (SNAP29) gene, complete cds | AF278704 | | |
| 4178 | 0.004203 | hypothetical protein (KIAA0536) | AB011108 | | NP_789770 |
| 4179 | 0.036914 | CD109 (CD109), mRNA /cds=(113,4450) /gb=NM_133493 /gi=19424129 /ug=Hs.55964 /len=5883 | NM_133493 | Hs.55964 | NP_598000 |
| 4181 | 0.027691 | KIAA0663 gene product (KIAA0663), mRNA /cds=(214,2646) /gb=NM_014827 /gi=7662231 /ug=Hs.17969 /len=4365 | NM_014827 | Hs.17969 | NP_055642 |
| 4185 | 0.021781 | APR-1 protein (MAGEH1), mRNA /cds=(271,930) /gb=NM_014061 /gi=18105051 /ug=Hs.279819 /len=1475 | NM_014061 | Hs.279819 | NP_054780 |
| 4189 | 0.01072 | fatty-acid-Coenzyme A ligase, long-chain 4 (FACL4), transcript variant 2, mRNA /cds=(507,2642) /gb=NM_022977 /gi=12669908 /ug=Hs.81452 /len=5356 | NM_022977 | Hs.81452 | NP_075266 |
| 4192 | 0.029363 | ribosomal 28S RNA | M11167 | | |
| 4194 | 0.031117 | peptidase D (PEPD), mRNA /cds=(17,1498) /gb=NM_000285 /gi=4557834 /ug=Hs.73947 /len=1888 | NM_000285 | Hs.73947 | NP_000276 |
| 4201 | 0.024587 | cytochrome c oxidase subunit VIb (COX6B), nuclear gene encoding mitochondrial protein, mRNA /cds=(163,423) /gb=NM_001863 /gi=17999530 /ug=Hs.431668 /len=578 | NM_001863 | Hs.431668 | NP_001854 |
| 4206 | 0.01072 | ring finger protein 4 (RNF4), mRNA /cds=(271,843) /gb=NM_002938 /gi=4506560 /ug=Hs.66394 /len=2918 | NM_002938 | Hs.66394 | NP_002929 |
| 4210 | 0.00489 | NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1, 7.5kDa (NDUFA1), nuclear gene encoding mitochondrial protein, mRNA /cds=(143,355) /gb=NM_004541 /gi=13699820 /ug=Hs.74823 /len=479 | NM_004541 | Hs.74823 | NP_004532 |
| 4220 | 0.00223 | ribosomal protein S2 (RPS2), mRNA /cds=(12,893) /gb=NM_002952 /gi=15055538 /ug=Hs.356360 /len=978 | NM_002952 | Hs.356360 | NP_002943 |

| Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension | | | | | |
|---|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 4221 | 0.0261 | ras inhibitor | M37190 | | NP_061866 |
| 4234 | 0.010015 | ribosomal protein S4, Y-linked (RPS4Y), mRNA /cds=(13,804) /gb=NM_001008 /gi=17981706 /ug=Hs.180911 /len=931 | NM_001008 | Hs.180911 | NP_000999 |
| 4246 | 0.009098 | hypothetical protein MGC10471 (MGC10471), mRNA /cds=(227,1417) /gb=NM_030818 /gi=13540613 /ug=Hs.24998 /len=1688 | NM_030818 | Hs.24998 | NP_110445 |
| 4261 | 0.010015 | epithelial membrane protein 3 (EMP3), mRNA /cds=(242,733) /gb=NM_001425 /gi=4503562 /ug=Hs.9999 /len=817 | NM_001425 | Hs.9999 | NP_001416 |
| 4263 | 0.036914 | testis expressed gene 292 (FLJ14728), mRNA /cds=(49,2109) /gb=NM_032830 /gi=14249535 /ug=Hs.151001 /len=2192 | NM_032830 | Hs.151001 | NP_116219 |
| 4294 | 0.006106 | hypothetical protein FLJ20729 (FLJ20729), mRNA /cds=(135,1547) /gb=NM_017953 /gi=20149642 /ug=Hs.5111 /len=2821 | NM_017953 | Hs.5111 | NP_060423 |
| 4296 | 0.023148 | splicing factor 3b, subunit 2, 145kD, clone IMAGE:2822659, mRNA, partial cds /cds=(1,2696) /gb=BC000401 /gi=12653264 /ug=Hs.406423 /len=2873 | BC000401 | Hs.406423 | |
| 4307 | 5.42E-04 | HT015 protein (HT015) | AF223466 | | NP_061049 |
| 4317 | 0.036914 | accessory protein BAP31 (DXS1357E), mRNA /cds=(137,877) /gb=NM_005745 /gi=10047078 /ug=Hs.291904 /len=1314 | NM_005745 | Hs.291904 | NP_005736 |
| 4347 | 7.88E-04 | flap structure-specific endonuclease 1 (FEN1), mRNA /cds=(373,1515) /gb=NM_004111 /gi=19718776 /ug=Hs.4756 /len=2265 | NM_004111 | Hs.4756 | NP_004102 |
| 4351 | 0.032959 | KIP gene | AB021866 | | |
| 4362 | 0.001232 | AD024 protein (AD024), mRNA /cds=(131,805) /gb=NM_020675 /gi=21314698 /ug=Hs.21137 /len=1376 | NM_020675 | Hs.21137 | NP_065726 |
| 4369 | 0.03489 | ribosomal protein L36 (RPL36), transcript variant 2, mRNA /cds=(153,470) /gb=NM_015414 /gi=16117793 /ug=Hs.433411 /len=545 | NM_015414 | Hs.433411 | NP_378669 |
| 4383 | 0.03489 | ribosomal protein S26 (RPS26), mRNA /cds=(26,373) /gb=NM_001029 /gi=15011935 /ug=Hs.299465 /len=459 | NM_001029 | Hs.299465 | NP_001020 |
| 4390 | 0.001596 | ataxia telangiectasia and Rad3 related (ATR), mRNA /cds=(106,8040) /gb=NM_001184 /gi=20143978 /ug=Hs.77613 /len=8265 | NM_001184 | Hs.77613 | NP_001175 |
| 4393 | 0.002625 | KIAA1316 protein, partial cds /cds=UNKNOWN /gb=AB037737 /gi=7243012 /ug=Hs.24255 /len=5477 | AB037737 | Hs.24255 | |

| Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension | | | | | |
|---|----------|---|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 4394 | 0.011469 | Likely ortholog of mouse tumor necrosis-alpha-induced adipose-related protein, cDNA FLJ14901 fis, clone PLACE1005409 (AK027807.1) | AK027807 | Hs.44208 | NP_078912 |
| 4401 | 0.01925 | T-box 15 (TBX15), mRNA /cds=(230,1093) /gb=NM_152380 /gi=23943887 /ug=Hs.164680 /len=2782 | NM_152380 | Hs.164680 | NP_689593 |
| 4405 | 0.041254 | CGI-116 protein (CGI-116), mRNA /cds=(108,692) /gb=NM_016053 /gi=7705621 /ug=Hs.18885 /len=860 | NM_016053 | Hs.18885 | NP_057137 |
| 4407 | 0.009349 | 15 kDa selenoprotein (SEP15), mRNA /cds=(5,493) /gb=NM_004261 /gi=20127464 /ug=Hs.90606 /len=1519 | NM_004261 | Hs.90606 | NP_004252 |
| 4420 | 5.96E-04 | Machado-Joseph disease (spinocerebellar ataxia 3, olivopontocerebellar ataxia 3, autosomal dominant, ataxin 3) (MJD), transcript variant 1, mRNA /cds=(59,1144) /gb=NM_004993 /gi=13518018 /ug=Hs.66521 /len=1900 | NM_004993 | Hs.66521 | NP_109376 |
| 4424 | 2.01E-04 | platelet glycoprotein IIB precursor | AAA60115 | | |
| 4438 | 0.007578 | trypsin-like serine protease (TLSP) gene | AF164623 | | |
| 4448 | 0.007578 | exostoses (multiple)-like 2 (EXTL2), mRNA /cds=(288,1280) /gb=NM_001439 /gi=14149608 /ug=Hs.61152 /len=2833 | NM_001439 | Hs.61152 | NP_001430 |
| 4450 | 0.016974 | glutathione S-transferase theta 2 (GSTT2) (GSTT1) genes | AF240786 | | |
| 4464 | 1.81E-04 | suCRase-isomaltase (SI) | M84646 | | |
| 4466 | 0.008722 | cDNA: FLJ21659 fis, clone COL08743. /gb=AK025312 /gi=10437802 /ug=Hs.248862 /len=2423 | AK025312 | Hs.248862 | |
| 4550 | 0.00242 | hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome) (HPRT1), mRNA /cds=(86,742) /gb=NM_000194 /gi=4504482 /ug=Hs.82314 /len=1331 | NM_000194 | Hs.82314 | NP_000185 |
| 4553 | 0.018081 | protein kinase (cAMP-dependent, catalytic) inhibitor beta (PKIB), mRNA /cds=(258,494) /gb=NM_032471 /gi=21359976 /ug=Hs.106106 /len=1209 | NM_032471 | Hs.106106 | NP_115860 |
| 4560 | 0.006106 | Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6 (ARHGEF6), mRNA /cds=(29,2359) /gb=NM_004840 /gi=22027524 /ug=Hs.79307 /len=4839 | NM_004840 | Hs.79307 | NP_004831 |
| 4565 | 0.001596 | Hypothetical protein(KIAA0469) | AB007938 | | NP_055666 |
| 4572 | 6.55E-04 | neuroigin 3 | AF217413 | | |
| 4577 | 0.015924 | biliverdin reductase A (BLVRA), mRNA /cds=(61,951) /gb=NM_000712 /gi=4502416 /ug=Hs.81029 /len=1070 | NM_000712 | Hs.81029 | NP_000703 |

| Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension | | | | | |
|---|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 4591 | 0.00489 | KIAA0484 | AB007953 | | |
| 4616 | 0.021781 | 603054284F1 NIH_MGC_122 cDNA clone IMAGE:5203652 5', mRNA sequence /clone=IMAGE:5203652 /clone_end=5' /gb=BI767055 /gi=15758633 /ug=Hs.356004 /len=1067 | BI767055 | Hs.356004 | |
| 4624 | 1.63E-04 | chromosome 11 open reading frame 17 (C11orf17), mRNA /cds=(77,709) /gb=NM_020642 /gi=21361869 /ug=Hs.131180 /len=1332 | NM_020642 | Hs.131180 | NP_065693 |
| 4636 | 0.020482 | thioredoxin (TXN), mRNA /cds=(64,381) /gb=NM_003329 /gi=4507744 /ug=Hs.432922 /len=501 | NM_003329 | Hs.432922 | NP_003320 |
| 4637 | 0.021781 | mitochondrion, complete genome | NC_001807 | | |
| 4639 | 0.048543 | ym45h08.s1 Soares infant brain 1NIB cDNA clone IMAGE:51273 3', mRNA sequence /clone=IMAGE:51273 /clone_end=3' /gb=H18675 /gi=884915 /ug=Hs.314777 /len=191 | H18675 | Hs.314777 | |
| 4643 | 2.01E-04 | zinc finger protein (AF020591), mRNA /cds=(246,2393) /gb=NM_014480 /gi=7656870 /ug=Hs.142634 /len=3743 | NM_014480 | Hs.142634 | NP_055295 |
| 4647 | 0.031117 | S-phase kinase-associated protein 1A (p19A) (SKP1A), transcript variant 1, mRNA /cds=(140,622) /gb=NM_006930 /gi=25777710 /ug=Hs.171626 /len=2172 | NM_006930 | Hs.171626 | NP_733779 |
| 4667 | 0.018081 | histone deacetylase 2 (HDAC2), mRNA /cds=(205,1671) /gb=NM_001527 /gi=4557640 /ug=Hs.3352 /len=1985 | NM_001527 | Hs.3352 | NP_001518 |
| 4680 | 0.03489 | U4/U6-associated RNA splicing factor (HPRP3P), mRNA /cds=(73,2124) /gb=NM_004698 /gi=4758555 /ug=Hs.11776 /len=2344 | NM_004698 | Hs.11776 | NP_004689 |
| 4683 | 0.036914 | nucleotide binding protein 1 (MinD E. coli) (NUBP1), mRNA /cds=(5,967) /gb=NM_002484 /gi=4505336 /ug=Hs.81469 /len=1213 | NM_002484 | Hs.81469 | NP_002475 |
| 4687 | 0.048543 | CREBBP/EP300 inhibitory protein 1 (CRI1), mRNA /cds=(63,626) /gb=NM_014335 /gi=7656937 /ug=Hs.381137 /len=1719 | NM_014335 | Hs.381137 | NP_055150 |
| 4698 | 0.01286 | retinoic acid receptor, beta (RARβ), transcript variant 1, mRNA /cds=(469,1815) /gb=NM_000965 /gi=14916493 /ug=Hs.171495 /len=3119 | NM_000965 | Hs.171495 | NP_057236 |
| 4699 | 0.031117 | chromodomain protein, Y chromosome-like (CDYL), transcript variant 2, mRNA /cds=(336,1970) /gb=NM_170751 /gi=25777618 /ug=Hs.16081 /len=3474 | NM_170751 | Hs.16081 | NP_736608 |

| Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension | | | | | |
|---|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | D scription | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 4701 | 4.93E-04 | ubiquitin-like 5 (UBL5), mRNA /cds=(66,287) /gb=NM_024292 /gi=13236509 /ug=Hs.13836 /len=413 | NM_024292 | Hs.13836 | NP_077268 |
| 4702 | 0.046005 | vascular cell adhesion molecule 1 (VCAM1), transcript variant 1, mRNA /cds=(121,2340) /gb=NM_001078 /gi=18201907 /ug=Hs.109225 /len=3119 | NM_001078 | Hs.109225 | NP_542413 |
| 4704 | 0.01925 | NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1, 8kDa (NDUFAB1), mRNA /cds=(25,495) /gb=NM_005003 /gi=4826851 /ug=Hs.5556 /len=663 | NM_005003 | Hs.5556 | NP_004994 |
| 4712 | 0.032959 | vacuolar protein sorting 35 (yeast) (VPS35), mRNA /cds=(48,2438) /gb=NM_018206 /gi=17999540 /ug=Hs.264190 /len=2707 | NM_018206 | Hs.264190 | NP_060676 |
| 4718 | 0.00527 | 3-oxoacid CoA transferase (OXCT), nuclear gene encoding mitochondrial protein, mRNA /cds=(99,1661) /gb=NM_000436 /gi=4557816 /ug=Hs.177584 /len=3337 | NM_000436 | Hs.177584 | NP_000427 |
| 4720 | 0.048543 | heterogeneous nuclear ribonucleoprotein R (HNRPR), mRNA /cds=(91,1992) /gb=NM_005826 /gi=14141188 /ug=Hs.15265 /len=2663 | NM_005826 | Hs.15265 | NP_005817 |
| 4738 | 0.048543 | hypothetical protein (KIAA1439) | AB037860 | | NP_005586 |
| 4740 | 0.004536 | mRNA for KIAA0934 protein, partial cds. /cds=(1,4759) /gb=AB023151 /gi=20521699 /ug=Hs.227716 /len=6594 | AB023151 | Hs.227716 | |
| 4743 | 0.009349 | KIAA0475 gene product (KIAA0475), mRNA /cds=(337,1566) /gb=NM_014864 /gi=7662149 /ug=Hs.5737 /len=5983 | NM_014864 | Hs.5737 | NP_055679 |
| 4751 | 0.039034 | hypothetical protein (HSPC117), mRNA /cds=(76,1593) /gb=NM_014306 /gi=7657014 /ug=Hs.10729 /len=2005 | NM_014306 | Hs.10729 | NP_055121 |
| 4764 | 0.039034 | mRNA for KIAA1025 protein, partial cds. /cds=(1,5755) /gb=AB028948 /gi=20521733 /ug=Hs.4084 /len=8444 | AB028948 | Hs.4084 | |
| 4774 | 0.014931 | ribosomal protein S19 (RPS19), mRNA /cds=(70,507) /gb=NM_001022 /gi=14591914 /ug=Hs.298262 /len=569 | NM_001022 | Hs.298262 | NP_001013 |
| 4778 | 0.007578 | ribosomal protein, large, P1 (RPLP1), mRNA /cds=(130,474) /gb=NM_001003 /gi=16905511 /ug=Hs.424299 /len=512 | NM_001003 | Hs.424299 | NP_000994 |
| 4782 | 0.018081 | CDC-like kinase1 (CLK1), mRNA /cds=(156,1610) /gb=NM_004071 /gi=4758007 /ug=Hs.2083 /len=1834 | NM_004071 | Hs.2083 | NP_004062 |

| Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension | | | | | |
|---|----------|---|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 4785 | 0.039034 | solute carrier family 38, member 2 (SLC38A2), mRNA /cds=(352,1872) /gb=NM_018976 /gi=21361601 /ug=Hs.298275 /len=4795 | NM_018976 | Hs.298275 | NP_061849 |
| 4801 | 0.027691 | growth hormone inducible transmembrane protein (GHITM), mRNA /cds=(130,1089) /gb=NM_014394 /gi=7657479 /ug=Hs.433957 /len=2374 | NM_014394 | Hs.433957 | NP_055209 |
| 4805 | 0.021781 | high-mobility group box 1 (HMGB1), mRNA /cds=(77,724) /gb=NM_002128 /gi=20149538 /ug=Hs.6727 /len=1207 | NM_002128 | Hs.6727 | NP_002119 |
| 4807 | 0.03489 | glypican 6 (GPC6), mRNA /cds=(616,2283) /gb=NM_005708 /gi=8051601 /ug=Hs.118407 /len=2760 | NM_005708 | Hs.118407 | NP_005699 |
| 4810 | 0.029363 | mRNA; cDNA DKFZp727I051 (from clone DKFZp727I051); partial cds /cds=(1,2099) /gb=AL117478 /gi=5911952 /ug=Hs.239370 /len=2480 | AL117478 | Hs.239370 | NP_056412 |
| 4814 | 0.023628 | ribosomal protein L10a (RPL10A), mRNA /cds=(16,669) /gb=NM_007104 /gi=15431287 /ug=Hs.425293 /len=700 | NM_007104 | Hs.425293 | NP_009035 |
| 4815 | 0.013991 | cDNA FLJ31247 fis, clone KIDNE2005296, weakly similar to ACTIN, CYTOPLASMIC 1. /gb=AK055809 /gi=16550632 /ug=Hs.170848 /len=2322 | AK055809 | Hs.170848 | |
| 4819 | 0.006566 | ribosomal protein L28 (RPL28), mRNA /cds=(43,456) /gb=NM_000991 /gi=13904865 /ug=Hs.356371 /len=500 | NM_000991 | Hs.356371 | NP_000982 |
| 4821 | 0.041254 | eukaryotic translation termination factor 1 (ETF1), mRNA /cds=(136,1449) /gb=NM_004730 /gi=4759033 /ug=Hs.77324 /len=3653 | NM_004730 | Hs.77324 | NP_004721 |
| 4833 | 0.007578 | ATP synthase, H transporting, mitochondrial F0 complex, subunit b, isoform 1 (ATP5F1), mRNA /cds=(98,868) /gb=NM_001688 /gi=21361564 /ug=Hs.81634 /len=1230 | NM_001688 | Hs.81634 | NP_001679 |
| 4839 | 0.007056 | tubulin alpha 6 (TUBA6), mRNA /cds=(1,1350) /gb=NM_032704 /gi=14389308 /ug=Hs.406578 /len=1350 | NM_032704 | Hs.406578 | NP_116093 |
| 4840 | 0.029363 | mRNA for KIAA1137 protein, partial cds. /cds=(1,2804) /gb=AB032963 /gi=6329896 /ug=Hs.43577 /len=4990 | AB032963 | Hs.43577 | |
| 4861 | 5.42E-04 | protein serine kinase H1 (PSKH1), mRNA /cds=(131,1405) /gb=NM_006742 /gi=27901802 /ug=Hs.150601 /len=3460 | NM_006742 | Hs.150601 | NP_006733 |

| Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension | | | | | |
|---|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 4862 | 0.004536 | mRNA for FLJ00005 protein, partial cds. /cds=(1,338) /gb=AK000005 /gi=7209310 /ug=Hs.367690 /len=4706 | AK000005 | Hs.367690 | |
| 4863 | 0.003079 | FLJ14819 fis, clone OVARC1000241, moderately similar to HYPOXIA-INDUCIBLE FACTOR 1 ALPHA | AK027725 | | NP_690009 |
| 4868 | 3.69E-04 | MLL septin-like fusion (MSF), mRNA /cds=(258,1964) /gb=NM_006640 /gi=19923366 /ug=Hs.181002 /len=3929 | NM_006640 | Hs.181002 | NP_006631 |
| 4876 | 0.006106 | solute carrier family 17 (anion/sugar transporter), member 5 (SLC17A5), mRNA /cds=(125,1612) /gb=NM_012434 /gi=21314648 /ug=Hs.117865 /len=3329 | NM_012434 | Hs.117865 | NP_036566 |
| 4877 | 0.003893 | chromosome 20 open reading frame 31 (C20orf31), mRNA /cds=(83,1819) /gb=NM_018217 /gi=8922666 /ug=Hs.93871 /len=1885 | NM_018217 | Hs.93871 | NP_060687 |
| 4886 | 0.011469 | proteasome (prosome, macropain) subunit, beta type, 4 (PSMB4), mRNA /cds=(24,818) /gb=NM_002796 /gi=22538466 /ug=Hs.89545 /len=925 | NM_002796 | Hs.89545 | NP_002787 |
| 4893 | 0.006566 | growth arrest and DNA-damage-inducible, beta (GADD45B), mRNA /cds=(101,586) /gb=NM_015675 /gi=9945331 /ug=Hs.110571 /len=1121 | NM_015675 | Hs.110571 | NP_056490 |
| 4898 | 0.016974 | cDNA FLJ12024 fis, clone HEMBB1001797. /gb=AK022086 /gi=10433407 /ug=Hs.8958 /len=1672 | AK022086 | Hs.8958 | |
| 4900 | 0.011469 | hypothetical protein FLJ10702 (FLJ10702), mRNA /cds=(175,735) /gb=NM_018184 /gi=8922600 /ug=Hs.104222 /len=2944 | NM_018184 | Hs.104222 | NP_060654 |
| 4904 | 0.014931 | tj44d11.x1 Soares_NSF_F8_9W_OT_PA_P_S1 cDNA clone IMAGE:2144373 3' similar to gb:Y00716 COMPLEMENT FACTOR H PRECURSOR mRNA sequence /clone=IMAGE:2144373 /clone_end=3' /gb=AI470482 /gi=4332572 /ug=Hs.387691 /len=384 | AI470482 | Hs.387691 | |
| 4905 | 0.0261 | cytoskeleton associated protein 2 (CKAP2), mRNA /cds=(97,2145) /gb=NM_018204 /gi=19923520 /ug=Hs.24641 /len=3626 | NM_018204 | Hs.24641 | NP_060674 |

| Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension | | | | | |
|---|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 4912 | 0.00489 | ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit g (ATP5L); mRNA /cds=(60,371) /gb=NM_006476 /gi=21359881 /ug=Hs.107476 /len=580 | NM_006476 | Hs.107476 | NP_006467 |
| 4919 | 0.013991 | KIAA0436 mRNA, partial cds. /cds=(1,2070) /gb=AB007896 /gi=2662152 /ug=Hs.110 /len=4661 | AB007896 | Hs.110 | |
| 4921 | 8.63E-04 | cDNA FLJ10423 fis, clone NT2RP1000259. /gb=AK001285 /gi=7022444 /ug=Hs.106909 /len=1837 | AK001285 | Hs.106909 | |
| 4928 | 0.016974 | mitochondrion, complete genome | NC_001807 | | |
| 4931 | 0.023148 | testis enhanced gene transcript (TEGT), mRNA /cds=(41,754) /gb=NM_003217 /gi=4507432 /ug=Hs.74637 /len=2600 | NM_003217 | Hs.74637 | NP_003208 |
| 4935 | 0.031117 | clone TCCCTA00211 mRNA sequence /gb=AY007115 /gi=9956010 /ug=Hs.355779 /len=1505 | AY007115 | Hs.355779 | |
| 4936 | 0.003079 | hypothetical protein FLJ20015 (FLJ20015), mRNA /cds=(32,523) /gb=NM_018996 /gi=9506648 /ug=Hs.375614 /len=1457 | NM_018996 | Hs.375614 | NP_061869 |
| 4939 | 0.0261 | UI-H-DH0-aul-p-19-0-UI.s1 NCI_CGAP_DH0 cDNA clone IMAGE:5871234 3', mRNA sequence /clone=IMAGE:5871234 /clone_end=3' /gb=BM994422 /gi=19719323 /ug=Hs.289721 /len=2081 | BM994422 | Hs.289721 | |
| 4943 | 0.005674 | DKFZp434N1717 (from clone DKFZp434N1717) | AL133655 | | NP_473357 |
| 4944 | 0.005674 | hypothetical protein FLJ20452 (FLJ20452), mRNA /cds=(15,614) /gb=NM_017828 /gi=21361660 /ug=Hs.351327 /len=1948 | NM_017828 | Hs.351327 | NP_060298 |
| 4945 | 0.018081 | eukaryotic translation initiation factor 3, subunit 5 epsilon, 47kDa (EIF3S5), mRNA /cds=(7,1080) /gb=NM_003754 /gi=4503518 /ug=Hs.7811 /len=1231 | NM_003754 | Hs.7811 | NP_003745 |
| 4946 | 0.013991 | myosin, light polypeptide 6, alkali, smooth muscle and non-muscle (MYL6), transcript variant 3, mRNA /cds=(41,514) /gb=NM_079425 /gi=17986263 /ug=Hs.77385 /len=717 | NM_079425 | Hs.77385 | NP_524149 |
| 4948 | 0.016974 | ovarian carcinoma immunoreactive antigen (OCIA), mRNA /cds=(168,905) /gb=NM_017830 /gi=8923426 /ug=Hs.132071 /len=1434 | NM_017830 | Hs.132071 | NP_060300 |

| Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension | | | | | |
|---|----------|--|--------------------|-----------------------|-----------------------|
| Spot | p-value | Description | Gene Accession No. | Unigene Accession No. | Protein Accession No. |
| 4949 | 2.23E-04 | carboxypeptidase A3 (mast cell) (CPA3), mRNA /cds=(12,1265) /gb=NM_001870 /gi=4503000 /ug=Hs.646 /len=1633 | NM_001870 | Hs.646 | NP_001861 |
| 4956 | 0.01072 | hypothetical protein FLJ20671 (FLJ20671), mRNA /cds=(43,465) /gb=NM_017924 /gi=19923511 /ug=Hs.180201 /len=2855 | NM_017924 | Hs.180201 | NP_060394 |
| 4962 | 0.031156 | mRNA for KIAA1320 protein, partial cds. /cds=(2051,3754) /gb=AB037741 /gi=7243020 /ug=Hs.117414 /len=5321 | AB037741 | Hs.117414 | |
| 4963 | 0.013102 | cytochrome c oxidase subunit VIIa polypeptide 2 (liver) (COX7A2), nuclear gene encoding mitochondrial protein, mRNA /cds=(76,327) /gb=NM_001865 /gi=18105035 /ug=Hs.70312 /len=470 | NM_001865 | Hs.70312 | NP_001856 |
| 4965 | 0.011469 | microtubule-associated protein, RP/EB family, member 1 (MAPRE1), mRNA /cds=(65,871) /gb=NM_012325 /gi=6912493 /ug=Hs.234279 /len=2540 | NM_012325 | Hs.234279 | NP_036457 |
| 4967 | 0.021781 | ah42f05.s1 Soares_testis_NHT cDNA clone 1292193 3' similar to P54687 BRANCHED-CHAIN AMINO ACID AMINOTRANSFERASE, CYTOSOLIC ;, mRNA sequence /clone=1292193 /clone_end=3' /gb=AA705851 /gi=2715769 /ug=Hs.443872 /len=412 | AA705851 | Hs.443872 | |
| 4971 | 5.96E-04 | muscle specific gene (M9), mRNA /cds=(172,828) /gb=NM_013234 /gi=10801344 /ug=Hs.283781 /len=911 | NM_013234 | Hs.283781 | NP_037366 |
| 4975 | 0.00223 | hypothetical protein MGC2747 (MGC2747), mRNA /cds=(93,248) /gb=NM_024104 /gi=13129111 /ug=Hs.194017 /len=1171 | NM_024104 | Hs.194017 | NP_077009 |
| 4979 | 0.010015 | ribosomal protein L6 (RPL6), mRNA /cds=(32,898) /gb=NM_000970 /gi=16753226 /ug=Hs.409045 /len=950 | NM_000970 | Hs.409045 | NP_000961 |
| 4980 | 0.008133 | Gene 33/Mig-6 (MIG-6), mRNA /cds=(213,1601) /gb=NM_018948 /gi=21314673 /ug=Hs.11169 /len=3099 | NM_018948 | Hs.11169 | NP_061821 |
| 4988 | 0.005674 | translocase of outer mitochondrial membrane 70 A (yeast) (TOMM70A), mRNA /cds=(92,1918) /gb=NM_014820 /gi=7662672 /ug=Hs.21198 /len=4017 | NM_014820 | Hs.21198 | NP_055635 |
| 4991 | 0.013102 | DNA sequence(chromosome 21q, section 38/105) | AP001694 | | |